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(74) Agent: **SIKS & CO.**; 8th Floor, Kyobashi-Nisshoku Bldg.,
8-7, Kyobashi 1-chome, Chuo-ku, Tokyo 104-0031 (JP).

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(71) Applicant (*for all designated States except US*): **ASAHI KASEI KABUSHIKI KAISHA** [JP/JP]; 2-6, Dojima-hama 1-chome, Kita-ku, Osaka-shi, Osaka 530-8205 (JP).

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(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **MATSUDA, Akio** [JP/JP]; 3629-1-404, Denbou, Fuji-shi, Shizuoka 417-0061 (JP). **MURAMATSU, Shuji** [JP/JP]; 17-13, Tadewara, Fuji-shi, Shizuoka 416-0931 (JP).

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(54) Title: **NF-KB ACTIVATING GENE**

(57) **Abstract:** Provided are proteins capable of activating NF-κB, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of NF-κB. Using plasmid pNFκB-Luc, cDNA encoding a protein capable of activating NF-κB has been cloned from a cDNA library constructed from human lung fibroblasts and the like, and the DNA sequence and the deduced amino acid sequence determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting NF-κB activation.



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DESCRIPTION

NF- κ B ACTIVATING GENE

TECHNICAL FIELD

The present invention relates to a protein capable of activating NF- κ B, a DNA sequence encoding the protein, a method for obtaining the DNA, a recombinant vector containing the DNA, a transformant containing the recombinant vector, and an antibody which specifically reacts with the protein. The present invention also relates to use of the protein, DNA or antibody of the invention in the diagnosis, treatment or prevention of diseases associated with the excessive activation or inhibition of NF- κ B.

The present invention also relates to a method for screening a substance capable of inhibiting or promoting NF- κ B activation by using the protein, DNA, recombinant vector and transformant.

BACKGROUND ART

The transcription factor NF- κ B (nuclear factor kappa B) plays an important role in the transcriptional regulation of various genes involved in inflammation and immunological reactions. NF- κ B is a homo- or heterodimer protein which belongs to the Rel family. In unstimulated conditions, NF- κ B normally resides in the cytoplasm as an inactive form by forming a complex with an I κ B (inhibitory protein of NF- κ B) to mask the nuclear transport signal of NF- κ B.

When cytokines such as interleukin (IL)-1 and tumor necrosis factor (TNF)- α stimulate cells, I κ B is phosphorylated by IKK (I κ B kinase) and degraded by the 26S proteasome through ubiquitination. The released NF- κ B moves to the nucleus, where it binds to the DNA sequence called the NF- κ B binding sequence and induces the transcription of the gene under control of NF- κ B. NF- κ B is believed to regulate the expression of genes such as those for immunoglobulins, inflammatory cytokines (e.g.,

IL-1 and TNF- α), interferons and cell adhesion factors. NF- κ B is involved in inflammation and immune responses through the expression induction of these genes.

The inhibition of the function or activation of NF- κ B may inhibit the expression of many factors (proteins) involved in inflammatory or immunological diseases or other diseases such as tumor proliferation. Thus, NF- κ B is a promising target for medicaments against diseases caused or characterized by autoimmunity or inflammation [see e.g., Clinical Chemistry 45, 7-17 (1999); J Clin. Pharmacol. 38, 981-993 (1998); Gut 43, 856-860 (1998); The New England Journal of Medicine 366, 1066-1071 (1997); TIPS 46-50 (1997); The FASEB Journal 9, 899-909 (1995); Nature 395, 225-226 (1998); Science 278, 818-819 (1997); Cell 91, 299-302 (1997)].

Extracellular information is converted into a certain signal, which passes through the cell membrane and goes through the cytoplasm to the nucleus, where it regulates the expression of the target gene and causes cell responses. Therefore the elucidation of the mechanism of intracellular signal transduction from extracellular stimuli to NF- κ B activation is of very important significance, because it provides very important means of developing new medicaments or therapies against autoimmune diseases and diseases exhibiting inflammatory symptoms.

It is believed that the signal transduction pathway from certain cell stimulation to NF- κ B activation includes many steps mediated by various transmitters such as protein kinases. Therefore it is desirable for more efficient drug discovery to identify the transmitters which play a key role in the pathway, and to focus research on the transmitters to establish a new drug-screening method. Some signaling molecules involved in NF- κ B activation have been identified [e.g., IKK, ubiquitination enzymes and the 26S proteasome described above, as well as TNF receptor associated factor 2 (TRAF2) and NF- κ B inducing kinase (NIK)]. However, most of the mechanism of NF- κ B activation remains unknown, and it has been desired to identify new signaling molecules and further to elucidate NF- κ B activation mechanism.

DISCLOSURE OF THE INVENTION

The object of the present invention is to identify a new gene and protein capable of directly, or indirectly, activating NF- κ B, and to provide a method of use of them in medicaments, diagnostics and therapy. That is, an object of the present invention is to provide a new protein capable of activating NF- κ B, a DNA sequence encoding the protein, a recombinant vector containing the DNA, a transformant containing the recombinant vector, a process for producing the protein, an antibody directed against the protein or a peptide fragment thereof, and a process for producing the antibody.

Another object of the present invention is to provide a method for screening a substance capable of inhibiting or promoting NF- κ B activation using the protein, the DNA, the recombinant vector or the transformant, a kit for the screening, a substance capable of inhibiting or promoting NF- κ B activation obtainable by the screening method or the screening kit, a process for producing the substance, a pharmaceutical composition containing a substance capable of inhibiting or promoting NF- κ B activation, etc.

The present inventors have intensively studied to solve the above problems. As a result, the present inventors have succeeded in constructing a full-length cDNA library by using the oligo-capping method; establishing a gene function assay system by expression cloning using 293-EBNA cells; and isolating a new DNA (cDNA) encoding a protein having a function of activating NF- κ B by using the assay system. This new DNA molecule induced NF- κ B activation by its expression in 293-EBNA cells. This result shows that this new DNA is a signal transduction molecule involved in NF- κ B activation. Thus, the present invention has been completed.

That is, the present invention provides the followings:

- (1) A purified protein selected from the group consisting of:
 - (a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,

98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF- κ B (Nuclear factor kappa B) and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(2) A purified protein that activates NF- κ B and comprises an amino acid sequence having at least 95% identity to the protein according to (1) over the entire length thereof.

(3) An isolated polynucleotide which comprises a nucleotide sequence encoding a protein selected from the group consisting of:

(a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168,

170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF- κ B and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(4) An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence

complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

(5) An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists

of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

(6) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to (3) over the entire length thereof.

(7) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to (4) or (5) over the entire length thereof.

(8) A purified protein encoded by the polynucleotide according to any one of (3) to (7).

(9) A recombinant vector which comprises a polynucleotide according to any one of (3) to (7).

(10) A agent for gene therapy which comprises the recombinant vector according to (9) as an active ingredient.

- (11) A transformed cell which comprises the recombinant vector according to (9).
- (12) A membrane of the cell according to (11), which has the protein according to (1) or (2) which is a membrane protein.
- (13) A process for producing a protein according to (1), (2) or (8) comprising the steps of;
- (a) culturing a transformed cell according to (11) under conditions providing expression of the protein according to (1), (2) or (8); and
 - (b) recovering the protein from the culture product.
- (14) A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of (1), (2) or (8) in a subject comprising the steps of:
- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
 - (b) analyzing the amount of expression of said protein in a sample derived from said subject.
- (15) A method for screening compounds capable of inhibiting or promoting NF- κ B activation, which comprises the steps of:
- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- κ B into a cell;
 - (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
 - (c) measuring the signal which can detect activation of NF- κ B; and
 - (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of

inhibiting or promoting NF- κ B activation.

(16) A method for screening compounds capable of inhibiting or promoting NF- κ B activation, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to (1), (2) or (8) into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- κ B; and
- (d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation.

(17) A compound capable of inhibiting or promoting NF- κ B activation, which is selected by the method for screening according to (15) or (16).

(18) A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- κ B into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- κ B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the

step of (d).

(19) A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to (1), (2) or (8) into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- κ B; and
- (d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

(20) A kit for screening a compound capable of inhibiting or promoting NF- κ B activation, which comprises:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- κ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- κ B; and
- (b) reagents for measuring the signal.

(21) A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to (1), (2) or (8).

(22) The monoclonal or polyclonal antibody or a fragment thereof according to (21), which inhibits the activity of promoting activation of NF- κ B by the protein according to (1), (2) or (8).

(23) A process for producing a monoclonal or polyclonal antibody according to (21) or (22), which comprises administering the protein according to (1), (2) or (8) or epitope-bearing fragments thereof to a non-human animal as an antigen.

(24) An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of (3) to (7), which prevents the expression of a protein which promotes NF- κ B activation.

(25) A ribozyme or deoxyribozyme capable of inhibiting NF- κ B activation, which has an action of cleavage of RNA that encodes the protein according to (1), (2) or (8) or an action of cleavage of RNA that encodes a protein involved in a pathway leading to NF- κ B activation.

(26) A method for treating a disease associated with NF- κ B activation, which comprises administering to a subject a compound screened by the process according to (15) or (16), and/or a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22), and/or an antisense oligonucleotide according to (24), and/or a ribozyme or deoxyribozyme according to (25) in an effective amount to treat a disease selected from the group consisting of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

(27) A pharmaceutical composition produced by the process according to (18) or (19) for inhibiting or promoting NF- κ B activation.

(28) The pharmaceutical composition according to (27) for the treatment of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and/or ischemic disorders.

(29) A method of treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders, which comprises administering a pharmaceutical composition produced by the process according to (18) or (19) to a patient suffering from a disease associated with NF- κ B activation.

(30) A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22) as an active ingredient.

(31) A pharmaceutical composition which comprises an antisense oligonucleotide according to (24) as an active ingredient.

(32) A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to (25) as an active ingredient.

(33) The pharmaceutical composition according to any one of (30) to (32) for the treatment and/or prevention of a disease which is selected from the group consisting of inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

(34) A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195,

197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(35) A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to (34) with data of said other nucleotide sequences and/or amino acid sequences.

(36) An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 are fixed.

(37) An insoluble substrate to which polypeptides comprising all or a part of the

amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed.

The contents of the specifications and/or drawings of Japanese Patent Applications Nos. 2001-368692 and 2002-291302 and U.S. Provisional Applications Nos. 60/335829 and 60/415,769, which from the bases of priority of the instant application, are incorporated herein.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a graph showing NF- κ B reporter activity inhibition by the proteasome inhibitor MG-132 in Example 3. The axis of abscissa is MG-132 concentration and the transversal axis is relative luciferase activity.

BEST MODE FOR CARRYING OUT THE INVENTION

At first, in order to further clarify the basic feature of the present invention, the present invention is explained by following how the present invention is completed. In order to obtain a new gene having a function of activating NF- κ B, the following experiments were carried out as shown in the examples.

First, using the oligo-capping method, a full-length cDNA was produced from mRNA prepared from normal human lung fibroblasts (purchased from Sanko Junyaku Co., Ltd.) and the like, and a full-length cDNA library was constructed in which the cDNA was inserted into the vector pME18S-FL3 (GenBank Accession AB009864).

Next, the cDNA library was introduced into E. coli cells, and plasmid preparation was carried out per clone. Then, the pNK κ B-Luc reporter plasmid (STRATAGENE) containing a DNA encoding luciferase and the above full-length cDNA plasmid were cotransfected into 293-EBNA cells (Invitrogen). After 24 or 48 hours of culture, luciferase activity was measured, and the plasmid with significantly increased luciferase activity compared to that of a control experiment (vector pME18S-FL3 is introduced into a cell in place of a full-length cDNA) was selected (the selected plasmid showed a 5-fold or more increase in luciferase activity compared to that of the control experiment), and the entire nucleotide sequence of the cDNA cloned into the plasmid was determined. The protein encoded by the cDNA thus obtained shows that this protein is a signal transduction molecule involved in NF- κ B activation.

The present invention is described in detail below.

In the present invention, activation of NF- κ B refers to activation of NF- κ B (including induction of NF- κ B activation) when a gene is introduced into a suitable cell and the protein encoded by the gene is excessively expressed. Activation of NF- κ B can be measured, for example, by an assay using an NF- κ B dependant reporter gene. Activation of NF- κ B is reflected by increasing the reporter activity compared to control cells (cells into which the vector only was introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 2 or more, and still more preferably by a factor of 5 or more.

Reporter activity can be measured by cloning a polynucleotide (e.g. cDNA) encoding the protein to be expressed into a suitable expression vector, co-transfecting the expression vector and an NF- κ B dependant reporter plasmid into a suitable cell, and after culturing for a certain period, then measuring reporter activity. Suitable expression vectors are well known to those skilled in the art, examples of which include pME18S-FL3, pcDNA3.1 (Invitrogen). The reporter gene can be one which enables a person skilled in the art to easily detect the expression thereof, and examples include a gene encoding luciferase, chloramphenicol acetyl transferase, or β -galactosidase. Use

of a gene encoding luciferase is most preferable, and examples of an NF- κ B dependent reporter plasmid include pNF- κ B-Luc (STRATAGENE). Suitable cells include cells which exhibit an NF- κ B activation response to stimulation by IL-1, TNF- α and the like. Examples include 293-EBNA cells. Cell culture and introduction of genes into cells (transfection) can be performed and optimized by a person skilled in the art by known techniques.

As a preferable method, 293-EBNA cells are inoculated on DMEM medium (Dulbecco's Modified Eagle Medium) containing 5% FBS (Fetal Bovine Serum) in a 96-well cell culture plate to a final cell density of 1×10^4 cells/well, and cultured for 24 hours at 37°C in the presence of 5% CO₂. Then, reporter plasmid pNF- κ B-Luc (STRATAGENE) and the expression vector are cotransfected into the cells in a well using FuGENE 6 (Roche). After 24 hours of culture at 37°C, NF- κ B activation is then measured by measuring luciferase activity using a long term luciferase assay system, Picagene LT2.0 (Toyo Ink Mfg). For example, luciferase activity can be measured using PerkinElmer's Wallac ARVOTMST 1420 MULTILABEL COUNTER. The method for gene introduction by FuGENE6, and measurement of luciferase activity by Picagene LT2.0 can be performed respectively according to the attached protocols. In a method of gene introduction with a 96-well plate using FuGENE6, the amount of FuGENE6 per 1 well is suitably 0.3 to 0.5 μ l, preferably 0.3 μ l; the amount of pNF- κ B-Luc plasmid is suitably 50 to 100ng, preferably 50ng; the amount of expression vector is suitably 50-100ng, and preferably 100ng. An ability to activate NF- κ B can be confirmed by an ability to increase the reporter activity (luciferase activity) relative to the control experiment (cells into which only a null vector was introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 2 or more, and still more preferably by a factor of 5 or more.

Related to the amino acid sequences of any one of SEQ ID NOS. 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104,

106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, the present invention provides the following proteins:

- (a) a protein which comprises one of the above amino acid sequences;
- (b) a peptide having one of the above amino acid sequences;
- (c) a protein which activates NF- κ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in the above amino acid sequences;
- (d) a protein which comprises an amino acid sequence, which has at least 95% identity, preferably at least 97-99% identity, to one of the above amino acid sequences over the entire length thereof.

As known in the art, "identity" used herein is a relationship between two or more protein sequence or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between protein or polynucleotide sequences, as determined by the match between protein or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods. Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. "Identity" can be determined by using the BLAST program (for example, Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschul SF, Madden TL, Schaffer AA, Zhang Z, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997)). Where software such as BLAST is used, it is preferable to use default values. The main initial conditions generally used in a BLAST search are as follows, but are not limited to these.

An amino acid substitution matrix is a matrix numerically representing the degree of analogy of each pairing of each of the 20 types of amino acid, and normally the default matrix of BLOSUM62 is used. The theory of this amino acid substitution matrix is shown in Altschul S.F., J. Mol. Biol. 219: 555-565 (1991), and applicability to DNA sequence comparison is shown on States D. J., Gish W., Altschul S.F., Methods, 3: 66-70 (1991). In this case, optimal gap cost is determined by experience and in the case of BLOSUM62 preferably parameters of Existence 11, Extension 1 are used. The expected value (EXPECT) is the threshold value concerning statistical significance for a match with a database sequence, and the default value is 10.

As one example, a protein having, for example, 95% or more identity to the amino acid sequence of SEQ ID NO: 2 may contain in the amino acid sequence up to 5 amino acid changes per 100 amino acids of the amino acid sequence of SEQ ID NO: 2. In other words, a protein having 95% or more amino acid sequence identity to a subject amino acid sequence, may have amino acids up to 5% of the total number of amino acids within the subject sequence, deleted or substituted by other amino acids, or amino acids up to 5% of the total number of amino acids within the subject sequence may be inserted within the subject sequence. These changes within the subject sequence, may exist at the amino terminus or the carboxy terminus of the subject sequence, or may exist at any position between these termini, or may form one or more groups of changes.

The Examples described below demonstrate that the protein consisting of an amino acid sequence of any one of the above SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, is capable of activating

NF- κ B.

Related to the polynucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or the polynucleotide of a coding region (CDS) of these sequences, the present invention further provides the following isolated polynucleotides:

- (a) a polynucleotide of any one of the above sequences;
- (b) a polynucleotide which encodes a protein that activates NF- κ B, and comprises a nucleotide sequence which has at least 95% identity, preferably at least 97-99% identity to any one of the above sequences; and
- (c) a polynucleotide having a nucleotide sequence which encodes a protein that activates NF- κ B and has an amino acid sequence which has at least 95% identity, preferably, at least 97-99% identity, to the amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

Polynucleotides which are identical or almost identical to nucleotide sequences contained in the above nucleotide sequences may be used as hybridization probes to isolate full-length cDNA and genomic clones encoding the protein of the present

invention, or cDNA or genomic clones of other genes that have a high sequence similarity to the above sequences, or genomic clones, or may be used as primers for nucleic acid amplification reactions. Typically, these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to the above sequences. The probes or primers will generally comprises at least 15 nucleotides, preferably 30 nucleotides and may have 50 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers have between 20 and 25 nucleotides.

The polynucleotide of the present invention may be either in the form of a DNA such as cDNA, a genomic DNA obtained by cloning or synthetically produced, or may be in the form of RNA such as mRNA. The polynucleotide may be single-stranded or double-stranded. The double-stranded polynucleotides may be double-stranded DNA, double-stranded RNA or DNA:RNA hybrid. The single-stranded polynucleotide may be sense strand also known as coding strand or antisense strand also known as non-coding strand.

Those skilled in the art can prepare a protein having the same activity that activates NF- κ B as the protein having an amino acid sequence of any one of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, by means of appropriate substitution of an amino acid in the protein using known methods. One such method involves using conventional mutagenesis procedures for the DNA encoding the protein. Another method is, for example, site-directed mutagenesis (e.g., Mutan-Super Express Km Kit from Takara Shuzo Co., Ltd.).

Mutations of amino acids in proteins may also occur in nature. Thus, the present invention also includes a mutated protein which is capable of activating NF- κ B and which has at least one amino acid deletion, substitution or addition relative to the protein of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, and the DNA encoding the protein. The number of mutations is preferably 1 to 10, more preferably 1 to 5, most preferably 1 to 3.

The substitutions of amino acids are preferably conservative substitutions, specific examples of which are substitutions within the following groups: (glycine, alanine), (valine, isoleucine, leucine), (aspartic acid, glutamic acid), (asparagine, glutamine), (serine, threonine), (lysine, arginine) and (phenylalanine, tyrosine).

Based on DNA (e.g., SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287) encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140,

142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 or a fragment thereof, those skilled in the art can routinely isolate a DNA with a high sequence similarity to these nucleotide sequences by using hybridization techniques and the like, and obtain proteins having the same activity that activates NF- κ B as the protein having of an amino acid sequence of any one of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288. Thus, the present invention also includes a protein that activates NF- κ B and comprises an amino acid sequence having a high identity to the amino acid sequence of any one of the above SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288. "High identity" refers to an amino acid sequence having an identity of at least 90%, preferably at least 97 to 99% over the entire length of an amino acid sequence expressed by any one of the above SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,

74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

The proteins of the present invention may be natural proteins derived from any human or animal cells or tissues, chemically synthesized proteins, or proteins obtained by genetic recombination techniques. The protein may or may not be subjected to post-translational modifications such as sugar chain addition or phosphorylation.

Examples of the proteins which are encoded by the genes of the present invention include secretion proteins (growth factors, cytokines, hormones, and the like), protein modification enzymes (protein kinase, protein phosphatase, protease, and the like), signal transduction molecules (protein-protein interaction molecules and the like), nuclear proteins (nuclear receptor, transcription factors and the like), and membrane proteins. The membrane proteins include receptors, cell adhesion molecules, ion channels, and transporters. When the protein is a membrane protein, a compound which is selected by the screening mentioned herein below is more useful as a research tool for a pharmaceutical compound since the compound is expected to easily move into a cell or transmit a signal into a cell.

The present invention also includes a polynucleotide encoding the above protein of the present invention. Examples of nucleotide sequences encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224,

226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 include nucleotide sequences of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287. The DNA includes cDNA, genomic DNA, and chemically synthesized DNA. In accordance with the degeneracy of the genetic code, at least one nucleotide in the nucleotide sequence encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 can be substituted with other nucleotides without altering the amino acid sequence of the protein produced from the gene. Therefore, the DNA sequences of the present invention also include nucleotide sequences altered by substitution based on the degeneracy of the genetic code. Such DNA sequences can be synthesized using known methods.

The DNA of the present invention includes a DNA which encodes a protein capable of activating NF- κ B and hybridizes under stringent conditions with the DNA sequence of the above nucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11,

13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287, or any complementary sequence thereof. Stringent conditions are apparent to those skilled in the art, and can be easily attained in accordance with various laboratory manuals such as T. Maniatis et al., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory 1982, 1989.

That is, "stringent conditions" refer to overnight incubation at 37°C in a hybridization solution containing 30% formamide, 5 x SSC (0.75 M NaCl, 75mM trisodium citrate), 5 x Denhardt's solution, 0.5% SDS, 100 µg/ml denatured, sheared salmon sperm DNA) followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 37°C (low stringency). Preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 40% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 42 °C (moderate stringency). More preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 50% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 50°C (high stringency). The DNA sequence thus obtained must encode a protein capable of activating NF- κ B.

The present invention also includes a polynucleotide comprising a nucleotide sequence which encodes a protein capable of activating NF- κ B and has a high sequence

similarity to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5). Typically these nucleotide sequence are 95% identical, preferably 97% identical, more preferably 98-99% identical, most preferably at least 99% identical to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5) over the entire length thereof.

The above DNA of the present invention can be used to produce the above protein using recombinant DNA techniques. In general, the DNA and peptide of the present invention can be obtained by:

- (A) cloning the DNA encoding the protein of the present invention;
- (B) inserting the DNA encoding the entire coding region of the protein or a part thereof into an expression vector to construct a recombinant vector;
- (C) transforming host cells with the recombinant vector thus constructed; and
- (D) culturing the obtained cells to express the protein or its analogue, and then purifying it by column chromatography.

General procedures necessary to handle DNA and recombinant host cells (e.g., *E. coli*) in the above steps are well known to those skilled in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. All the enzymes, reagents, etc., used in these procedures are commercially available, and unless otherwise stated, such commercially available products can be used according to the use conditions specified by the manufacturer's instructions to attain completely its objects. The above steps (A) to (D) can be further illustrated in more details as follows.

Techniques for cloning the DNA encoding the protein of the present invention in the above step (A) include, in addition to the methods described in the specification of the present application, PCR amplification using a synthetic DNA having a part of the nucleotide sequence of the present invention (e.g., any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139,

141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287) as a primer, and selection of the DNA inserted into a suitable vector by hybridization with a labeled DNA fragment encoding a partial or full coding region of the protein of the present invention or a labeled synthetic DNA. Another technique involves direct amplification from total RNAs or mRNA fractions prepared from cells or tissues, using the reverse transcriptase polymerase chain reaction (RT-PCR method).

As a DNA inserted into a suitable vector, for example, a commercially available library (e.g., from CLONTECH and STRATAGENE) can be used. Techniques for hybridization are normally used in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. Depending on the intended purpose, the cloned DNA encoding the protein of the present invention can be used as such or if desired after digestion with a restriction enzyme or addition of a linker. The DNA thus obtained may have a nucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287, or a polynucleotide of above items (3) to (7). The DNA sequence to be inserted into an expression vector in the above step (B) may be a full-length cDNA or a DNA fragment encoding the above full-length protein, or a DNA fragment constructed so that it expresses a part thereof.

Thus, the present invention also provides a recombinant vector, which comprises

the above DNA sequence. The expression vector for the protein of the present invention can be produced, for example, by excising the desired DNA fragment from the DNA encoding the protein of the present invention, and ligating the DNA fragment downstream of a promoter in a suitable expression vector.

Expression vectors for use in the present invention may be any vectors derived from prokaryotes (e.g., *E. coli*), yeast, fungi, insect viruses and vertebrate viruses so long as such vectors are replicable. However, the vectors should be selected to be compatible with microorganisms or cells used as hosts. Suitable combinations of host cell – expression vector systems are selected depending on the desired expression product.

When microorganisms are used as hosts, plasmid vectors compatible with these microorganisms are generally used as replicable expression vectors for recombinant DNA molecules. For example, the plasmids pBR322 and pBR327 can be used to transform *E. coli*. Plasmid vectors normally contain an origin of replication, a promoter, and a marker gene conferring upon a recombinant DNA a phenotype useful for selecting the cells transformed with the recombinant DNA. Example of such promoters include a β -lactamase promoter, lactose promoter and tryptophan promoter. Examples of such marker genes include an ampicillin resistance gene, and a tetracycline resistance gene. Examples of suitable expression vectors include the plasmids pUC18 and pUC19 in addition to pBR322, pBR327.

In order to express the DNA of the present invention in yeast, for example, YEp24 can be used as a replicable vector. The plasmid YEp24 contains the URA3 gene, which can be employed as a marker gene. Examples of promoters in expression vectors for yeast cells include promoters derived from genes for 3-phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase and alcohol dehydrogenase.

Examples of promoters and terminators for use in expression vectors to express the DNA of the present invention in fungal cells include promoters and terminators derived from genes for phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dehydrogenase (GAPD) and actin. Examples of suitable expression vectors include the

plasmids pPGACY2 and pBSFAHY83.

Examples of promoters for use in expression vectors to express the DNA of the present invention in insect cells include a polyhedrin promoter and P10 promoter. Examples of expression vectors which are suitable for insect cells include baculo virus vector.

Recombinant vectors used to express the DNA of the present invention in animal cells normally contain functional sequences to regulate genes, such as an origin of replication, a promoter to be placed upstream of the DNA of the present invention, a ribosome-binding site, a polyadenylation site and a transcription termination sequence. Such functional sequences, which can be used to express the DNA of the present invention in eukaryotic cells, can be obtained from viruses and viral substances.

Examples of such functional sequences include an SR α promoter, SV40 promoter, LTR promoter, CMV (cytomegalovirus) promoter and HSV-TK promoter. Among them, a CMV promoter and SR α promoter can be preferably used. As promoters to be placed inherently upstream of the gene encoding the protein of the present invention, any promoters can be used so long as they are suitable for use in the above host-vector systems. Examples of origins of replication include foreign origins of replication, for example, those derived from viruses such as adenovirus, polyoma virus and SV40 virus. When vectors capable of integration into host chromosomes are used as expression vectors, origins of replication of the host chromosomes may be employed. Examples of suitable expression vectors include the plasmids pSV-dhfr (ATCC 37146), pBPV-1(9-1) (ATCC 37111), pcDNA3.1 (INVITROGEN) and pME18S-FL3.

The present invention also provides a transformed cell, which comprises the above recombinant vector. Microorganisms or cells transformed with the replicable recombinant vector of the present invention can be selected from remaining untransformed parent cells based on at least one phenotype conferred by the recombinant vector as mentioned above. Phenotypes can be conferred by inserting at least one marker gene into the recombinant vector. Marker genes naturally contained in

replicable vectors can be employed. Examples of marker genes include drug resistance genes such as neomycin resistance genes, and genes encoding dihydrofolate reductase.

As hosts for use in the above step (C), any of prokaryotes (e.g., *E. coli*), microorganisms (e.g., yeast and fungi) as well as insect and animal cells can be used so long as such hosts are compatible with the expression vectors used. Examples of such microorganisms include *Escherichia coli* strains such as *E. coli* K12 strain 294 (ATCC 31446), *E. coli* X1776 (ATCC 31537), *E. coli* C600, *E. coli* JM109 and *E. coli* B strain; bacterial strains belonging to the genus *Bacillus* such as *Bacillus subtilis*; intestinal bacteria other than *E. coli*, such as *Salmonella typhimurium* or *Serratia marcescens*; and various strains belonging to the genus *Pseudomonas*. Examples of such yeast include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and *Pichia pastoris*. Examples of such fungi include *Aspergillus nidulans*, and *Acremonium chrysogenum* (ATCC 11550).

As insect cells, for example, *Spodoptera frugiperda* (Sf cells), High FiveTM cells derived from eggs of *Trichoplusia*, etc., can be used when the virus is AcNPV. Examples of such animal cells include HEK 293 cells, COS-1 cells, COS-7 cells, Hela cells, and Chinese hamster ovary (CHO) cells. Among them, CHO cells and HEK 293 cells are preferred. When cells are used as hosts, combinations of expression vectors and host cells to be used vary with experimental objects. According to such combinations, two types of expression (i.e. transient expression and constitutive expression) can be included.

"Transformation" of microorganisms and cells in the above step (C) refers to introducing DNA into microorganisms or cells by forcible methods or phagocytosis of cells and then transiently or constitutively expressing the trait of the DNA in a plasmid or an intra-chromosome integrated form. Those skilled in the art can carry out transformation by known methods [see e.g., "Idenshi Kougaku Handbook (Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.]. For example, in the case of animal cells, DNA can be

introduced into cells by known methods such as DEAE-dextran method, calcium-phosphate-mediated transfection, electroporation, lipofection, etc. For stable expression of the protein of the present invention using animal cells, there is a method in which selection can be carried out by clonal selection of the animal cells containing the chromosomes into which the introduced expression vectors have been integrated. For example, transformants can be selected using the above selectable marker as an indication of successful transformation. In addition, the animal cells thus obtained using the selectable marker can be subjected to repeated clonal selection to obtain stable animal cell strains highly capable of expressing the protein of the present invention. When a dihydrofolate reductase (DHFR) gene is used as a selectable marker, one can culture animal cells while gradually increasing the concentration of methotrexate (MTX) and select the resistant strains, thereby amplifying the DNA encoding the protein of the present invention together with the DHFR gene in the cell to obtain animal cell strains having higher levels of expression.

The above transformed cells can be cultured under conditions which permit the expression of the DNA encoding the protein of the present invention to produce and accumulate the protein of the present invention. In this manner, the protein of the present invention can be produced. Thus, the present invention also provides a process for producing a protein, which comprises culturing a transformed cell comprising the isolated polynucleotide according to above item (3) to (7) under conditions providing expression of the encoded protein, and recovering the protein from the culture (that is, cells or culture medium).

The above transformed cells can be cultured by methods known to those skilled in the art (see e.g., "Bio Manual Series 4", YODOSHA CO., LTD.). For example, animal cells can be cultured by various known animal cell culture methods including attachment culture such as Petri dish culture, multitray type culture and module culture, attachment culture in which cells are attached to cell culture carriers (microcarriers), suspension culture in which productive cells themselves are suspended. Examples of

media for use in the culture include media commonly used for animal cell culture, such as D-MEM and RPMI 1640.

In order to separate and purify the protein of the present invention from the above culture, suitable combinations of per se known separation and purification methods can be used. Examples such methods include methods based on solubility, such as salting-out and solvent precipitation; methods based on the difference in charges, such as ion-exchange chromatography; methods mainly based on the difference in molecular weights, such as dialysis, ultrafiltration, gel filtration and SDS-polyacrylamide gel electrophoresis; methods based on specific affinity, such as affinity chromatography; methods based on the difference in hydrophobicity, such as reverse phase high performance liquid chromatography; and methods based on the difference in isoelectric points, such as isoelectric focusing. For example, a protein of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation or purification.

The protein of the present invention can also be produced as a fusion protein with another protein. These fusion proteins are also included within the present invention. For the expression of such fusion proteins, any vectors can be used so long as the DNA encoding the protein can be inserted into the vectors and the vectors can express the fusion protein. Examples of proteins to which a polypeptide of the present invention can be fused include glutathione S-transferase (GST) and a hexa-histidine sequence (6 x His). The fusion protein of the protein of the present invention with another protein can be advantageously purified by affinity chromatography using a substance with an affinity

for the fusion partner protein. For example, fusion proteins with GST can be purified by affinity chromatography using glutathione as a ligand.

When the protein of the present invention is a membrane protein, a transformed cell into which DNA encoding the protein of the present invention has been introduced can express the protein on its membrane. The membrane which is prepared from such transformed cells and contains the protein of the present invention is also included within the present invention. As used herein, "membrane of a cell" includes cell membrane, and membrane of cell organelle. The membrane of a cell can be prepared by a method known to those skilled in the art. For example, cells are collected from the culture where transformed cells are cultured, and suspended in a suitable buffer. Then, the cells are lysed by a homogenizer or by vortex after addition of glassbeads. The obtained solution is centrifuged to remove uncrushed cells and the like, and the supernatant is ultracentrifuged under a suitable condition, and the obtained precipitate is suspended in a buffer to prepare a membrane fraction. The condition for ultracentrifugation can be suitably selected depending on the type of membrane and the like.

The present invention also includes a protein capable of inhibiting the activity of the protein of the present invention. Examples of such proteins include antibodies, or other proteins that bind to active sites of the protein of the present invention, thereby inhibiting the expression of their activity.

The present invention also relates to an antibody that reacts with the protein of the present invention or a fragment thereof, and to production of such an antibody. More preferably, the present invention relates to an antibody that specifically react with the protein of the present invention or a fragment thereof, and to production of such an antibody. As used herein, "specifically" means that cross-reactivity is low, more preferably cross-reactivity is not present.

The antibody of the present invention is not specifically limited so long as it can recognize the protein of the present invention. Examples of such antibodies include polyclonal antibodies, monoclonal antibodies and their fragments, single chain antibodies

and humanized antibodies. Antibody fragments can be produced by known techniques. Examples of such antibody fragments include, but not limited to, F(ab')₂ fragments, Fab' fragments, Fab fragments and Fv fragments. For example, a monoclonal or polyclonal antibody can be produced by administering the protein according to above item (1) or (2) as an antigen or epitope-bearing fragments to a non-human animal. The antibody against the protein of the present invention can be produced by using the protein of the present invention or a peptide thereof as an immunogen according to per se known process for producing antibodies or antisera. Such methods are described, for example, in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition, an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

In the case of polyclonal antibodies, for example, the protein of the present invention or a peptide thereof can be injected to animals such as rabbits to produce antibodies directed against the protein or peptide, and then their blood can be collected. The polyclonal antibodies can be purified from the blood, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

In the case of monoclonal antibodies, for example, animals such as mice are immunized with the protein of the present invention, their spleen is removed and homogenized to obtain spleen cells, which are then fused with mouse myeloma cells by using a reagent such as polyethylene glycol. From the resulting hybrid cells (i.e. hybridoma cells), the clone producing the antibody directed against the protein of the present invention can be selected. Then, the resulting clonal hybridoma cells can be implanted intraperitoneally into mice, the ascitic fluid recovered from the mice. The resulting monoclonal antibody can be purified, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

When the resulting antibody is used to administer it to humans, it is preferably

used as a humanized antibody or human antibody in order to reduce its immunogenicity. The humanized antibody can be produced using transgenic mice or other mammals. For a general review of these humanized antibodies and human antibodies, see, for example, Morrison, S.L. et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984); Jones, P.T. et al., Nature 321:522-525 (1986); Hiroshi Noguchi, Igaku no Ayumi (J. Clin. Exp. Med.) 167:457-462 (1993); Takashi Matsumoto, Kagaku to Seibutsu (Chemistry and Biology) 36:448-456 (1998). Humanized chimeric antibodies can be produced by linking a V region of a mouse antibody to a C region of a human antibody. Humanized antibodies can be produced by substituting a sequence derived from a human antibody for a region other than a complementarity-determining region (CDR) from a mouse monoclonal antibody.

In addition, human antibodies can be directly produced in the same manner as the production of conventional monoclonal antibodies by immunizing the mice whose immune systems have been replaced with human immune systems. These antibodies can be used to isolate or to identify clones expressing the protein.

Also, these antibodies can be used to purify the protein of the present invention from a cell extract or transformed cells producing the protein of the present invention. These proteins can also be used to construct ELISA, RIA (radioimmunoassay) and western blotting systems. These assay systems can be used for diagnostic purposes for detecting an amount of the protein of the present invention present in a body sample in a tissue or a fluid in the blood of an animal, preferably human. For example, they can be used for diagnosis of a disease characterized by undesirable activation of HF- κ B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

In order to provide a basis for diagnosis of a disease, a standard value (that is, a normal value for the expression of the protein of the present invention) must be established. However, this is a well-known technique to those skilled in the art. For

example, a method of calculating the standard value comprises binding a body fluid or a cell extract of normal individual of a human or an animal to an antibody against the protein of the present invention under a suitable condition for the complex formation, detecting the amount of the antibody-protein complex by chemical or physical means and then calculating the standard value for the normal sample using a standard curve prepared from a standard solution containing a known amount of an antigen (the protein of the present invention). The presence of a disease can be confirmed by deviation from the standard value obtained by comparison of the standard value with the value obtained from a sample of an individual latently suffering from a disease associated with the protein of the present invention. These antibodies can also be used as reagents for studying functions of the protein of the present invention.

The antibody of the present invention can be used as a medicament as mentioned below. When the antibody of the present invention is used as a medicament, it is preferred to use an antibody capable of inhibiting the activity of activating NF- κ B of the protein of the present invention (that is, neutralizing antibody).

The antibodies of the present invention can be purified and then administered to patients of a disease characterized by undesirable activation of NF- κ B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus in another aspect, the present invention is a pharmaceutical composition which comprises the above antibody as an active ingredient, and a method for therapy and/or prevention using the antibody of the present invention. In such pharmaceutical compositions, the active ingredient may be combined with other therapeutically or preventively active ingredients or inactive ingredients (e.g., conventional pharmaceutically acceptable carriers or diluents such as immunogenic adjuvants) and physiologically non-toxic stabilizers and excipients. The resulting combinations can be sterilized by filtration, and formulated into vials after lyophilization or into various dosage forms in stabilized and preservable aqueous

preparations.

Administration to a patient can be intra-arterial administration, intravenous administration and subcutaneous administration, which are well known to those skilled in the art. The dosage range depends upon the weight and age of the patient, route of administration and the like. Suitable dosages can be determined by those skilled in the art. These antibodies exhibit therapeutic activity by inhibiting the NF- κ B activation mediated by the protein of the present invention. More specifically, the antibody of the present invention is useful as a medicament for treating or preventing a disease associated with abnormality of NF- κ B activity such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

The DNA of the present invention can also be used to isolate, identify and clone other proteins involved in intracellular signal transduction processes. For example, the DNA sequence encoding the protein of the present invention can be used as a "bait" in yeast two-hybrid systems (see e.g., Nature 340:245-246 (1989)) to isolate and clone the sequence encoding a protein ("prey") which can associate with the protein of the present invention. In a similar manner, it can be determined whether the protein of the present invention can associate with other cellular proteins (e.g., NIK and TRAF2). In another method, proteins which can associate with the protein of the present invention can be isolated from cell extracts by immunoprecipitation [see e.g., "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] using antibodies directed against the protein of the present invention. In still another method, the protein of the present invention can be expressed as a fusion protein with another protein as described above, and immunoprecipitated with an antibody directed against the fusion protein in order to isolate a protein which can associate with the protein of the present invention.

The present invention provides a process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of present

invention in a subject comprising the steps of:

- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
- (b) analyzing the amount of expression of said protein in a sample derived from said subject.

The diagnostic assays offer a process for diagnosing diseases or determining a susceptibility to the diseases through detection of mutation in a gene for the protein of the present invention which has a function of activating NF- κ B, by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of protein or mRNA.

The determination of the presence or absence of a mutation in the nucleotide sequence of a the gene encoding the protein of the present invention which has a function of activating NF- κ B, may involve RT-PCR using a part of the nucleotide sequences of genes encoding these proteins as a primer, followed by conventional DNA sequencing to detect the presence or absence of the mutation. PCR-SSCP [Genomics 5:874-879 (1989); "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] can also be used to determine the presence or absence of the mutation.

Decreased or increased expression of a gene in a sample can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, for example, nucleic acid amplification methods such as RT-PCR, and methods such as RNase protection assay, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein in a sample derived from a host are well-known to those skilled in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assays. When an expression level is determined at a protein level, the antibody of the present invention mentioned above can be used.

The degree of abnormality of expression level of gene in a sample is not particularly limited. For example, when the level of the expressed protein is 2 or more times, or 1/2 or less, as compared with normal case, the subject may be diagnosed to be a disease. In another example, when the level of the expressed protein is 3 or more times, or 1/3 or less, as compared with normal case, the subject may be diagnosed to be a disease.

The DNA of the present invention can be used to detect abnormality in the DNA or mRNA encoding the protein of the present invention or a peptide fragment thereof. Therefore, the DNA is useful for gene diagnosis such as detection of damage, mutation, decreased, increased or excessively increased expression of said DNA or mRNA.

When the nucleotide sequence encoding the protein of the present invention in a genome of an individual contains a mutation, the mutation may cause a disease associated with the expression and/or activity of NF- κ B.

When the amount of the expression of the protein in a sample from an individual is different from the normal value, the abnormal expression of the novel protein of the present invention which acts to activate NF- κ B may be responsible for diseases associated with the expression and/or activity of NF- κ B.

The present invention also relates to a method for screening compounds which inhibit or promote NF- κ B activation using the proteins of the invention.

A compound which inhibits NF- κ B activation has an activity as an inhibitor of NF- κ B in vivo or in vitro as a result of this function, while a compound which promotes NF- κ B activation has an activity as an activator of NF- κ B in vivo or in vitro as a result of this function. Therefore, an activity as an inhibitor or activator of NF- κ B is screened in the method for screening of the present invention. The above compounds have an activity as an inhibitor or activator of NF- κ B.

The method for screening comprises the steps of:

(a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to the present invention and a gene encoding a signal

which can detect activation of NF- κ B into a cell;

(b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring the signal which can detect activation of NF- κ B; and

(d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation.

Further, it is preferable to isolate or identify as an activator compound, a compound that increases said detectable signal 2-fold or higher than normal, and to isolate or identify as an inhibitor compound, a compound that decreases said detectable signal half or less than normal.

Examples of genes encoding a signal which can detect activation of NF- κ B include reporter genes. Reporter genes are used instead of directly detecting the activation of transcription factors of interest. The transcriptional activity of a promoter of a gene is analyzed by linking the promoter to a reporter gene and measuring the activity of the product of the reporter gene ("Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Any peptide or protein can be used so long as those skilled in the art can measure the activity or amount of the expression product (including the amount of the produced mRNA) of the reporter genes. For example, enzymatic activity of chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., can be measured. Any reporter plasmids can be used to evaluate NF- κ B activation so long as the reporter plasmids have an NF- κ B recognition sequence inserted upstream of the reporter gene. For example, pNF- κ B-Luc (STRATAGEGE) can be used. Other examples include NF- κ B dependent reporter plasmids described in Tanaka S. et al., J. Vet. Med. Sci. Vol.59 (7); Rothe M. et al., Science Vol.269, p.1424-1427 (1995).

Any host cells may be used so long as NF- κ B activation can be detected in the host cells. Preferred host cells are mammalian cells such as 293-EBNA cells.

Transformation and culture of the cells can be carried out as described above.

In a specific embodiment, the method for screening a compound which inhibits or promotes NF- κ B activation comprises culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. The reporter activity can be measured by methods known in the art (see e.g., "Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Examples of test compounds include, but not limited to, low molecular weight compounds, high molecular compounds, and peptides. Test compounds may be artificially synthesized compounds or naturally occurring compounds. Test compounds may be a single compound or mixtures. Usable examples include a library of low molecular weight compounds, a compound library which was synthesized by combinatorial chemistry, a naturally occurring product containing cells, plants, animals or a part thereof, or an extracted product of such naturally occurring product. When a mixture containing several compounds is used as a test substance for screening, the test substance which shows an activity of inhibiting or promoting NF- κ B activation can be further screened to isolate a single substance having the activity. Isolation and purification of a desired compound from a mixture can be carried out by using any known method such as filtration, extraction, washing, drying, concentration, crystallization or various chromatography in combination.

The method for screening according to the present invention can be carried out by the following steps:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to the present invention into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- κ B; and

(d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation.

Methods for measuring the activation of NF- κ B in the above method include a method of analyzing the binding of NF- κ B to its binding sequence using cell extraction solution by gel shift (for example, Hayashi T. et al. J.Biol.Chem.268, p.26790-26795 (1993), Nauman M. et al. EMBO J. 13, p4597-4607 (1994)). Alternatively, the amount of mRNA or proteins for genes whose expression is known to be induced by NF- κ B activation (e.g., genes for IL-1 and TNF- α), can be measured. The amount of mRNA can be measured, for example, by northern hybridization, RT-PCR, etc. The amount of proteins can be measured, for example, by using antibodies. The antibodies may be produced by known methods. Commercially available antibodies (from, e.g., Wako Pure Chemical Industries, Ltd.) can also be used.

The present invention further provided a method of producing a pharmaceutical composition, which comprises the following steps (a) to (f):

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to the present invention and a gene encoding a signal which can detect activation of NF- κ B into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- κ B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the present invention, a pharmaceutical composition can be produced by the following steps:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to the present invention into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- κ B; and
- (d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the step (d) of the method of producing a pharmaceutical composition, it is preferable to isolate or identify as an activator compound, a compound that increases said detectable signal 2-fold or higher than normal, and to isolate or identify as an inhibitor compound, a compound that decreases said detectable signal half or less than normal.

The protein of the present invention may also be used in a method for the structure-based design of an agonist, antagonist or inhibitor of the protein, by:

- (a) determining in the first instance the three-dimensional structure of the protein;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
- (c) synthesising candidate compounds that are predicted to bind to or react with the deduced binding or reactive site; and
- (d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitor.

The present invention also provides a compound which is selected by the above screening method. This compound has a function of inhibiting or promoting NF- κ B activation. More specifically, this compound has a function of inhibiting or promoting NF- κ B activation by the protein of the present invention.

The compounds obtained by the above screening methods have a function of inhibiting or promoting NF- κ B activation, they are useful as therapeutic or preventive

pharmaceuticals for the treatment of diseases resulting from unfavorable activation or inactivation of NF- κ B.

When obtainment of a salt of the compounds is desired, a compound which is obtained in the form of a salt can be purified as it is. A compound which is obtained in the free form can be converted into a salt by isolating and purifying a salt obtained by dispersing or dissolving the compound into a suitable solvent and then adding a desired acid or base. Examples of a step to optimize the compounds or salts thereof obtained by the method of the present invention as a pharmaceutical composition, include methods of formulating according to ordinary processes such as the following. The above compounds or their pharmaceutically acceptable salts in an amount effective as an active ingredient, and pharmaceutically acceptable carriers can be mixed. A form of formulation suitable for the mode of administration is selected. A composition suitable for oral administration includes a solid form such as tablet, granule, capsule, pill and powder, and solution form such as solution, syrup, elixir and dispersion. A form useful for parenteral administration includes sterile solution, dispersion, emulsion and suspension. The above carriers include, for example, sugars such as gelatin, lactose and glucose, starches such as corn, wheat, rice and maize, fatty acids such as stearic acid, salts of fatty acids such as calcium stearate, magnesium stearate, talc, vegetable oil, alcohol such as stearyl alcohol and benzyl alcohol, gum, and polyalkylene glycol. Examples of such liquid carriers include generally water, saline, sugar solution of dextrose and the like, glycols such as ethylene glycol, propylene glycol and polyethylene glycol.

The present invention also provides a kit for screening compounds which inhibit or promote NF- κ B activation. The kit comprises reagents and the like necessary for screening compounds which inhibit or promote NF- κ B activation, including:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- κ B according to the present invention and a gene encoding a signal which can detect activation of NF- κ B; and
- (b) reagents for measuring the signal.

In another aspect, the present invention relates to a diagnostic kit which comprises:

(a) a polynucleotide of the present invention having a nucleotide sequence expressed by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide having a nucleotide sequence complementary to that of (a);

(c) a protein of the present invention having an amino acid sequence expressed by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, or a fragment thereof; or

(d) an antibody to the protein of the present invention of (c).

A kit comprising at least one of (a) to (d) is useful for diagnosing a disease or susceptibility to a disease such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

Because NF- κ B is involved in a wide variety of pathological conditions such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders, it is an attractive target for drug

design and therapeutic intervention. Many experiments show that NF- κ B activity may have significant physiological effects [see e.g., *Ann. Rheum. Dis.* 57:738-741 (1998); *American Journal of Pathology* 152:793-803 (1998); *ARTHRITIS & RHEUMATISM* 40:226-236 (1997); *Am. J. Respir. Crit. Care Med.* 158:1585-1592 (1998); *J. Exp. Med.* 188:1739-1750 (1998); *Gut* 42:477-484 (1998); *The Journal of Immunology* 161:4572-4582 (1998); *Nature Medicine* 3:894-899 (1997)].

The finding of the new protein described herein capable of activating NF- κ B has provided a new medicament and method for controlling an abnormal NF- κ B function. Thus, the present invention also relates to a method of use of a compound which inhibits the function of the protein capable of activating NF- κ B described above, for inhibiting NF- κ B activation. Further, the present invention relates to a method of using a compound which activates the function of the protein capable of activating NF- κ B described above, for promoting NF- κ B activation. The compound obtained by the above screening method, which inhibits NF- κ B activation, is useful as a medicament to treat or prevent diseases characterized by undesirable activation of NF- κ B, such as inflammation, autoimmune diseases (such as rheumatoid arthritis, systemic lupus erythematosus, asthma, etc), infectious diseases, bone diseases, and graft rejection. Recently, it has also become apparent that NF- κ B activation controls apoptosis of cells. The compound obtained by the above screening method, which inhibits NF- κ B activation, may be capable of stimulating apoptosis. Diseases which may be treated by the induction of apoptosis include tumors.

Further, examples of diseases related to abnormality in NF- κ B activation include AIDS (acquired immunodeficiency syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, etc.), ischemic disorders (i.e. those caused by cardiac infarction, reperfusion injury, etc), myelogenesis incompetency syndrome (aplastic anemia, etc), skin diseases (Toxic epidermal necrolysis, etc), proliferative nephritis (IgA nephritis, purpuric nephritis, lupus nephritis, etc) and fulminant hepatitis. Thus, a compound obtained by the above screening method, which

inhibits or promotes NF- κ B activation, is useful as a medicament to treat or prevent these diseases.

In addition, the gene encoding the protein of the present invention is useful for gene therapy to treat various diseases such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. "Gene therapy" refers to administering into the human body a gene or a cell into which a gene has been introduced for the purpose of therapy of diseases. The protein of the present invention and the DNA encoding the protein can also be used for diagnostic purposes. Thus, the present invention provides a agent for gene therapy which comprises a gene encoding the protein of the present invention.

The form of the agent for gene therapy is not particularly limited, but includes a pharmaceutical composition which comprises a expression vector containing a gene of the present invention in a pharmaceutical carrier of physiological buffer. The pharmaceutical carrier may contain suitable stabilizer (for example, nuclease inhibitor), chelate agent (for example, EDTA), and/or other auxiliary agent. Alternatively, the agent for gene therapy of the present invention may be provided as a complex of an expression vector containing a gene of the present invention and a liposome. The agent for gene therapy may be applied using a catheter. For example, the agent for gene therapy of the present invention can be directly injected into a blood vessel of patient and the like.

The dosage of the agent for gene therapy of the present invention should be selected depending on the conditions such as age, sex, body weight and symptom of patient, and administration route, and is generally about 1 μ g/kg to about 1000 mg/kg, more preferably about 10 μ g/kg to about 100 mg/kg, as an amount of DNA (which is an effective ingredient) per one administration for adult. The number of administration is not particularly limited.

The compound obtained by the screening method of the present invention or a salt thereof can be formulated into the above pharmaceutical compositions (e.g., tablets,

capsules, elixirs, microcapsules, sterile solutions and suspensions) according to conventional procedures. The formulations thus obtained are safe and of low toxicity, and can be administered, for example, to humans and mammals (e.g., rats, rabbits, sheep, pigs, cattle, cats, dogs and monkeys). Administration to patients can be carried out by methods known in the art, such as intra-arterial injection, intravenous injection and subcutaneous injection. The dosage and administration mode may vary with the weight and age of the patient, but those skilled in the art can appropriately select suitable administration mode and can appropriately select suitable dosage depending on the administration mode. When the compound can be encoded by DNA, the DNA can be inserted into a vector for gene therapy, and gene therapy can be carried out. Thus, the present invention relates to a medicament which comprises a compound capable of inhibiting or promoting NF- κ B activation as an active ingredient.

In addition, the above compound is useful as a medicament to treat or prevent diseases characterized by abnormal NF- κ B activity, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus, the present invention also relates to a medicament to treat or prevent inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, ischemic disorders and the like, which comprises a compound capable of inhibiting or promoting NF- κ B activation. Specifically, the compound is useful as a therapeutic and/or prophylactic drug against, for example, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, diabetes, sepsis, asthma, allergic rhinitis, ischemic heart diseases, inflammatory intestinal diseases, subarachnoid hemorrhage, viral hepatitis, AIDS, atherosclerosis, atopic dermatitis, viral infections, Crohn's disease, gout, hepatitis, multiple sclerosis, cardiac infarction, nephritis, osteoporosis, Alzheimer's, Parkinson's disease, Huntington's chorea, psoriasis, amyotrophic lateral sclerosis, or aplastic anemia.

The present invention also relates to the use of the above compound for manufacturing a medicament for the therapy and/or prevention of inflammation,

autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, ischemic disorders and the like.

The present invention also provides an antisense oligonucleotide against the polynucleotide of any one of above items (3) to (7). An antisense oligonucleotide refers to an oligonucleotide complementary to the target gene sequence. The antisense oligonucleotide can inhibit the expression of the target gene by inhibiting RNA functions such as translation to proteins, transport to the cytoplasm and other activity necessary for overall biological functions. In this case, the antisense oligonucleotide may be RNA or DNA. The DNA sequence of the present invention can be used to produce an antisense oligonucleotide capable of hybridizing with the mRNA transcribed from the gene encoding the protein of the present invention. It is known that an antisense oligonucleotide generally has an inhibitory effect on the expression of the corresponding gene (see e.g., Saibou Kougaku Vol.13, No.4 (1994)). The oligonucleotide containing an antisense coding sequence against a gene encoding the protein of the present invention can be introduced into a cell by standard methods. The oligonucleotide effectively blocks the translation of mRNA of the gene encoding the protein of the present invention, thereby blocking its expression and inhibiting undesirable activity.

The antisense oligonucleotide of the present invention may be a naturally occurring oligonucleotide or its modified form [see e.g., Murakami & Makino, Saibou Kougaku Vol.13, No.4, p.259-266 (1994); Akira Murakami, Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol.40, No.10, p.1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14, No. 4 p85-95(1996)]. Thus, the oligonucleotide may have modified sugar moieties or inter-sugar moieties. Examples of such modified forms include phosphothioates and other sulfur-containing species used in the art. According to several preferred embodiments of the present invention, at least one phosphodiester bond in the oligonucleotide is substituted with the structure which can enhance the ability of the composition to permeate cellular regions where RNA with the activity to be regulated is

located.

Such substitution preferably involves a phosphorothioate bond, a phosphoramidate bond, methylphosphonate bond, or a short-chain alkyl or cycloalkyl structure. The antisense oligonucleotide may also contain at least some modified base forms. Thus, it may contain purine and pyrimidine derivatives other than naturally occurring purine and pyrimidine. Similarly, the furanosyl moieties of the nucleotide subunits can be modified so long as the essential purpose of the present invention is attained. Examples of such modifications include 2'-O-alkyl and 2'-halogen substituted nucleotides. Examples of modifications in sugar moieties at their 2-position include OH, SH, SCH₃, OCH₃, OCN or O(CH₂)_nCH₃, wherein n is 1 to about 10, and other substituents having similar properties. All the analogues are included in the scope of the present invention so long as they can hybridize with the mRNA of the gene of the present invention to inhibit functions of the mRNA.

The antisense oligonucleotide of the present invention contains about 3 to about 50 nucleotides, preferably about 8 to about 30 nucleotides, more preferably about 12 to about 25 nucleotides. The oligonucleotide of the present invention can be produced by the well-known solid phase synthesis technique. Devices for such synthesis are commercially available from some manufactures including Applied Biosystems. Other oligonucleotides such as phosphothioates can also be produced by methods known in the art.

The antisense oligonucleotide of the present invention is designed to hybridize with the mRNA transcribed from the gene of the present invention. Those skilled in the art can easily design an antisense oligonucleotides based on a given gene sequence (For example, Murakami and Makino: Saibou Kougaku Vol. 13 No.4 p259-266 (1994), Akira Murakami: Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol. 40 No.10 p1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14 No. 4 p85-95 (1996)). Recent sutudy suggests that antisense oligonucleotides which are designed in a region containing 5' region of

mRNA, preferably, the translation initiation site, are most effective for the inhibition of the expression of a gene. The length of the antisense oligonucleotides is preferably 15 to 30 nucleotides and more preferably 20 to 25 nucleotides. It is important to confirm no interaction with other mRNA and no formation of secondary structure in the oligonucleotide sequence by homology search. The evaluation of whether the designed antisense oligonucleotide is functional or not can be determined by introducing the antisense oligonucleotide into a suitable cell and measuring the amount of the target mRNA, for example by northern blotting or RT-PCR, or the amount of the target protein, for example by western blotting or fluorescent antibody technique, to confirm the effect of expression inhibition.

Another method includes the triple helix technique. This technique involves forming a triple helix on the targeted intra-nuclear DNA sequence, thereby regulating its gene expression, mainly at the transcription stage. The oligonucleotide is designed mainly in the gene region involved in the transcription and inhibits the transcription and the production of the protein of the present invention. Such RNA, DNA and oligonucleotide can be produced using known synthesizers.

The antisense oligonucleotide may be introduced into the cells containing the target nucleic acid sequence by any of DNA transfection methods such as calcium phosphate method, electroporation, lipofection, microinjection, or gene transfer methods including the use of gene transfer vectors such as viruses. An antisense oligonucleotide expression vector can be prepared using a suitable retrovirus vector, then the expression vector can be introduced into the cells containing the target nucleic acid sequence by contacting the vector with the cells in vivo or ex vivo.

The DNA of the present invention can be used in the antisense RNA/DNA technique or the triple helix technique to inhibit NF- κ B activation mediated by the protein of the present invention.

The antisense oligonucleotide against the gene encoding the protein of the present invention is useful as a medicament to treat or prevent diseases characterized by

undesirable activation of NF- κ B, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus, the present invention also provides a medicament which comprises the above antisense oligonucleotide as an active ingredient. The antisense oligonucleotide can also be used to detect such diseases using northern hybridization or PCR.

The present invention also provides a ribozyme or deoxyribozyme which inhibits NF- κ B activation. A ribozyme and deoxyribozyme is an RNA capable of recognizing a nucleotide sequence of a nucleic acid and cleaving the nucleic acid (see e.g., Hiroshi Yanagawa, "Jikken Igaku (Experimental Medicine) Bioscience 12: New Age of RNA). The ribozyme or deoxyribozyme can be produced so that it cleaves the selected target RNA (e.g., mRNA encoding the protein of the present invention). Based on the nucleotide sequence of the DNA encoding the protein of the present invention, the ribozyme or deoxyribozyme specifically cleaving the mRNA of the protein of the present invention can be designed. Such ribozyme has a complementary sequence to the mRNA for the protein of the present invention, complementarily associates with the mRNA and then cleaves the mRNA, which results in reduction or entire loss of the expression of the protein of the present invention. The level of the reduction of the expression is dependent on the level of the ribozyme or deoxyribozyme expression in the target cells.

There are two types of ribozyme or deoxyribozyme commonly used: a hammerhead ribozyme and a hairpin ribozyme. In particular, hammerhead ribozymes or deoxyribozymes have been well studied regarding their primary and secondary structure necessary for their cleavage activity, and those skilled in the art can easily design the ribozymes nucleotided solely on the nucleotide sequence information for the DNA encoding the protein of the present invention [see e.g., Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994)]. It is known that the hammerhead ribozymes or deoxyribozymes have a structure consisting of two recognition sites (recognition site I and recognition site II forming a chain complementary to target RNA) and an active site,

and cleave the target RNA at the 3' end of its sequence NUX (wherein N is A or G or C or U, and X is A or C or U) after the formation of a complementary pair with the target RNA in the recognition sites. In particular, the sequence GUC (or GUA) has been found to have the highest activity [see e.g., Koizumi, M. et al., *Nucl. Acids Res.* 17:7059-7071 (1989); Iida et al., *Saibou Kougaku* Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, *Jikken Igaku (Experimental Medicine)* Vol.12, No.12, p.83-88 (1994); Kawasaki & Taira, *Jikken Igaku (Experimental Medicine)* Vol.18, No.3, p.381-386 (2000)].

Therefore the sequence GTC (or GTA) is searched out, and a ribozyme is designed to form several, up to 10 to 20 complementary base pairs around that sequence. The suitability of the designed ribozyme can be evaluated by checking whether the prepared ribozyme can cleave the target mRNA in vitro according to the method described for example in Ohkawa & Taira, *Jikken Igaku (Experimental Medicine)* Vol.12, No.12, p.83-88 (1994). The ribozyme can be prepared by methods known in the art to synthesize RNA molecules.

Alternatively, the sequence of the ribozyme can be synthesized on a DNA synthesizer and inserted into various vectors containing a suitable RNA polymerase promoter (e.g., T7 or SP6) to enzymatically synthesize an RNA molecule in vitro. Such ribozymes can be introduced into cells by gene transfer methods such as microinjection. Another method involves inserting a ribozyme DNA into a suitable expression vector and introducing the vector into cell strains, cells or tissues. Suitable vectors can be used to introduce the ribozyme into a selected cell. Examples of vectors commonly used for such purpose include plasmid vectors and animal virus vectors (e.g., retrovirus, adenovirus, herpes or vaccinia virus vectors). Such ribozymes are capable of inhibiting the NF- κ B activation mediated by the protein of the present invention.

The present invention further provides a process for obtaining a new gene having a function, which comprises using the oligo-capping method to construct a full-length cDNA library, and detecting the presence of a protein having the function by using a signal factor. An example of such signal factor is a reporter gene.

Methods using a cDNA library containing a lot of non-full-length cDNAs are inefficient in obtaining many genes (cDNAs) having functions. Therefore libraries with a high ratio of the number of the full-length cDNA clones to the total number of the clones are necessary. "Full-length cDNA" refers to a complete DNA copy of mRNA from a gene. The cDNA libraries produced using the oligo-capping method contain full-length cDNA clones in a ratio of 50 to 80%, namely, a 5 to 10-fold increase in full-length cDNA clones compared to the cDNA libraries produced by prior art methods (Sumio Sugano, the monthly magazine BIO INDUSTRY Vol.16, No.11, p.19-26). Full-length cDNA clones are essential for protein expression in functional analyses of genes, and full-length cDNA clones themselves are very important materials for activity measurement. Thus, cloning of full-length cDNA is necessary for functional analyses of genes. Sequencing of the cDNA not only provides important information for establishing the primary sequence of the protein encoded by the cDNA, but also reveals the entire exon sequence. Thus, the full-length cDNA provides valuable information for identifying a gene, such as information for determining the primary sequence of a protein, exon-intron structure, the transcription initiation site of mRNA, the location of a promoter, etc.

The construction of full-length cDNA libraries by the oligo-capping method can be carried out, for example, according to the method described in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD. The oligo-capping method used herein involves substituting a cap structure with a synthetic oligo sequence by using BAP, TAP and an RNA ligase, as described in Suzuki & Sugano, "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

The reporter gene which can be used as a signal factor which indicates the presence of a protein having a function contains one or more suitable expression regulation sequence portion to which a protein factor such as a transcriptional factor can

bind, and a structural gene portion which allows the measurement of the activation of the proteins factor. The structural gene portion may encode any peptide or protein so long as those skilled in the art can measure the activity or amount of its expression product (including the amount of the mRNA produced). For example, chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., can be used and their enzymatic activity measured.

Examples of reporter genes which indicate the presence of a protein having a function include reporter genes containing a CREB (cAMP responsive element binding protein) binding sequence or AP-1 (activator protein-1) binding sequence at the expression regulation sequence region of the reporter genes, in addition to the NF- κ B reporter genes described herein.

For example, if a gene capable of activating CREB is to be obtained, a CREB-dependent reporter plasmid and an expression vector comprising full-length cDNA produced by the oligo-capping method can be cotransfected into cells, and an expression vector having increased reporter activity can be selected from the cells to attain the purpose. If a gene capable of inhibiting CREB is to be obtained, a CREB-dependent reporter plasmid and an expression vector comprising full-length cDNA produced by the oligo-capping method can be cotransfected into cells, and an expression vector having decreased reporter activity can be selected from the cells to attain the purpose. These procedures may be carried out in the presence of a certain stimulus to the cells. The cDNA clone (expression vector) to be transfected into the cells may be a single clone or multiple clones which may be transfected simultaneously. One embodiment of the process of the present invention is detailed in Examples herein. Alternatively, a screening system for obtaining a gene capable of inhibiting NF- κ B activation can also be constructed by cotransfecting an expression vector comprising full-length cDNA and a reporter gene into cells, stimulating the cells with IL-1 or TNF- α and the like, and selecting a clone having subnormally increased reporter activity. By preparing a reporter gene suitably, a gene encoding a protein capable of activating various

factors (for example, MAP kinase, transcription factor) can be obtained in addition to a gene encoding the protein capable of activating NF- κ B.

The process of the present invention uses an in vitro system or a cell-based system, preferably a cell-based system. Examples of such cells include cells of prokaryotes such as E. coli, microorganisms such as yeast and fungi, as well as insects and animals. Preferred examples include animal cells, in particular, 293-EBNA cells and NIH3T3 cells.

Because the cDNA of the present invention is full-length, its 5' end sequence is the transcription initiation site of the corresponding mRNA. Therefore the cDNA sequence can be used to identify the promoter region of the gene by comparing the cDNA with the genomic nucleotide sequence. Genomic nucleotide sequences are available from various databases when the sequences have been deposited in the databases. Alternatively, the cDNA can also be used to clone the desired sequence from a genomic library, for example, by hybridization, and determine its nucleotide sequence. Thus, by comparing the nucleotide sequence of the cDNA of the present invention with a genomic sequence, the promoter region of the gene located upstream the cDNA can be identified. In addition, the promoter fragment thus identified can be used to construct a reporter plasmid for evaluating the expression of the gene. In general, the DNA fragment spanning 2kb (preferably 1kb) upstream from the transcription initiation site can be inserted upstream of the reporter gene to produce the reporter plasmid. The reporter plasmid can be used to screen for a compound which enhances or reduces the expression of the gene. For example, such screening can be carried out by transforming a suitable cell with the reporter plasmid, culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. These methods are also included in the scope of the present invention.

The present invention also relates to a computer-readable medium on which a

sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

In another aspect, the present invention relates to a method for calculating a homology, which comprises comparing data on the above medium with data of other nucleotide sequences. Thus, the gene and amino acid sequence of the present invention provide valuable information for determining their secondary and tertiary structure, e.g., information for identifying other sequence having a similar function and high homology. These sequences are stored on the computer-readable medium, then a database is searched using data stored in a known macromolecule structure program and a known search tool such as GCG. In this manner, a sequence in a database having a certain homology can be easily found.

The computer-readable medium may be any composition of materials used to

store information or data. Examples of such media include commercially available floppy disks, tapes, chips, hard drives, compact disks and video disks. The data on the medium allows a method for calculating a homology by comparing the data with other nucleotide sequence data. This method comprises the steps of providing a first polynucleotide sequence containing the polynucleotide sequence of the present invention for the computer-readable medium, and then comparing the first polynucleotide sequence with at least one-second polynucleotide or polypeptide sequence to identify the homology.

The present invention also relates to an insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 are fixed. A plurality of the various polynucleotides which are DNA probes are fixed on a specifically processed solid substrate such as slide glass to form a DNA microarray and then a labeled target polynucleotide is hybridized with the fixed polynucleotides to detect a signal from each of the probes. The data obtained is analyzed and the gene expression is determined.

The present invention further relates to an insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160,

162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed. By mixing organism-derived cell extract with the insoluble substrate on which these proteins are fixed, it is possible to isolate or identify cell-derived components such as proteins captured on the insoluble substrate that can be expected to be useful in diagnosis or drug development.

EXAMPLES

The following examples further illustrate, but do not limit the present invention.

Example 1: Construction of a full-length cDNA library using the oligo-capping method

(1) Preparation of RNA from human lung fibroblasts (Cryo NHLF)

Human lung fibroblasts (Cryo NHLF: purchased from Sanko Junyaku Co., Ltd.) were cultured according to the manufacture's protocol. After repeating subculturing the cells to obtain fifty 10cm dishes containing the resulting culture, the cells were recovered with a cell scraper. Then, total RNA was obtained from the recovered cells by using the RNA extraction reagent ISOGEN (purchased from NIPPON GENE) according to the manufacturer's protocol. Then, poly A⁺ RNA was obtained from the total RNA by using an oligo-dT cellulose column according to Maniatis et al., supra.

(2) Preparation of RNA from mouse ATDC5 cells

ATDC5, a cell strain cloned from mouse EC (embryonal carcinoma) (Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116)(1990) was repeatedly subcultured to obtain fifty 10cm dishes containing the resultant culture. Thereafter, poly A⁺ RNA was obtained by a method similar to that of (1) above. Culture of ATDC5 cells was performed according to the method described in Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116 (1990).

(3) Preparation of RNA from Jurkat cells

From Jurkat cells, a human T cell strain (purchased from DAINIPPON PHARMACEUTICAL CO.,LTD), poly A⁺ RNA was obtained in the same way as in the

above (1). Jurkat cells were cultured in PRMI 1640 medium (GIBCO) containing 10%FBS (Fetal Bovine Serum: GIBCO) and 10mM HEPES (GIBCO) in the presence of 5% CO₂ at 37°C.

(4) Preparation of RNA from RAW264.7 cells

RAW264.7 cells, a mouse macrophage-like cell strain (ATCC Number TIB-71), were cultured to obtain poly A⁺ RNA in the same way as in the above (1).

(5) Construction of a full-length cDNA library by the oligo-capping method

A full-length cDNA library was constructed from poly A⁺ RNA of the above human lung fibroblasts, ATDC5 cells, Jurkat cells and RAW264.7 cells by the oligo-capping method according to the method of Sugano S. et al. [e.g., Maruyama, K. & Sugano, S., *Gene*, 138:171-174 (1994); Suzuki, Y. et al., *Gene*, 200:149-156 (1997); Suzuki, Y. & Sugano, S. "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.].

(6) Preparation of plasmid DNA

The full-length cDNA library constructed as above was transformed into *E. coli* strain TOP 10 by electroporation, then spread on LB agar medium containing 100 μ g/ml of ampicillin, and incubated overnight at 37°C. Then, using QIAwell 96 Ultra Plasmid Kit (QIAGEN) according to the manufacturer's protocol, the plasmids were recovered from the colonies grown on ampicillin-containing LB agar medium.

Example 2: Cloning of DNA capable of activating NF- κ B

(1) Screening of the cDNA encoding the protein capable of activating NF- κ B

293-EBNA cells (purchased from Invitrogen) were seeded on DMEM medium containing 5% FBS in a 96 well cell culture plate to a final cell density of 1×10^4 cells/100 μ l/well, and cultured for 24 hours at 37°C in the presence of 5% CO₂. Then, 50ng of pNF κ B-Luc (purchased from STRATAGENE) and 2 μ l of the full-length cDNA expression vector prepared in above Example 1.(6) were cotransfected into the cells in a

well using FuGENE 6 (purchased from Roche) according to the manufacturer's protocol. After 24 hours of culture at 37°C, the reporter activity of NF- κ B (luciferase activity) was measured using long-term luciferase assay system, PIKKA GENE LT2.0 (TOYO INK) according to the attached manufacturer's instructions. The luciferase activity was measured using Wallac ARVO™ST 1420 MULTILABEL COUNTER (Perkin Elmer).

(2) DNA sequencing

The above screening was carried out, and plasmids showing a 5-fold or more increase in luciferase activity compared to that of the control experiment (luciferase activity of the cell into which vacant vector pME18S-FL3 is introduced instead of full-length cDNA expression vector) were selected. One pass sequencing was carried out from the 5' end of the cloned cDNA (sequencing primer: 5'-CTTCTGCTCTAAAAGCTGCG-3' (SEQ ID NO: 289)) and from the 3' end (sequencing primer: 5'-CGACCTGCAGCTCGAGCACA-3' (SEQ ID NO: 290)) so that as long sequence as possible is determined. The sequencing was carried out using the reagent Thermo Sequenase II Dye Terminator Cycle Sequencing Kit (Amersham Pharmacia Biotech) or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit (Applied Biosystems) and the device ABI PRISM 377 sequencer or ABI PRISM 3100 sequencer according to the manufacturer's instructions.

(3) Full-length sequencing

The full-length DNA sequences for the 144 new clones which were obtained by the above screening, were determined (SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287). The

amino acid sequences of the protein coding regions (open reading frames) were deduced (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288).

The results of measurement of NF- κ B reporter activity (luciferase activity) of 41 clones among the above obtained clones are shown in Table 1 below. The value of activity shown in Table 1 is a relative value to the value of control experiment (luciferase activity of a cell into which pME183-FL3 vector containing no insert has been introduced in place of full length cDNA).

Table 1

Clone	activity (-fold)
SEQ ID NO:7	9
SEQ ID NO:9	12
SEQ ID NO:19	6
SEQ ID NO:23	5
SEQ ID NO:29	92
SEQ ID NO:35	54
SEQ ID NO:37	33
SEQ ID NO:39	22
SEQ ID NO:43	31
SEQ ID NO:47	63
SEQ ID NO:51	12

SEQ ID NO:75	9
SEQ ID NO:77	13
SEQ ID NO:85	13
SEQ ID NO:91	7
SEQ ID NO:103	7
SEQ ID NO:111	70
SEQ ID NO:115	11
SEQ ID NO:119	9
SEQ ID NO:123	10
SEQ ID NO:143	6
SEQ ID NO:151	10
SEQ ID NO:157	29
SEQ ID NO:165	145
SEQ ID NO:171	134
SEQ ID NO:175	19
SEQ ID NO:181	22
SEQ ID NO:185	33
SEQ ID NO:195	6
SEQ ID NO:197	5
SEQ ID NO:199	14
SEQ ID NO:201	31
SEQ ID NO:205	32
SEQ ID NO:211	16
SEQ ID NO:229	13
SEQ ID NO:237	7
SEQ ID NO:239	23
SEQ ID NO:247	15
SEQ ID NO:257	5

SEQ ID NO:261 17

SEQ ID NO:287 66

Example 3: Screening compounds inhibiting NF- κ B activation

293-EBNA cells were seeded on DMEM medium containing 5% FBS in a 96-well cell culture plate to a final cell density of 1×10^4 cells/100 μ l/well, and cultured for 24 hours at 37°C in the presence of 5% CO₂. Then, 50ng of the plasmid comprising the gene encoding NF- κ B activating protein of SEQ ID NO: 12 which was obtained in Example 2 above, and 50ng of the reporter plasmid pNF κ B-Luc were cotransfected into the cells in a well using FuGENE 6. After 1 hour, the proteasome inhibitor MG-132 (purchased from CALBIOCHEM) (Uehara T. et al., J. Biol. Chem. 274, p.15875-15882 (1999); Wang X. C. et al., Invest. Ophthalmol. Vis. Sci. 40, p.477-486) was added to the culture to final concentrations of 1.0 μ M. After 24 hours of culture at 37°C, the reporter activity was measured using PIKKA GENE LT2.0. The results showed that MG132 inhibited the expression of the reporter gene (Fig. 1).

INDUSTRIAL APPLICABILITY

As described above, the present invention provides industrially highly useful proteins capable of activating NF- κ B and genes encoding the proteins. The proteins of the present invention and the genes encoding the proteins allow not only screening for compounds useful for treating and preventing diseases associated with the excessive activation or inhibition of NF- κ B, but also production of diagnostics for such diseases. The genes of the present invention are also useful as a gene source used for gene therapy.

All publications, patents and patent applications cited herein are incorporated herein in their entirety.

CLAIMS

1. A purified protein selected from the group consisting of:
 - (a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and
 - (b) a protein that activates NF- κ B (Nuclear factor kappa B) and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.
2. A purified protein that activates NF- κ B and comprises an amino acid sequence having at least 95% identity to the protein according to claim 1 over the entire length thereof.
3. An isolated polynucleotide which comprises a nucleotide sequence encoding a

protein selected from the group consisting of:

(a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF- κ B and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

4. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,

179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

5. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243,

245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

6. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to claim 3 over the entire length thereof.

7. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to claim 4 or 5 over the entire length thereof.

8. A purified protein encoded by the polynucleotide according to any one of claims 3 to 7.

9. A recombinant vector which comprises a polynucleotide according to any one of claims 3 to 7.
10. A agent for gene therapy which comprises the recombinant vector according to claim 9 as an active ingredient.
11. A transformed cell which comprises the recombinant vector according to claim 9.
12. A membrane of the cell according to claim 11, which has the protein according to claim 1 or 2 which is a membrane protein.
13. A process for producing a protein according to claim 1, 2 or 8 comprising the steps of;
- (a) culturing a transformed cell according to claim 11 under conditions providing expression of the protein according to claim 1, 2 or 8; and
 - (b) recovering the protein from the culture product.
14. A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of claim 1, 2 or 8 in a subject comprising the steps of:
- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
 - (b) analyzing the amount of expression of said protein in a sample derived from said subject.
15. A method for screening compounds capable of inhibiting or promoting NF- κ B activation, which comprises the steps of:
- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes

activation of NF- κ B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- κ B into a cell;

(b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring the signal which can detect activation of NF- κ B; and

(d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation.

16. A method for screening compounds capable of inhibiting or promoting NF- κ B activation, which comprises the steps of:

(a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to claim 1, 2 or 8 into a cell;

(b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring the activation of NF- κ B; and

(d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation.

17. A compound capable of inhibiting or promoting NF- κ B activation, which is selected by the method for screening according to claim 15 or 16.

18. A process for producing a pharmaceutical composition, which comprises the steps of:

(a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- κ B into a cell;

- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- κ B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

19. A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- κ B according to claim 1, 2 or 8 into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- κ B; and
- (d) selecting a candidate compound which can change the activation of NF- κ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- κ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

20. A kit for screening a compound capable of inhibiting or promoting NF- κ B activation, which comprises:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- κ B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- κ B; and
- (b) reagents for measuring the signal.

21. A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to claim 1, 2 or 8.
22. The monoclonal or polyclonal antibody or a fragment thereof according to claim 21, which inhibits the activity of promoting activation of NF- κ B by the protein according to claim 1, 2 or 8.
23. A process for producing a monoclonal or polyclonal antibody according to claim 21 or 22, which comprises administering the protein according to claim 1, 2 or 8 or epitope-bearing fragments thereof to a non-human animal as an antigen.
24. An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of claims 3 to 7, which prevents the expression of a protein which promotes NF- κ B activation.
25. A ribozyme or deoxyribozyme capable of inhibiting NF- κ B activation, which has an action of cleavage of RNA that encodes the protein according to claim 1, 2 or 8 or an action of cleavage of RNA that encodes a protein involved in a pathway leading to NF- κ B activation.
26. A method for treating a disease associated with NF- κ B activation, which comprises administering to a subject a compound screened by the process according to claim 15 or 16, and/or a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22, and/or an antisense oligonucleotide according to claim 24, and/or a ribozyme or deoxyribozyme according to claim 25 in an effective amount to treat a disease selected from the group consisting of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and

ischemic disorders.

27. A pharmaceutical composition produced by the process according to claim 18 or 19 for inhibiting or promoting NF- κ B activation.

28. The pharmaceutical composition according to claim 27 for the treatment of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and/or ischemic disorders.

29. A method of treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders, which comprises administering a pharmaceutical composition produced by the process according to claim 18 or 19 to a patient suffering from a disease associated with NF- κ B activation.

30. A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22 as an active ingredient.

31. A pharmaceutical composition which comprises an antisense oligonucleotide according to claim 24 as an active ingredient.

32. A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to claim 25 as an active ingredient.

33. The pharmaceutical composition according to any one of claims 30 to 32 for the treatment and/or prevention of a disease which is selected from the group consisting of inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

34. A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

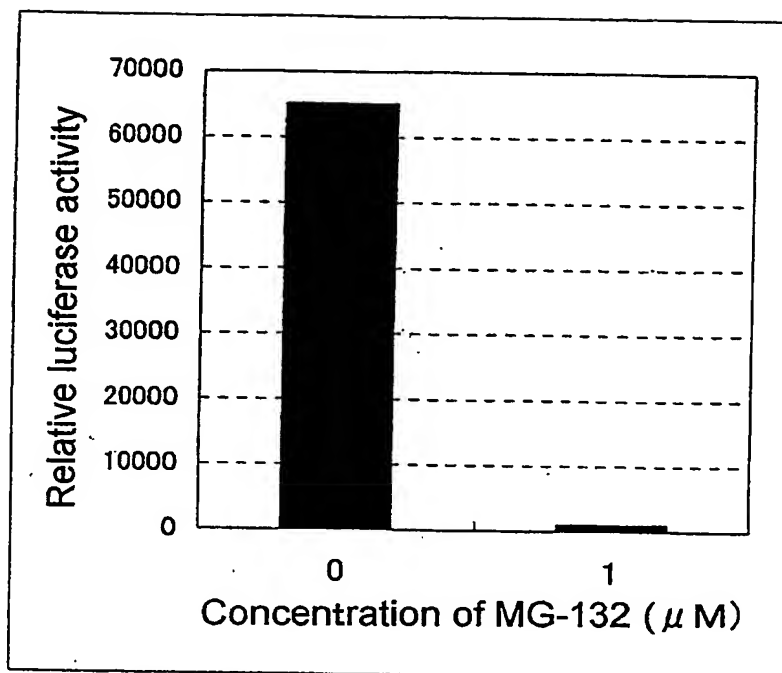
35. A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to claim 34 with data of said other nucleotide sequences and/or amino acid sequences.

36. An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,

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37. An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed.

Fig. 1



BEST AVAILABLE COPY

SEQUENCE LISTING

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 Glu Ser Phe Ala Arg Ile Gln Val Arg Phe Ala Glu Leu Lys Ala Ile
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Gln Glu Pro Asp Asp Ala Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn
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 Cys Lys Lys Phe Ala Phe Val His Ile Ser Phe Ala Gln Phe Glu Leu
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 Ser Gln Gly Asn Val Lys Lys Ser Lys Gln Leu Leu Gln Lys Ala Val
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Lys Pro Ser Gly Asn Asp Ser Cys Glu Leu Arg Asn Leu Lys Ser Val	
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Ser Leu Leu Ala Lys Leu Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu	
365 370 375	
gtt cca gag agt aac cag aaa cag tgg caa tct aag aga aag tca gag	1265
Val Pro Glu Ser Asn Gln Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu	
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Cys Ile Asn Gln Asn Pro Ala Ala Ser Ser Asn His Trp Gln Ile Pro	
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Glu Leu Ala Arg Lys Val Asn Thr Glu Gln Lys His Thr Thr Phe Glu
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 Lys Trp Phe Asp Pro Lys Ser Ile Cys Lys Thr Pro Ser Ser Asn Thr
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 510 515 520
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 Arg Ile Tyr Ser Ile Leu Lys Gln Ile Gly Ser Gly Gly Ser Ser Lys
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Val Asn Leu Glu Glu Ala Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn
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 Glu Ile Ala Tyr Leu Asn Lys Leu Gln Gln His Ser Asp Lys Ile Ile
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 Arg Leu Tyr Asp Tyr Glu Ile Thr Asp Gln Tyr Ile Tyr Met Val Met
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 635 640 645 650
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 Gln Val Gly Thr Val Asn Tyr Met Pro Pro Glu Ala Ile Lys Asp Met
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 tct tcc tcc aga gag aat ggg aaa tct aag tca aag ata agc ccc aaa 2225

Ser Ser Ser Arg Glu Asn Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys
 700 705 710
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 Lys Thr Pro Phe Gln Gln Ile Ile Asn Gln Ile Ser Lys Leu His Ala
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 Asp Leu Gln Asp Val Leu Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln
 765 770 775
 agg ata tcc att cct gag ctc ctg gct cat ccc tat gtt caa att caa 2465
 Arg Ile Ser Ile Pro Glu Leu Leu Ala His Pro Tyr Val Gln Ile Gln
 780 785 790
 act cat cca gtt aac caa atg gcc aag gga acc act gaa gaa atg aaa 2513
 Thr His Pro Val Asn Gln Met Ala Lys Gly Thr Thr Glu Glu Met Lys
 795 800 805 810
 tat gtt ctg ggc caa ctt gtt ggt ctg aat tct cct aac tcc att ttg 2561
 Tyr Val Leu Gly Gln Leu Val Gly Leu Asn Ser Pro Asn Ser Ile Leu
 815 820 825
 aaa gct gct aaa act tta tat gaa cac tat agt ggt ggt gaa agt cat 2609
 Lys Ala Ala Lys Thr Leu Tyr Glu His Tyr Ser Gly Gly Glu Ser His
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 aat tct tca tcc tcc aag act ttt gaa aaa aaa agg gga aaa aaa 2654

Asn Ser Ser Ser Ser Lys Thr Phe Glu Lys Lys Arg Gly Lys Lys

845

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 aaaaaattca gtagattatc tttaaaagaa aactgtaaaa atagcaacca cttatggtac 2834
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Thr Asp Glu Leu Ser Leu Asn Lys Ile Ser Ala Asp Thr Thr Asp Asn

35

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45

Ser Gly Thr Val Asn Gln Ile Met Met Met Ala Asn Asn Pro Glu Asp

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Trp Leu Ser Leu Leu Leu Lys Leu Glu Lys Asn Ser Val Pro Leu Ser

65

70

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Asp Ala Leu Leu Asn Lys Leu Ile Gly Arg Tyr Ser Gln Ala Ile Glu

85

90

95

Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser Phe Ala Arg Ile

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Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys Lys Phe Ala Phe			
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Val His Ile Ser Phe Ala Gln Phe Glu Leu Ser Gln Gly Asn Val Lys			
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Lys Ser Lys Gln Leu Leu Gln Lys Ala Val Glu Arg Gly Ala Val Pro			
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Leu Glu Met Leu Glu Ile Ala Leu Arg Asn Leu Asn Leu Gln Lys Lys			
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Gln Leu Leu Ser Glu Glu Glu Lys Lys Asn Leu Ser Ala Ser Thr Val			
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Leu Tyr Gly Glu Asn Met Pro Pro Gln Asp Ala Glu Ile Gly Tyr Arg			
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Asn Ser Leu Arg Gln Thr Asn Lys Thr Lys Gln Ser Cys Pro Phe Gly			
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Asp Asp Ser Val Val Pro Cys Phe Met Lys Arg Gln Thr Ser Arg Ser			
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Glu Cys Arg Asp Leu Val Val Pro Gly Ser Lys Pro Ser Gly Asn Asp			
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340 345 350
Ser Ile Thr Leu Lys Asn Lys Thr Glu Ser Ser Leu Leu Ala Lys Leu
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Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu Val Pro Glu Ser Asn Gln
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Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu Cys Ile Asn Gln Asn Pro
385 390 395 400
Ala Ala Ser Ser Asn His Trp Gln Ile Pro Glu Leu Ala Arg Lys Val
405 410 415
Asn Thr Glu Gln Lys His Thr Thr Phe Glu Gln Pro Val Phe Ser Val
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Ser Lys Gln Ser Pro Pro Ile Ser Thr Ser Lys Trp Phe Asp Pro Lys
435 440 445
Ser Ile Cys Lys Thr Pro Ser Ser Asn Thr Leu Asp Asp Tyr Met Ser
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Cys Phe Arg Thr Pro Val Val Lys Asn Asp Phe Pro Pro Ala Cys Gln
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Gln Ile Leu Ala Thr Pro Leu Gln Asn Leu Gln Val Leu Ala Ser Ser
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Ser Ala Asn Glu Cys Ile Ser Val Lys Gly Arg Ile Tyr Ser Ile Leu
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545 550 555 560
Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn Glu Ile Ala Tyr Leu Asn
 565 570 575
Lys Leu Gln Gln His Ser Asp Lys Ile Ile Arg Leu Tyr Asp Tyr Glu
 580 585 590
Ile Thr Asp Gln Tyr Ile Tyr Met Val Met Glu Cys Gly Asn Ile Asp
 595 600 605
Leu Asn Ser Trp Leu Lys Lys Lys Lys Ser Ile Asp Pro Trp Glu Arg
 610 615 620
Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala Val His Thr Ile His Gln
625 630 635 640
His Gly Ile Val His Ser Asp Leu Lys Pro Ala Asn Phe Leu Ile Val
 645 650 655
Asp Gly Met Leu Lys Leu Ile Asp Phe Gly Ile Ala Asn Gln Met Gln
 660 665 670
Pro Asp Thr Thr Ser Val Val Lys Asp Ser Gln Val Gly Thr Val Asn
 675 680 685
Tyr Met Pro Pro Glu Ala Ile Lys Asp Met Ser Ser Ser Arg Glu Asn
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Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys Ser Asp Val Trp Ser Leu
705 710 715 720
Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly Lys Thr Pro Phe Gln Gln
 725 730 735
Ile Ile Asn Gln Ile Ser Lys Leu His Ala Ile Ile Asp Pro Asn His
 740 745 750

Glu Ile Glu Phe Pro Asp Ile Pro Glu Lys Asp Leu Gln Asp Val Leu

755

760

765

Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile Ser Ile Pro Glu

770

775

780

Leu Leu Ala His Pro Tyr Val Gln Ile Gln Thr His Pro Val Asn Gln

785

790

795

800

Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val Leu Gly Gln Leu

805

810

815

Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys Ala Ala Lys Thr Leu

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Gly Glu Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp	
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Val His Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu	
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Lys Thr Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu	
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Leu Gln Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser	
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Leu Glu Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser	
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Ser Ile Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met	
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24/861

Tyr Tyr Arg Ser Tyr Val Gly Arg Leu Met Lys Val Gln Tyr Glu Glu
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 Glu Leu Lys Lys His Lys Pro Asn Phe
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 Arg His Tyr Ser Lys Gln Val Glu Leu Glu Leu Gln Gln Ile Glu Gln
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 Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser Glu Asn Ile Ala Ser Leu
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His Asn Gln Ile Thr Ala Cys Asp Ala Val Leu Glu Arg Met Glu Gln
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Arg Thr Leu Gln Glu Gln Ser Gly Ala Met Asn Ile Arg Leu Arg Asn
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Val Pro Ser Ala Leu Val Thr Ala Ile Leu Glu Ala Pro Val Thr Glu
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Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu Asp Ala Lys Ala Ala Ala
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Val Arg Glu Gln Glu Ala Met Gly Thr Ala Ala Cys Ala Asp Val Arg
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Gly Val Leu Asp Arg Leu Arg Val Lys Ala Val Thr Lys Ile Arg Glu
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Gln Ile Pro Gln Ala Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe
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275 280 285
Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Val
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Gly Arg Leu Met Lys Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp
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	450		455		460										
Leu	Asp	Arg	Tyr	Trp	Glu	Gln	Val	Leu	Ala	Leu	Leu	Trp	Pro	Arg	Phe
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Glu	Leu	Ile	Leu	Glu	Met	Asn	Val	Gln	Ser	Val	Arg	Ser	Thr	Asp	Pro
	485		490		495										
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Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met
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Glu Arg Ala Ala Asp Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu
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tgaggctgcg ggga atg gcc gcc gct gcg acc atg gcg gct gcg gcc cgg 170
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gaa ctg gtg ttg cgg gct ggg acc tca gat atg gag gag gaa gag ggc 218
Glu Leu Val Leu Arg Ala Gly Thr Ser Asp Met Glu Glu Glu Glu Gly
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ccg ctg gcg ggt ggt cct ggg ctc cag gaa cca ctg caa ctt ggg gag 266
Pro Leu Ala Gly Gly Pro Gly Leu Gln Glu Pro Leu Gln Leu Gly Glu
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Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp Val His
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Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu Lys Thr
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ggg gta gat ctc cgt cac tat tca aag caa gtt gag ctg gag cta cag 410
Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu Leu Gln
              80              85              90
cag att gaa cag aaa tcc att cgg gat tat att caa gag agt gag aat 458
Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser Glu Asn

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Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser Ser Ile			
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Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met Asn Ile			
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Arg Leu Arg Asn Arg Gln Ala Val Arg Gly Lys Leu Gly Glu Leu Val			
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Asp Gly Leu Val Val Pro Ser Ala Leu Val Thr Ala Ile Leu Glu Ala			
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Pro Val Thr Glu Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu Asp Ala			
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Lys Ala Ala Ala Val Arg Glu Gln Glu Ala Arg Gly Thr Ala Ala Cys			
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gca gat gtc aga ggc gtg ctc gat cgg ctc cgg gtc aag gca gtg acg			842
Ala Asp Val Arg Gly Val Leu Asp Arg Leu Arg Val Lys Ala Val Thr			
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Phe Tyr Gln Phe Leu Leu Gly Asn Glu Arg Ala Thr Ala Lys Glu Ile			
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Arg Asp Glu Tyr Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser Tyr Tyr			
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Thr Arg Gly Ser Val Ile Ser Pro Thr Glu Leu Glu Ala Pro Ile Leu			
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Val Pro His Thr Ala Gln Arg Gly Glu Gln Arg Tyr Pro Phe Glu Ala			
365	370	375	380
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Leu Phe Arg Ser Gln His Tyr Ala Leu Leu Asp Asn Ser Cys Arg Glu			

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Tyr Leu Phe Ile Cys Glu Phe Phe Val Val Ser Gly Pro Ala Ala His			
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Asp Leu Phe His Ala Val Met Gly Arg Thr Leu Ser Met Thr Leu Lys			
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His Leu Asp Ser Tyr Leu Ala Asp Cys Tyr Asp Ala Ile Ala Val Phe			
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ctc tgt atc cac att gtt ctc cgg ttc cgt aac att gca gca aag agg			1514
Leu Cys Ile His Ile Val Leu Arg Phe Arg Asn Ile Ala Ala Lys Arg			
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gat gtt cct gcc ctg gac agg tac tgg gaa cag gtg ctt gcc ttg cta			1562
Asp Val Pro Ala Leu Asp Arg Tyr Trp Glu Gln Val Leu Ala Leu Leu			
465	470	475	
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Trp Pro Arg Phe Glu Leu Ile Leu Glu Met Asn Val Gln Ser Val Arg			
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Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro His Tyr			
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Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser Ala Leu Val Ser Ile Asn			
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Gln Thr Ile Pro Asn Glu Arg Thr Met Gln Leu Leu Gly Gln Leu Gln			

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Glu Leu Ile Leu Glu Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro			
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Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg			
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660

665

670

Ile Ile Gln Gly Ala Leu Thr Gln Leu Ile Gln Leu Tyr His Arg Phe

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680

685

His Arg Val Leu Ser Gln Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala

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Pro Asn Phe

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15

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Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
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Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
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Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
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tat gaa gat gtg gag cac aag gtg aca aca gta ttt gga caa cct ctt 402
Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
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Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
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Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
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aaa agc ctt agg ata ttg ctg ttg tcc cag gac aga aac cat aac agt 546
Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
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Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
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 Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
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 Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
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375	380
385	390
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Thr	Arg	Lys	Tyr	Thr	Arg	Gln	Ile	Leu	Glu	Gly	Met	Ser	Tyr	Leu	His		
				490					495					500			
agc	aac	atg	att	gtt	cac	cgg	gac	att	aag	gga	gcc	aac	atc	ctc	cga	1650	
Ser	Asn	Met	Ile	Val	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	Arg		
			505					510						515			
gac	tct	gct	ggg	aat	gta	aag	ctg	ggg	gac	ttt	ggg	gcc	agc	aaa	cgc	1698	
Asp	Ser	Ala	Gly	Asn	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ala	Ser	Lys	Arg		
			520					525						530			
ctg	cag	acg	atc	tgt	atg	tcg	ggg	acg	ggc	atg	cgc	tcc	gtc	act	ggc	1746	
Leu	Gln	Thr	Ile	Cys	Met	Ser	Gly	Thr	Gly	Met	Arg	Ser	Val	Thr	Gly		
535					540					545				550			
act	ccc	tac	tgg	atg	agc	cct	gag	gtg	atc	agc	ggc	gag	ggc	tat	gga	1794	
Thr	Pro	Tyr	Trp	Met	Ser	Pro	Glu	Val	Ile	Ser	Gly	Glu	Gly	Tyr	Gly		
					555					560				565			
agg	aaa	gca	gac	gtg	tgg	agc	ctg	ggc	tgc	act	gtg	gtg	gag	atg	ctg	1842	
Arg	Lys	Ala	Asp	Val	Trp	Ser	Leu	Gly	Cys	Thr	Val	Val	Glu	Met	Leu		
				570					575					580			
aca	gag	aaa	cca	ccg	tgg	gca	gag	tat	gaa	gct	atg	gcc	gcc	atc	ttc	1890	
Thr	Glu	Lys	Pro	Pro	Trp	Ala	Glu	Tyr	Glu	Ala	Met	Ala	Ala	Ile	Phe		
				585					590					595			
aag	att	gcc	acc	cag	ccc	acc	aat	cct	cag	ctg	ccc	tcc	cac	atc	tct	1938	

Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser
 600 605 610
 gaa cat ggc cgg gac ttc ctg agg cgc att ttt gtg gag gct cgc cag 1986
 Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln
 615 620 625 630
 aga cct tca gct gag gag ctg ctc aca cac cac ttt gca cag ctc atg 2034
 Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met
 635 640 645
 tac tgagctctca cgccacaca gctgccggtc gccctttgct gcatggcagg 2087
 Tyr
 gggctgctgc tgggctcagt gaagttgctg cttctcccag gcaaggctgt ggaccatgga 2147
 gtggcagccc agccagcgtc ggtctgtgcc cttccgcca ctggggctca gagccggggt 2207
 ggggtggctg cagcctcagg actgggagcc ccagcctgt cagatccagg agctccagtg 2267
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 agagcccag gaggtgtctc aggctgcctg agtcgtgacc tgctaggcca gagcccactc 3047
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<211> 647

<212> PRT

<213> Homo sapiens

<400> 10

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				20				25					30		
Lys	Lys	His	Asn	Ser	Ser	Ser	Ser	Ala	Leu	Leu	Asn	Ser	Pro	Thr	Val
		35					40					45			
Thr	Thr	Ser	Ser	Cys	Ala	Gly	Ala	Ser	Glu	Lys	Lys	Lys	Phe	Leu	Ser
		50					55					60			
Asp	Val	Arg	Ile	Lys	Phe	Glu	His	Asn	Gly	Glu	Arg	Arg	Ile	Ile	Ala
	65				70					75				80	
Phe	Ser	Arg	Pro	Val	Lys	Tyr	Glu	Asp	Val	Glu	His	Lys	Val	Thr	Thr
				85						90				95	
Val	Phe	Gly	Gln	Pro	Leu	Asp	Leu	His	Tyr	Met	Asn	Asn	Glu	Leu	Ser
			100						105					110	
Ile	Leu	Leu	Lys	Asn	Gln	Asp	Asp	Leu	Asp	Lys	Ala	Ile	Asp	Ile	Leu
			115					120						125	

Asp Arg Ser Ser Ser Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln
 130 135 140
 Asp Arg Asn His Asn Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln
 145 150 155 160
 Val Arg Ile Lys Ala Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr
 165 170 175
 Gln Pro Pro Glu Pro Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn
 180 185 190
 Pro Gly Arg Ser Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln
 195 200 205
 His Ile Ala Arg Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu
 210 215 220
 Phe Ile Pro Glu Thr Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser
 225 230 235 240

 Ala Glu Asn Ser Leu Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala
 245 250 255
 Asp Ser Pro Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe
 260 265 270
 Pro Asp Asn Arg Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp
 275 280 285
 Lys Gly Val Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val
 290 295 300
 His His Lys Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg
 305 310 315 320
 Arg His Gln Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu
 325 330 335

Ser Thr Asn Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro
340 345 350

Arg Gly Arg Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln
355 360 365

Glu Arg Asn Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg
370 375 380

Arg Gly Lys Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys
385 390 395 400

Tyr Asp Val Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe
405 410 415

Asp Pro Asp Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys
420 425 430

Glu Ile Gln Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr
435 440 445

Tyr Gly Cys Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met
450 455 460

Glu Tyr Met Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly
465 470 475 480

Ala Leu Thr Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu
485 490 495

Gly Met Ser Tyr Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys
500 505 510

Gly Ala Asn Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp
515 520 525

Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly
530 535 540

Met Arg Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile

545 550 555 560
 Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys
 565 570 575
 Thr Val Val Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu
 580 585 590
 Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln
 595 600 605
 Leu Pro Ser His Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile
 610 615 620
 Phe Val Glu Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His
 625 630 635 640
 His Phe Ala Gln Leu Met Tyr
 645

<210> 11

<211> 3352

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (2037)

<400> 11

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 Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu
 1 5 10
 gtg gcc ctc cag atg aac cga cgt cac cgg atg cct gga tat gag acc 156

Val	Ala	Leu	Gln	Met	Asn	Arg	Arg	His	Arg	Met	Pro	Gly	Tyr	Glu	Thr				
15					20					25					30				
atg	aag	aac	aaa	gac	aca	ggt	cac	tca	aat	agg	cag	aaa	aaa	cac	aac	204			
Met	Lys	Asn	Lys	Asp	Thr	Gly	His	Ser	Asn	Arg	Gln	Lys	Lys	His	Asn				
				35					40					45					
agc	agc	agc	tca	gcc	ctt	ctg	aac	agc	ccc	aca	gta	aca	aca	agc	tca	252			
Ser	Ser	Ser	Ser	Ala	Leu	Leu	Asn	Ser	Pro	Thr	Val	Thr	Thr	Ser	Ser				
				50					55					60					
tgt	gca	ggg	gcc	agt	gag	aaa	aag	aaa	ttt	ttg	agt	gac	gtc	aga	atc	300			
Cys	Ala	Gly	Ala	Ser	Glu	Lys	Lys	Lys	Phe	Leu	Ser	Asp	Val	Arg	Ile				
		65						70					75						
aag	ttc	gag	cac	aac	ggg	gag	agg	cga	att	ata	gcg	ttc	agc	cgg	cct	348			
Lys	Phe	Glu	His	Asn	Gly	Glu	Arg	Arg	Ile	Ile	Ala	Phe	Ser	Arg	Pro				
		80					85				90								
gtg	aaa	tat	gaa	gat	gtg	gag	cac	aag	gtg	aca	aca	gta	ttt	gga	caa	396			
Val	Lys	Tyr	Glu	Asp	Val	Glu	His	Lys	Val	Thr	Thr	Val	Phe	Gly	Gln				
		95					100				105				110				
cct	ctt	gat	cta	cat	tac	atg	aac	aat	gag	ctc	tcc	atc	ctg	ctg	aaa	444			
Pro	Leu	Asp	Leu	His	Tyr	Met	Asn	Asn	Glu	Leu	Ser	Ile	Leu	Leu	Lys				
				115						120				125					
aac	caa	gat	gat	ctt	gat	aaa	gca	att	gac	att	tta	gat	aga	agc	tca	492			
Asn	Gln	Asp	Asp	Leu	Asp	Lys	Ala	Ile	Asp	Ile	Leu	Asp	Arg	Ser	Ser				
				130					135				140						
agc	atg	aaa	agc	ctt	agg	ata	ttg	ctg	ttg	tcc	cag	gac	aga	aac	cat	540			
Ser	Met	Lys	Ser	Leu	Arg	Ile	Leu	Leu	Leu	Ser	Gln	Asp	Arg	Asn	His				
		145						150				155							
aac	agt	tcc	tct	ccc	cac	tct	ggg	gtg	tcc	aga	cag	gtg	cgg	atc	aag	588			

Asn Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys
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 Ala Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu
 175 180 185 190
 ccc aga agc agg cac ctc tct gtc agc tcc cag aac cct ggc cga agc 684
 Pro Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser
 195 200 205
 tca cct ccc cct ggc tat gtt cct gag cgg cag cag cac att gcc cgg 732
 Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg
 210 215 220
 cag ggg tcc tac acc agc atc aac agt gag ggg gag ttc atc cca gag 780
 Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu
 225 230 235
 acc agc gag cag tgc atg ctg gat ccc ctg agc agt gca gaa aat tcc 828
 Thr Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser
 240 245 250
 ttg tct gga agc tgc caa tcc ttg gac agg tca gca gac agc cca tcc 876
 Leu Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser
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 Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg
 275 280 285
 cag gaa tac tca gat cgg gaa act cag ctt tat gac aaa ggg gtc aaa 972
 Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys
 290 295 300
 ggt gga acc tac ccc cgg cgc tac cac gtg tct gtg cac cac aag gac 1020

Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp	
305	310
315	
tac agt gat ggc aga aga aca ttt ccc cga ata cgg cgt cat caa ggc	1068
Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly	
320	325
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aac ttg ttc acc ctg gtg ccc tcc agc cgc tcc ctg agc aca aat ggc	1116
Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly	
335	340
345	350
gag aac atg ggt ctg gct gtg caa tac ctg gac ccc cgt ggg cgc ctg	1164
Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu	
355	360
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cgg agt gcg gac agc gag aat gcc ctc tct gtg cag gag agg aat gtg	1212
Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val	
370	375
380	
cca acc aag tct ccc agt gcc ccc atc aac tgg cgc cgg gga aag ctc	1260
Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu	
385	390
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ctg ggc cag ggt gcc ttc ggc agg gtc tat ttg tgc tat gac gtg gac	1308
Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp	
400	405
410	
acg gga cgt gaa ctt gct tcc aag cag gtc caa ttt gat cca gac agt	1356
Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser	
415	420
425	430
cct gag aca agc aag gag gtg agt gct ctg gag tgc gag atc cag ttg	1404
Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu	
435	440
445	
cta aag aac ttg cag cat gag cgc atc gtg cag tac tat ggc tgt ctg	1452

Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu
 450 455 460
 cgg gac cgc gct gag aag acc ctg acc atc ttc atg gag tac atg cca 1500
 Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro
 465 470 475
 ggg ggc tcg gtg aaa gac cag ttg aag gct tac ggt gct ctg aca gag 1548
 Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu
 480 485 490
 agc gtg acc cga aag tac acg cgg cag atc ctg gag ggc atg tcc tac 1596
 Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr
 495 500 505 510
 ctg cac agc aac atg att gtt cac cgg gac att aag gga gcc aac atc 1644
 Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile
 515 520 525
 ctc cga gac tct gct ggg aat gta aag ctg ggg gac ttt ggg gcc agc 1692
 Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser
 530 535 540
 aaa cgc ctg cag acg atc tgt atg tcg ggg acg ggc atg cgc tcc gtc 1740
 Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val
 545 550 555
 act ggc act ccc tac tgg atg agc cct gag gtg atc agc ggc gag ggc 1788
 Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly
 560 565 570
 tat gga agg aaa gca gac gtg tgg agc ctg ggc tgc act gtg gtg gag 1836
 Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu
 575 580 585 590
 atg ctg aca gag aaa cca ccg tgg gca gag tat gaa gct atg gcc gcc 1884

Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala
595 600 605
atc ttc aag att gcc acc cag ccc acc aat cct cag ctg ccc tcc cac 1932
Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His
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Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala
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Leu Met Tyr
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<212> PRT

<213> Homo sapiens

<400> 12

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			20					25					30		
Asn	Lys	Asp	Thr	Gly	His	Ser	Asn	Arg	Gln	Lys	Lys	His	Asn	Ser	Ser
		35					40					45			
Ser	Ser	Ala	Leu	Leu	Asn	Ser	Pro	Thr	Val	Thr	Thr	Ser	Ser	Cys	Ala
	50				55					60					
Gly	Ala	Ser	Glu	Lys	Lys	Lys	Phe	Leu	Ser	Asp	Val	Arg	Ile	Lys	Phe
65				70					75					80	
Glu	His	Asn	Gly	Glu	Arg	Arg	Ile	Ile	Ala	Phe	Ser	Arg	Pro	Val	Lys
			85					90						95	

Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
 100 105 110
 Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
 115 120 125
 Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
 130 135 140
 Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
 145 150 155 160
 Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
 165 170 175
 Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
 180 185 190
 Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
 195 200 205
 Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
 210 215 220
 Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
 225 230 235 240
 Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
 245 250 255
 Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
 260 265 270
 Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
 275 280 285
 Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
 290 295 300
 Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser

305	310	315	320
Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu			
	325	330	335
Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn			
	340	345	350
Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser			
	355	360	365
Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr			
	370	375	380
Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly			
385	390	395	400
Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly			
	405	410	415
Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu			
	420	425	430
Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys			
	435	440	445
Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp			
	450	455	460
Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly			
465	470	475	480
Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val			
	485	490	495
Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His			
	500	505	510
Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg			
	515	520	525

Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg
530 535 540
Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly
545 550 555 560
Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly
565 570 575
Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu
580 585 590
Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe
595 600 605
Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser
610 615 620
Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln
625 630 635 640
Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met
645 650 655
Tyr

<210> 13

<211> 2447

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (9).. (1802)

<400> 13

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cgg gga gct ggc ctc tgc ttc act ttc gtc tct gct caa caa aac agt 98
Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser Ala Gln Gln Asn Ser
15 20 25 30
cct tct tct acg ggt tct ggc aat aca gaa cat tct tgc agc tcc caa 146
Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln
35 40 45
aaa cag atc tcc atc cag cac aga cag acc cag tct gac ctc aca ata 194
Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile
50 55 60
gaa aaa ata tct gca cta gaa aac agt aag aac tct gac tta gag aag 242
Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys
65 70 75
aag gaa gga aga ata gat gat tta tta aga gcc aac tgt gat ttg aga 290
Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg
80 85 90
cga cag ata gat gaa cag caa aag atg cta gag aaa tac aag gaa cga 338
Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg
95 100 105 110
tta aat aga tgt gtc acc atg agc aag aag ctc ctt ata gaa aag tca 386
Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser
115 120 125
aaa caa gag aag atg gcg tgc aga gat aag agc atg cag gac cgg ttg 434
Lys Gln Glu Lys Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu
130 135 140
cga tta ggc cac ttt act act gtc cgg cat gga gcc tcg ttt act gag 482

Arg Leu Gly His Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu
 145 150 155
 cag tgg aca gat ggt tat gct ttc caa aac ctc atc aag caa cag gaa 530
 Gln Trp Thr Asp Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu
 160 165 170
 agg ata aat tca cag aga gaa gag ata gaa agg caa cgg aaa atg tta 578
 Arg Ile Asn Ser Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu
 175 180 185 190
 gca aaa cgg aaa cct cct gcc atg ggt cag gcc cct cct gca acc aat 626
 Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn
 195 200 205
 gag cag aaa caa cgg aaa agc aag act aat gga gct gaa aat gaa acg 674
 Glu Gln Lys Gln Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr
 210 215 220
 tta acg tta gcc gag tac cat gaa caa gag gaa atc ttc aaa ctt aga 722
 Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg
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 Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu
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 Arg Leu Glu Arg Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile
 255 260 265 270
 cat aat gaa gac aat tcg cag ttt aaa gac cat cca aca cta aat gac 866
 His Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp
 275 280 285
 aga tat ttg ttg tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt 914

Arg Tyr Leu Leu Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val
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 Tyr Lys Ala Phe Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile
 305 310 315
 cac cag tta aat aaa aac tgg aga gat gag aaa aag gag aat tac cac 1010
 His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His
 320 325 330
 aag cat gcg tgt agg gaa tac cgg att cac aag gag ctg gac cac ccc 1058
 Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro
 335 340 345 350
 agg ata gtg aag ctg tat gat tac ttt tca ctg gac act gac tcg ttt 1106
 Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe
 355 360 365
 tgt aca gta tta gaa tac tgt gaa ggg aat gac ctg gac ttc tac cta 1154
 Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu
 370 375 380
 aaa cag cac aaa tta atg tcg gag aaa gaa gcc cga tcc att att atg 1202
 Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met
 385 390 395
 cag att gtg aat gct tta aag tac tta aat gaa ata aaa cct ccc atc 1250
 Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile
 400 405 410
 ata cac tat gac ctc aaa cca ggt aat atc ctt tta gta aat ggt aca 1298
 Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr
 415 420 425 430
 gca tgt gga gag ata aaa att aca gat ttt ggt ctt tcc aag atc atg 1346

Ala Cys Gly Glu Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met	
435	440
gat gat gat agc tac aat tca gtg gat ggc atg gag ctg acg tca caa	1394
Asp Asp Asp Ser Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln	
450	455
gga gct ggt act tat tgg tat tta cca cca gag tgt ttt gtg gtt ggg	1442
Gly Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly	
465	470
aaa gag cca cca aag atc tca aat aaa gtc gat gtt tgg tca gtg ggt	1490
Lys Glu Pro Pro Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly	
480	485
gtg atc ttc tac cag tgt ctt tat ggg agg aag cct ttt ggc cat aac	1538
Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn	
495	500
cag tcc cag caa gat att cta caa gag aat act att ctt aag gct act	1586
Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr	
515	520
gaa gta cag ttc ccg cca aag cca gta gta aca cct gaa gca aag gca	1634
Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala	
530	535
ttt atc agg aga tgt ctg gcc tat cga aag gaa gat cgc att gat gtg	1682
Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val	
545	550
cag cag ctg gcc tgt gac ccc tac ttg ttg cct cac atc cga aag tca	1730
Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser	
560	565
gtc tcc aca agt agc cct gca gga gct gct att gca tca acc tct ggg	1778

35	40	45
Ile Ser Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys		
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Ile Ser Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu		
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Gly Arg Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln		
85	90	95
Ile Asp Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn		
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Arg Cys Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln		
115	120	125
Glu Lys Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu		
130	135	140
Gly His Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp		
145	150	155
Thr Asp Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile		
165	170	175
Asn Ser Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys		
180	185	190
Arg Lys Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln		
195	200	205
Lys Gln Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr		
210	215	220
Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg Leu Gly		
225	230	235
His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu		
245	250	255

Glu Arg Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile His Asn
 260 265 270
 Glu Asp Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr
 275 280 285
 Leu Leu Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys
 290 295 300
 Ala Phe Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln
 305 310 315 320
 Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His
 325 330 335
 Ala Cys Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro Arg Ile
 340 345 350
 Val Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr
 355 360 365
 Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln
 370 375 380
 His Lys Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile
 385 390 395 400
 Val Asn Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His
 405 410 415
 Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys
 420 425 430
 Gly Glu Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp
 435 440 445
 Asp Ser Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala
 450 455 460
 Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu

465 470 475 480
Pro Pro Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile
 485 490 495
Phe Tyr Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser
 500 505 510
Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val
 515 520 525
Gln Phe Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile
 530 535 540
Arg Arg Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln
545 550 555 560
Leu Ala Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser
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Thr Ser Ser Pro Ala Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser
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<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (2393)

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 cggcggcggc ggcggcagca gaaatg atg gaa gaa ttg cat agc ctg gac cca 173

Met Glu Glu Leu His Ser Leu Asp Pro

1

5

cga cgg cag gaa tta ttg gag gcc agg ttt act gga gta ggt gtt agt 221
 Arg Arg Gln Glu Leu Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser

10

15

20

25

aag gga cca ctt aat agt gag tct tcc aac cag agc ttg tgc agc gtc 269
 Lys Gly Pro Leu Asn Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val

30

35

40

gga tcc ttg agt gat aaa gaa gta gag act ccc gag aaa aag cag aat 317
 Gly Ser Leu Ser Asp Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn

45

50

55

gac cag cga aat cgg aaa aga aaa gct gaa cca tat gaa act agc caa 365
 Asp Gln Arg Asn Arg Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln

60

65

70

ggg aaa ggc act cct agg gga cat aaa att agt gat tac ttt gag ttt 413
 Gly Lys Gly Thr Pro Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Phe

75

80

85

gct ggg gga agc gcg cca gga acc agc cct ggc aga agt gtt cca cca 461
 Ala Gly Gly Ser Ala Pro Gly Thr Ser Pro Gly Arg Ser Val Pro Pro

90

95

100

105

gtt gca cga tcc tca ccg caa cat tcc tta tcc aat ccc tta ccg cga 509
 Val Ala Arg Ser Ser Pro Gln His Ser Leu Ser Asn Pro Leu Pro Arg

110

115

120

cga gta gaa cag ccc ctc tat ggt tta gat ggc agt gct gca aag gag 557
 Arg Val Glu Gln Pro Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu

125	130	135	
gca acg gag gag cag tct gct ctg cca acc ctc atg tca gtg atg cta			605
Ala Thr Glu Glu Gln Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu			
140	145	150	
gca aaa cct cgg ctt gac aca gag cag ctg gcg caa agg gga gct ggc			653
Ala Lys Pro Arg Leu Asp Thr Glu Gln Leu Ala Gln Arg Gly Ala Gly			
155	160	165	
ctc tgc ttc act ttt gtt tca gct cag caa aac agt ccc tca tct acg			701
Leu Cys Phe Thr Phe Val Ser Ala Gln Gln Asn Ser Pro Ser Ser Thr			
170	175	180	185
gga tct ggc aac aca gag cat tcc tgc agc tcc caa aaa cag atc tcc			749
Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser			
190	195	200	
atc cag cac aga cag acc cag tcc gac ctc aca ata gaa aaa ata tct			797
Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser			
205	210	215	
gca cta gaa aac agt aag aat tct gac tta gag aag aag gag gga aga			845
Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg			
220	225	230	
ata gat gat tta tta aga gcc aac tgt gat ttg aga cgg cag att gat			893
Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp			
235	240	245	
gaa cag caa aag atg cta gag aaa tac aag gaa cga tta aat aga tgt			941
Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn Arg Cys			
250	255	260	265
gtg aca atg agc aag aaa ctc ctt ata gaa aag tca aaa caa gag aag			989
Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys			

270	275	280	
atg gcg tgt aga gat aag agc atg caa gac cgc ttg aga ctg ggc cac			1037
Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His			
285	290	295	
ttt act act gtc cga cac gga gcc tca ttt act gaa cag tgg aca gat			1085
Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp			
300	305	310	
ggt tat gct ttt cag aat ctt atc aag caa cag gaa agg ata aat tca			1133
Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile Asn Ser			
315	320	325	
cag agg gaa gag ata gaa aga caa cgg aaa atg tta gca aag cgg aaa			1181
Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys			
330	335	340	345
cct cct gcc atg ggt cag gcc cct cct gca acc aat gag cag aaa cag			1229
Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln			
350	355	360	
cgg aaa agc aag acc aat gga gct gaa aat gaa acg tta acg tta gca			1277
Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala			
365	370	375	
gaa tac cat gaa caa gaa gaa atc ttc aaa ctc aga tta ggt cat ctt			1325
Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg Leu Gly His Leu			
380	385	390	
aaa aag gag gaa gca gag atc cag gca gag ctg gag aga cta gaa agg			1373
Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg			
395	400	405	
gtt aga aat cta cat atc agg gaa cta aaa agg ata cat aat gaa gat			1421
Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile His Asn Glu Asp			

410	415	420	425	
aat tca caa ttt aaa gat cat cca acg cta aat gac aga tat ttg ttg				1469
Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu				
	430	435	440	
tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt tac aag gca ttt				1517
Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys Ala Phe				
	445	450	455	
gat cta aca gag caa aga tac gta gct gtg aaa att cac cag tta aat				1565
Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln Leu Asn				
	460	465	470	
aaa aac tgg aga gat gag aaa aag gag aat tac cac aag cat gca tgt				1613
Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His Ala Cys				
	475	480	485	
agg gaa tac cgg att cat aaa gag ctg gat cat ccc aga ata gtt aag				1661
Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro Arg Ile Val Lys				
490	495	500	505	
ctg tat gat tac ttt tca ctg gat act gac tcg ttt tgt aca gta tta				1709
Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr Val Leu				
	510	515	520	
gaa tac tgt gag gga aat gat ctg gac ttc tac ctg aaa cag cac aaa				1757
Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln His Lys				
	525	530	535	
tta atg tcg gag aaa gag gcc cgg tcc att atc atg cag att gtg aat				1805
Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile Val Asn				
	540	545	550	
gct tta aag tac tta aat gaa ata aaa cct ccc atc ata cac tat gac				1853
Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His Tyr Asp				

555	560	565	
ctc aaa cca ggt aat att ctt tta gta aat ggt aca gcg tgt gga gag			1901
Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys Gly Glu			
570	575	580	585
ata aaa att aca gat ttt ggt ctt tcg aag atc atg gat gat gat agc			1949
Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp Asp Ser			
	590	595	600
tac aat tca gtg gat ggc atg gag cta aca tca caa ggt gct ggt act			1997
Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala Gly Thr			
	605	610	615
tat tgg tat tta cca cca gag tgt ttt gtg gtt ggg aaa gaa cca cca			2045
Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro			
	620	625	630
aag atc tca aat aaa gtt gat gtg tgg tcg gtg ggt gtg atc ttc tat			2093
Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr			
	635	640	645
cag tgt ctt tat gga agg aag cct ttt ggc cat aac cag tct cag caa			2141
Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln			
650	655	660	665
gac atc cta caa gag aat acg att ctt aaa gct act gaa gtg cag ttc			2189
Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val Gln Phe			
	670	675	680
ccg cca aag cca gta gta aca cct gaa gca aag gcg ttt att cga cga			2237
Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg			
	685	690	695
tgc ttg gcc tac cga aag gag gac cgc att gat gtc cag cag ctg gcc			2285
Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala			

700	705	710	
tgt gat ccc tac ttg ttg cct cac atc cga aag tca gtc tct aca agt			2333
Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser			
715	720	725	
agc cct gct gga gct gct att gca tca acc tct ggg gcg tcc aat aac			2381
Ser Pro Ala Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser Asn Asn			
730	735	740	745
agt tct tct aat tgagactgac tccaaggcca caaactgttc aacacacaca			2433
Ser Ser Ser Asn			
aagtggacaa atggcggttca gcagcgggtt tggaacatag cgaatccgaa tggatctgat			2493
gaaacctgta ccaggtgctt ttattttctt gcttttttcc catccataga gcatgacagc			2553
atcgattctc attgaggaga aaccttgggc agctccggcc aggccttgta ggaaaaggcc			2613
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taaaaagaaa aactggttcc atgtactgtg aacttgaaaa cttgcagact caggggggtc			2733
cctgatgcag tgcttcagat gaagaatgtg gacttgaaaa tacagactgg gctagtccag			2793
tgtctatatt taaacttggt cttttctttt aataaagttt aggtaacatc tcctgaaaag			2853
cttgtagcac aaaggctcag ctggggatgg tgtttgactt cggaggaaaa aagttgctat			2913
tgcccgttaa aggcactaga gtagtggtt tatccctaaa taatttcaat ttttaaaac			2973
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tggtctcctg tttgcaattg cttccctcat ctgagtaggg aaaaaattga gtgggagtac			3153
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tctctctagg ttttcaacta tttcttcaca atttgaacac ttgacggttg tcccttttaa			3273
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<211> 749

<212> PRT

<213> Homo sapiens

<400> 16

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Ser Ser Asn Gln Ser Leu Cys Ser Val Gly Ser Leu Ser Asp Lys Glu
35 40 45
Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg Asn Arg Lys Arg
50 55 60
Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly Thr Pro Arg Gly
65 70 75 80
His Lys Ile Ser Asp Tyr Phe Glu Phe Ala Gly Gly Ser Ala Pro Gly
85 90 95
Thr Ser Pro Gly Arg Ser Val Pro Pro Val Ala Arg Ser Ser Pro Gln
100 105 110
His Ser Leu Ser Asn Pro Leu Pro Arg Arg Val Glu Gln Pro Leu Tyr
115 120 125
Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu Glu Gln Ser Ala
130 135 140
Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro Arg Leu Asp Thr
145 150 155 160
Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser
165 170 175
Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His
180 185 190

Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln
 195 200 205
 Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn
 210 215 220
 Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala
 225 230 235 240
 Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu
 245 250 255
 Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu
 260 265 270
 Leu Ile Glu Lys Ser Lys Gln Glu Lys Met Ala Cys Arg Asp Lys Ser
 275 280 285
 Met Gln Asp Arg Leu Arg Leu Gly His Phe Thr Thr Val Arg His Gly
 290 295 300
 Ala Ser Phe Thr Glu Gln Trp Thr Asp Gly Tyr Ala Phe Gln Asn Leu
 305 310 315 320
 Ile Lys Gln Gln Glu Arg Ile Asn Ser Gln Arg Glu Glu Ile Glu Arg
 325 330 335
 Gln Arg Lys Met Leu Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Ala
 340 345 350
 Pro Pro Ala Thr Asn Glu Gln Lys Gln Arg Lys Ser Lys Thr Asn Gly
 355 360 365
 Ala Glu Asn Glu Thr Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu
 370 375 380
 Ile Phe Lys Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile
 385 390 395 400
 Gln Ala Glu Leu Glu Arg Leu Glu Arg Val Arg Asn Leu His Ile Arg

405	410	415
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Pro Thr Leu Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Gly Arg Gly		
435	440	445
Gly Phe Ser Glu Val Tyr Lys Ala Phe Asp Leu Thr Glu Gln Arg Tyr		
450	455	460
Val Ala Val Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys		
465	470	475
480		
Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys		
485	490	495
Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu		
500	505	510
Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp		
515	520	525
Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala		
530	535	540
Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu		
545	550	555
560		
Ile Lys Pro Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu		
565	570	575
Leu Val Asn Gly Thr Ala Cys Gly Glu Ile Lys Ile Thr Asp Phe Gly		
580	585	590
Leu Ser Lys Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Asp Gly Met		
595	600	605
Glu Leu Thr Ser Gln Gly Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu		
610	615	620

Cys Phe Val Val Gly Lys Glu Pro Pro Lys Ile Ser Asn Lys Val Asp
 625 630 635 640
 Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys
 645 650 655
 Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr
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 Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr
 675 680 685
 Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu
 690 695 700
 Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro
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<220>

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<222> (147).. (2297)

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cggcggcggc ggccggcagca gaaatg atg gaa gaa ttg cat agc ctg gac cca 173
 Met Glu Glu Leu His Ser Leu Asp Pro
 1 5
 cga cgg cag gaa tta ttg gag gcc agg ttt act gga gta ggt gtt agt 221
 Arg Arg Gln Glu Leu Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser
 10 15 20 25
 aag gga cca ctt aat agt gag tct tcc aac cag agc ttg tgc agc gtc 269
 Lys Gly Pro Leu Asn Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val
 30 35 40
 gga tcc ttg agt gat aaa gaa gta gag act ccc gag aaa aag cag aat 317
 Gly Ser Leu Ser Asp Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn
 45 50 55
 gac cag cga aat cgg aaa aga aaa gct gaa cca tat gaa act agc caa 365
 Asp Gln Arg Asn Arg Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln
 60 65 70
 ggg aaa ggc act cct agg gga cat aaa att agt gat tac ttt gag cga 413
 Gly Lys Gly Thr Pro Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Arg
 75 80 85
 cga gta gaa cag ccc ctc tat ggt tta gat ggc agt gct gca aag gag 461
 Arg Val Glu Gln Pro Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu
 90 95 100 105
 gca acg gag gag cag tct gct ctg cca acc ctc atg tca gtg atg cta 509
 Ala Thr Glu Glu Gln Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu
 110 115 120
 gca aaa cct cgg ctt gac aca gag cag ctg gcg caa agg gga gct ggc 557
 Ala Lys Pro Arg Leu Asp Thr Glu Gln Leu Ala Gln Arg Gly Ala Gly
 125 130 135

ctc tgc ttc act ttt gtt tca gct cag caa aac agt ccc tca tct acg 605
 Leu Cys Phe Thr Phe Val Ser Ala Gln Gln Asn Ser Pro Ser Ser Thr
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 gga tct ggc aac aca gag cat tcc tgc agc tcc caa aaa cag atc tcc 653
 Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser
 155 160 165
 atc cag cac aga cag acc cag tcc gac ctc aca ata gaa aaa ata tct 701
 Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser
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 Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg
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 Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp
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 gaa cag caa aag atg cta gag aaa tac aag gaa cga tta aat aga tgt 845
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 Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys
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 Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His
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 Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp
 270 275 280

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 Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile Asn Ser
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 cag agg gaa gag ata gaa aga caa cgg aaa atg tta gca aag cgg aaa 1085
 Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys
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 Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln
 315 320 325
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 Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala
 330 335 340 345
 gaa tac cat gaa caa gaa gaa atc ttc aaa ctc aga tta ggt cat ctt 1229
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 aaa aag gag gaa gca gag atc cag gca gag ctg gag aga cta gaa agg 1277
 Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg
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 380 385 390
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 Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu
 395 400 405
 tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt tac aag gca ttt 1421
 Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys Ala Phe
 410 415 420 425

gat cta aca gag caa aga tac gta gct gtg aaa att cac cag tta aat 1469
Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln Leu Asn
430 435 440
aaa aac tgg aga gat gag aaa aag gag aat tac cac aag cat gca tgt 1517
Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His Ala Cys
445 450 455
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Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro Arg Ile Val Lys
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Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr Val Leu
475 480 485
gaa tac tgt gag gga aat gat ctg gac ttc tac ctg aaa cag cac aaa 1661
Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln His Lys
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Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile Val Asn
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gct tta aag tac tta aat gaa ata aaa cct ccc atc ata cac tat gac 1757
Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His Tyr Asp
525 530 535
ctc aaa cca ggt aat att ctt tta gta aat ggt aca gcg tgt gga gag 1805
Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys Gly Glu
540 545 550
ata aaa att aca gat ttt ggt ctt tcg aag atc atg gat gat gat agc 1853
Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp Asp Ser
555 560 565

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Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala Gly Thr	
570 575 580 585	
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Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro	
590 595 600	
aag atc tca aat aaa gtt gat gtg tgg tcg gtg ggt gtg atc ttc tat	1997
Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr	
605 610 615	
cag tgt ctt tat gga agg aag cct ttt ggc cat aac cag tct cag caa	2045
Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln	
620 625 630	
gac atc cta caa gag aat acg att ctt aaa gct act gaa gtg cag ttc	2093
Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val Gln Phe	
635 640 645	
ccg cca aag cca gta gta aca cct gaa gca aag gcg ttt att cga cga	2141
Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg	
650 655 660 665	
tgc ttg gcc tac cga aag gag gac cgc att gat gtc cag cag ctg gcc	2189
Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala	
670 675 680	
tgt gat ccc tac ttg ttg cct cac atc cga aag tca gtc tct aca agt	2237
Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser	
685 690 695	
agc cct gct gga gct gct att gca tca acc tct ggg gcg tcc aat aac	2285
Ser Pro Ala Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser Asn Asn	

700

705

710

agt tct tct aat tgagactgac tccaaggcca caaactgttc aacacacaca 2337

Ser Ser Ser Asn

715

aagtggacaa atggcggttca gcagcgggtt tggaacatag cgaatccgaa tggatctgat 2397

gaaacctgta ccaggtgctt ttattttctt gcttttttcc catccataga gcatgacagc 2457

atcgattctc attgaggaga aaccttgggc agctccggcc aggccttgta ggaaaaggcc 2517

ccgcccagg ttccagcgtc aacggccact gtgtgtggct gctctgagtg aggaaaaaat 2577

taaaaagaaa aactggttcc atgtactgtg aacttgaaaa cttgcagact caggggggtc 2637

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<212> PRT

<213> Homo sapiens

<400> 18

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Ser Ser Asn Gln Ser Leu Cys Ser Val Gly Ser Leu Ser Asp Lys Glu
35 40 45
Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg Asn Arg Lys Arg
50 55 60
Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly Thr Pro Arg Gly
65 70 75 80
His Lys Ile Ser Asp Tyr Phe Glu Arg Arg Val Glu Gln Pro Leu Tyr
85 90 95
Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu Glu Gln Ser Ala
100 105 110
Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro Arg Leu Asp Thr
115 120 125
Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser
130 135 140
Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His
145 150 155 160
Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln
165 170 175
Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn
180 185 190
Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala
195 200 205
Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu
210 215 220
Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu

85/861

Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys
450 455 460
Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu
465 470 475 480
Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp
485 490 495
Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala
500 505 510
Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu
515 520 525
Ile Lys Pro Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu
530 535 540
Leu Val Asn Gly Thr Ala Cys Gly Glu Ile Lys Ile Thr Asp Phe Gly
545 550 555 560
Leu Ser Lys Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Asp Gly Met
565 570 575
Glu Leu Thr Ser Gln Gly Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu
580 585 590
Cys Phe Val Val Gly Lys Glu Pro Pro Lys Ile Ser Asn Lys Val Asp
595 600 605
Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys
610 615 620
Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr
625 630 635 640
Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr
645 650 655
Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu

660	665	670
Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro		
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His Ile Arg Lys Ser Val Ser Thr Ser Ser Pro Ala Gly Ala Ala Ile		
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Ala Ser Thr Ser Gly Ala Ser Asn Asn Ser Ser Ser Asn		
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<213> Mus musculus

<220>

<221> CDS

<222> (220).. (627)

<400> 19

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ctcccgtgtg cagcggcggc agcaggcggc cgccaggctc gcggtcggag acgtcacagc 180
ccggtgcggg gcaccggtgg ccggtgttaa gcaggcgcg atg tta ttc tcg ctg    234
                                     Met Leu Phe Ser Leu
                                     1           5
cgg gag ctg gtg cag tgg ctg agc ttc gcc acc ttt gag ata ttc gtg    282
Arg Glu Leu Val Gln Trp Leu Ser Phe Ala Thr Phe Glu Ile Phe Val
          10           15           20
cac ctg ctg gcc ctg ttg gtg ttc tcc gta ctg ttg gca ctg cga gtg    330
His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu Ala Leu Arg Val

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Asp Gly Leu Thr Pro Gly Leu Ser Trp Trp Asn Val Phe Val Pro Phe			
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ttc gcc gcc gac ggg ctc agt acc tac ttc acc acc atc gtt tcc gtt			426
Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr Ile Val Ser Val			
55	60	65	
cga ctc ttc caa gat ggg gag aag cga ctg gct gtg ctg cgc ctc ttc			474
Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val Leu Arg Leu Phe			
70	75	80	85
tgg gtt ctc acc gtc ctt agc ctc aag ttt gtc ttt gag atg ttg ctg			522
Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val Phe Glu Met Leu Leu			
90	95	100	
tgc cag aag cta gtg gag cag act cga gag ctc tgg ttc ggc ctg atc			570
Cys Gln Lys Leu Val Glu Gln Thr Arg Glu Leu Trp Phe Gly Leu Ile			
105	110	115	
acg tct cgc gtc ttc att ctc ctg cag ctg ctc atg atc cgg gct tgt			618
Thr Ser Pro Val Phe Ile Leu Leu Gln Leu Leu Met Ile Arg Ala Cys			
120	125	130	
cgc gtc aac tagcctcttg cagtggctgg aaatggagca ctgcgcagct			667
Arg Val Asn			
135			
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gaaatcagtg tttgcttggtg ccagttttac tgtccagttt tctttatata taagatcggt			787
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<210> 20

<211> 136

<212> PRT

<213> Mus musculus

<400> 20

Met Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Ser Phe Ala Thr

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Leu Ala Leu Arg Val Asp Gly Leu Thr Pro Gly Leu Ser Trp Trp Asn

35 40 45

Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr

50 55 60

Thr Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala

65 70 75 80

Val Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val

85 90 95

Phe Glu Met Leu Leu Cys Gln Lys Leu Val Glu Gln Thr Arg Glu Leu

100 105 110

Trp Phe Gly Leu Ile Thr Ser Pro Val Phe Ile Leu Leu Gln Leu Leu

115 120 125

Met Ile Arg Ala Cys Arg Val Asn

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<210> 21

<211> 1563

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (234).. (641)

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Met

1

ctc ttc tcg ctc cgg gag ctg gtg cag tgg cta ggc ttc gcc acc ttc 284
 Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr Phe

5

10

15

gag atc ttc gtg cac ctg ctg gcc ctg ttg gtg ttc tct gtg ctg ctg 332
 Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu

20

25

30

gca ctg cgt gtg gat ggc ctg gtc ccg ggc ctc tcc tgg tgg aac gtg 380
 Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn Val

35

40

45

ttc gtg cct ttc ttc gcc gct gac ggg ctc agc acc tac ttc acc acc 428
 Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr

50

55

60

65

atc gtg tcc gtg cgc ctc ttc cag gat gga gag aag cgg ctg gcg gtg 476
 Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val

70

75

80

ctc cgc ctt ttc tgg gta ctt acg gtc ctg agt ctc aag ttc gtc ttc 524
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Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu Trp			
100	105	110	
ttc ggc ctc att acg tcc ccg ctc ttc att ctc ctg cag ctg ctc atg			620
Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu Met			
115	120	125	
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Ile Arg Ala Cys Arg Val Asn			
130	135		
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aagcttgtga gtggcccatc tttgttggtc tacgaacttt ggtttgatgc cagtcaggtg			1511
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<210> 22

<211> 136

<212> PRT

<213> Homo sapiens

<400> 22

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Leu Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn

35 40 45

Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr

50 55 60

Thr Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala

65 70 75 80

Val Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val

85 90 95

Phe Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu

100 105 110

Trp Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu

115 120 125

Met Ile Arg Ala Cys Arg Val Asn

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<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (9)..(659)

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agc ggc ggg gag agt ggc ggc gac ggg agc ccg ggt ggc gcc gga gcg 98

Ser Gly Gly Glu Ser Gly Gly Asp Gly Ser Pro Gly Gly Ala Gly Ala

15

20

25

30

acg gcg gtg agg agc agt tgg gtg gcg gcg ctg ctg gcg acg ggc ggg 146

Thr Ala Val Arg Ser Ser Trp Val Ala Ala Leu Leu Ala Thr Gly Gly

35

40

45

gag atg ctg ctg aac gtg gcg ctg gtg gcg ctg gtg ctg ctg ggg gcc 194

Glu Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala

50

55

60

tac cgg ctg tgg gtg cgc tgg ggg cgg cgt ggt ctg tgc tgc gga ccc 242

Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Cys Ser Gly Pro

65

70

75

ggg gcg ggc gag gag agc ccg gcc gcc acg ctg ccg cgc atg aag aag 290

Gly Ala Gly Glu Glu Ser Pro Ala Ala Thr Leu Pro Arg Met Lys Lys

80

85

90

cgg gac ttc agc ctg gag cag ctg cgc cag tac gac ggg gcg cgc acg 338

Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ala Arg Thr

95

100

105

110

ccg cgc atc ctg ctc gcg gtc aat ggg aaa gtc ttc gac gtg acc aaa 386

Pro Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys

115

120

125

ggc agc aag ttc tac ggc ccc gcg ggt cca tat ggc atc ttt gct ggc 434

Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly

130

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140

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Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala

145

150

155

ctt aga gat gga tat gac gac ctc tca gat ttg aac gca gtg caa atg 530

Leu Arg Asp Gly Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met

160

165

170

gag agt gtt cga gaa tgg gaa atg cag ttt aaa gaa aaa tat gat tat 578

Glu Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr

175

180

185

190

gta ggc aga ctc cta aag cca ggg gag gag cca tca gag tac aca gat 626

Val Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp

195

200

205

gag gag gac acc aag gat cac agt aaa cag gac tgaactttgt gagcaaccaa 679

Glu Glu Asp Thr Lys Asp His Ser Lys Gln Asp

210

215

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<210> 24

<211> 217

<212> PRT

<213> Mus musculus

<400> 24

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				20					25					30	
Val	Arg	Ser	Ser	Trp	Val	Ala	Ala	Leu	Leu	Ala	Thr	Gly	Gly	Glu	Met
				35					40					45	
Leu	Leu	Asn	Val	Ala	Leu	Val	Ala	Leu	Val	Leu	Leu	Gly	Ala	Tyr	Arg
				50					55					60	
Leu	Trp	Val	Arg	Trp	Gly	Arg	Arg	Gly	Leu	Cys	Ser	Gly	Pro	Gly	Ala
				65					70					75	
Gly	Glu	Glu	Ser	Pro	Ala	Ala	Thr	Leu	Pro	Arg	Met	Lys	Lys	Arg	Asp
				85					90					95	
Phe	Ser	Leu	Glu	Gln	Leu	Arg	Gln	Tyr	Asp	Gly	Ala	Arg	Thr	Pro	Arg
				100					105					110	
Ile	Leu	Leu	Ala	Val	Asn	Gly	Lys	Val	Phe	Asp	Val	Thr	Lys	Gly	Ser
				115					120					125	
Lys	Phe	Tyr	Gly	Pro	Ala	Gly	Pro	Tyr	Gly	Ile	Phe	Ala	Gly	Arg	Asp

130 135 140
 Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg
 145 150 155 160
 Asp Gly Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser
 165 170 175
 Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly
 180 185 190
 Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu Glu
 195 200 205
 Asp Thr Lys Asp His Ser Lys Gln Asp
 210 215

<210> 25

<211> 1850

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (7).. (675)

<400> 25

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 agt ggc agc gag agc agc aac gac ggc ggc agc gag agt cca ggc gac 96
 Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp
 15 20 25 30
 gcg gga gcg gca gcg gaa ggg gga ggc tgg gcg gcg gcg gcg ttg gcg 144

Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala
 35 40 45
 ctt ctg acg ggg ggc ggg gaa atg ctg ctg aac gtg gcg ctg gtg gct 192
 Leu Leu Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala
 50 55 60
 ctg gtg ctg ctg ggg gcc tac cgg ctg tgg gtg cgc tgg ggg cgg cgg 240
 Leu Val Leu Leu Gly Ala Tyr Arg-Leu Trp Val Arg Trp Gly Arg Arg
 65 70 75
 ggt ctg ggg gcc ggg gcc ggg gcg ggc gag gag agc ccc gcc acc tct 288
 Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser
 80 85 90
 ctg cct cgc atg aag aag cgg gac ttc agc ttg gag cag ctg cgc cag 336
 Leu Pro Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln
 95 100 105 110
 tac gac ggc tcc cgc aac ccg cgc atc ctg ctc gcg gtc aat ggg aaa 384
 Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys
 115 120 125
 gtc ttc gac gtg acc aaa ggc agc aag ttc tac ggc ccg gcg ggt cca 432
 Val Phe Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro
 130 135 140
 tat gga ata ttt gct ggt agg gat gcc tcc aga gga ctg gcc aca ttt 480
 Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
 145 150 155
 tgc cta gat aaa gat gca ctt aga gat gaa tat gat gat ctc tca gat 528
 Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp
 160 165 170
 ttg aat gca gta caa atg gag agt gtt cga gaa tgg gaa atg cag ttt 576

99/861

gggtgtcagt atggatgtgt ctgaatgtgt gaggccttgg aagggactct ttctgcagat 1805
actgtaaata caagtacat ttttaataaag catgtacaat aaacc 1850

<210> 26

<211> 223

<212> PRT

<213> Homo sapiens

<400> 26

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Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu

35 40 45

Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala Leu Val

50 55 60

Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu

65 70 75 80

Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro

85 90 95

Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp

100 105 110

Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe

115 120 125

Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly

130 135 140

Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu

145 150 155 160
 Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn
 165 170 175
 Ala Val Gln Met Glu Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu
 180 185 190
 Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser
 195 200 205
 Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp His Asn Lys Gln Asp
 210 215 220

<210> 27

<211> 2156

<212> DNA

<213> Homo sapiens.

<220>

<221> CDS

<222> (241)..(981)

<400> 27

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 cggccagcga aagaagggag ggggcgggag atccgagaca acgttaccac gtcaacaccc 180
 aatcaggagc cggcctgacc ccgccccctc ttctcacgtt attggctgag aggccccag 240
 atg ggc ggg gcc ggc cgt ggg gtt ggg gag ggc agg ggg cgg gga gga 288
 Met Gly Gly Ala Gly Arg Gly Val Gly Glu Gly Arg Gly Arg Gly Gly
 1 5 10 15
 gga gga agg cgc tgg cgg gca gtg atg gcg gct ggt gat ggg gac gtg 336
 Gly Gly Arg Arg Trp Arg Ala Val Met Ala Ala Gly Asp Gly Asp Val

20	25	30	
aag cta ggc acc ctg ggg agt ggc agc gag agc agc aac gac ggc ggc			384
Lys Leu Gly Thr Leu Gly Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly			
35	40	45	
agc gag agt cca ggc gac gcg gga gcg gca gcg gaa ggg gga ggc tgg			432
Ser Glu Ser Pro Gly Asp Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp			
50	55	60	
gcg gcg gcg gcg ttg gcg ctt ctg acg ggg ggc ggg gaa atg ctg ctg			480
Ala Ala Ala Ala Leu Ala Leu Leu Thr Gly Gly Gly Glu Met Leu Leu			
65	70	75	80
aac gtg gcg ctg gtg gct ctg gtg ctg ctg ggg gcc tac cgg ctg tgg			528
Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp			
85	90	95	
gtg cgc tgg ggg cgg cgg ggt ctg ggg gcc ggg gcc ggg gcg ggc gag			576
Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu			
100	105	110	
gag agc ccc gcc acc tct ctg cct cgc atg aag aag cgg gac ttc agc			624
Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg Asp Phe Ser			
115	120	125	
ttg gag cag ctg cgc cag tac gac ggc tcc cgc aac ccg cgc atc ctg			672
Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu			
130	135	140	
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Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly Ser Lys Phe			
145	150	155	160
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Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser			

165	170	175	
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Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu			
180	185	190	
tat gat gat ctc tca gat ttg aat gca gta caa atg gag agt gtt cga			864
Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser Val Arg			
195	200	205	
gaa tgg gaa atg cag ttt aaa gaa aaa tat gat tat gta ggc aga ctc			912
Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu			
210	215	220	
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Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu Glu Asp Thr			
225	230	235	240
aag gat cac aat aaa cag gat tgaactttgt aaacaaccaa agtcaggggc			1011
Lys Asp His Asn Lys Gln Asp			
245			
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<210> 28

<211> 247

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Leu Gly Thr Leu Gly Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly

35 40 45

Ser Glu Ser Pro Gly Asp Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp

50 55 60

Ala Ala Ala Ala Leu Ala Leu Leu Thr Gly Gly Gly Glu Met Leu Leu

65 70 75 80

Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp

85 90 95

Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu
100 105 110
Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg Asp Phe Ser
115 120 125
Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu
130 135 140
Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly Ser Lys Phe
145 150 155 160
Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser
165 170 175
Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu
180 185 190
Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser Val Arg
195 200 205
Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu
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Lys Asp His Asn Lys Gln Asp
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<210> 29

<211> 2906

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (61).. (2229)

<400> 29

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Met Asp Arg Asp Asp Asn Gln Asp Gly Arg Arg Ser Lys Ser Ile Glu
      1              5              10              15
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Glu Arg Glu Glu Glu Tyr Gln Arg Val Arg Glu Arg Ile Phe Ala Arg
              20              25              30
gag acc ggc cag aat gga tat ctg aat gac atc agg gga aac cgg gaa 204
Glu Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile Arg Gly Asn Arg Glu
              35              40              45
ggg ctg agc cgt acc tca agc agc cga cag agc agc aca gac agc gag 252
Gly Leu Ser Arg Thr Ser Ser Ser Arg Gln Ser Ser Thr Asp Ser Glu
              50              55              60
ctc aag tcc ctg gag cca cgg cct tgg agc agc aca gac tca gac ggc 300
Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly
              65              70              75              80
tct gtc cgc agc atg cga cct cct gtc acc aaa gcc agc agc ttc agt 348
Ser Val Arg Ser Met Arg Pro Pro Val Thr Lys Ala Ser Ser Phe Ser
              85              90              95
gga atc tcc atc ctc acc cga ggc gac agc att ggc agc agt aaa ggc 396
Gly Ile Ser Ile Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly
              100              105              110
ggc agt gca ggc agg ctc tcc agg cca ggc atg gca cta ggt gcc cca 444
Gly Ser Ala Gly Arg Leu Ser Arg Pro Gly Met Ala Leu Gly Ala Pro
              115              120              125

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 Leu Pro Ala Leu Pro Pro Thr Pro Gln His Gln Pro Pro Leu Asn Asn
 165 170 175
 cac atg att tca cag gca gaa gac ctc agc aac ccc ttt gga caa atg 636
 His Met Ile Ser Gln Ala Glu Asp Leu Ser Asn Pro Phe Gly Gln Met
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 195 200 205
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 210 215 220
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 225 230 235 240
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 Met Gln Pro Pro Gln Gln Ile Gln Val Ser Tyr Tyr Pro Pro Gly Gln
 260 265 270

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Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu Ser His Pro Val Ala	
275	280
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Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln Ala Ser Gln Gln Pro	
290	295
300	
ggc tta cag ccc atg atg tct aac cag cag cag acg gct tac caa ggc	1020
Gly Leu Gln Pro Met Met Ser Asn Gln Gln Gln Thr Ala Tyr Gln Gly	
305	310
315	320
atg ctt ggg gtc cag cag cct cag aac cag ggc cta ctc agc aac cag	1068
Met Leu Gly Val Gln Gln Pro Gln Asn Gln Gly Leu Leu Ser Asn Gln	
325	330
335	
agg agc agc atg gga ggc cag atg caa ggc ctg gtg gtg cag tac act	1116
Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val Gln Tyr Thr	
340	345
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cca ctg cct tct tac caa gtc cct gtg ggc agt gac tca caa aac gtg	1164
Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser Gln Asn Val	
355	360
365	
gtc cag cca tcc ttc cag cag ccc atg ctg gtt cct gcc agc cag tct	1212
Val Gln Pro Ser Phe Gln Gln Pro Met Leu Val Pro Ala Ser Gln Ser	
370	375
380	
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Val Gln Gly Gly Leu Pro Thr Gly Gly Val Pro Val Tyr Tyr Ser Met	
385	390
395	400
atc cca cca gct cag cag aac gga acg agc cct tct gtg ggc ttt ctg	1308
Ile Pro Pro Ala Gln Gln Asn Gly Thr Ser Pro Ser Val Gly Phe Leu	
405	410
415	

cag cct cct ggc tct gag cag tac cag atg cct cag tct ccc tct ccc 1356
 Gln Pro Pro Gly Ser Glu Gln Tyr Gln Met Pro Gln Ser Pro Ser Pro
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 Cys Ser Pro Pro Gln Met Ser Gln Gln Tyr Ser Gly Val Ser Pro Ser
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 gga cca ggt gtg gtg gtc atg caa ctg aat gtc cct aac gga ccc cag 1452
 Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn Gly Pro Gln
 450 455 460
 gcc ccc cag aat cca tcc atg gtc caa tgg agt cac tgc aaa tac tac 1500
 Ala Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys Lys Tyr Tyr
 465 470 475 480
 agc gtg gag cag cgt ggt cag aag cct gga gac ctg tac agc cct gat 1548
 Ser Val Glu Gln Arg Gly Gln Lys Pro Gly Asp Leu Tyr Ser Pro Asp
 485 490 495
 ggg agc ccc cag gcc aac gca caa atg ggc agc agc ccc gtc aca tct 1596
 Gly Ser Pro Gln Ala Asn Ala Gln Met Gly Ser Ser Pro Val Thr Ser
 500 505 510
 cct acc cag tct cca gca ccc tct cct gtc acg agc ctc agc aac gtc 1644
 Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu Ser Asn Val
 515 520 525
 tgc act gga ctc agc ccc ctg cct gtc ctc aca cca ttc ccc cgg cct 1692
 Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Pro Phe Pro Arg Pro
 530 535 540
 ggg ggt cct gca cag ggt gac ggg cgc tat tcc cta ctg ggt cag cca 1740
 Gly Gly Pro Ala Gln Gly Asp Gly Arg Tyr Ser Leu Leu Gly Gln Pro
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Leu Gln Tyr Asn Leu Ser Ile Cys Pro Pro Leu Leu His Gly Gln Ser	
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act tac acg gtg cac cag gga cag agc gga ttg aag cac gga aac cgg	1836
Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu Lys His Gly Asn Arg	
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Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr Asp Leu Gly Thr Ala	
595 600 605	
gat gtt gtg ctt gga agg gtg ctg gag gtg act gac ctc cct gaa gga	1932
Asp Val Val Leu Gly Arg Val Leu Glu Val Thr Asp Leu Pro Glu Gly	
610 615 620	
atc acc cgt acg gag gct gac aaa ctc ttc acc cag ctt gcc atg tct	1980
Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr Gln Leu Ala Met Ser	
625 630 635 640	
ggg gcc aag atc cag tgg ctt aag gat gct cag ggg ctg cct ggt gca	2028
Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln Gly Leu Pro Gly Ala	
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ggc ggg ggg gac aac agt ggg act gct gag aac ggc cgc cac ccg gac	2076
Gly Gly Gly Asp Asn Ser Gly Thr Ala Glu Asn Gly Arg His Pro Asp	
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ctc gca gcc ctg tac acg ata gtg gct gtg ttc ccc agc ccc ctg gcc	2124
Leu Ala Ala Leu Tyr Thr Ile Val Ala Val Phe Pro Ser Pro Leu Ala	
675 680 685	
gcc cag aac gcc tcc ctt cgc ctc aac aac tct gtg agt cgc ttc aaa	2172
Ala Gln Asn Ala Ser Leu Arg Leu Asn Asn Ser Val Ser Arg Phe Lys	
690 695 700	

ctc cga gtg gct aaa aag aac tac gac ctg agg atc ctg gaa cga gct 2220
 Leu Arg Val Ala Lys Lys Asn Tyr Asp Leu Arg Ile Leu Glu Arg Ala
 705 710 715 720
 agc tct caa tagctggggg aggggagggg ctggcacagt gggagcaaag 2269
 Ser Ser Gln
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<212> PRT

<213> Mus musculus

<400> 30

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Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly		
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Ser Val Arg Ser Met Arg Pro Pro Val Thr Lys Ala Ser Ser Phe Ser		
85	90	95
Gly Ile Ser Ile Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly		
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Gly Ser Ala Gly Arg Leu Ser Arg Pro Gly Met Ala Leu Gly Ala Pro		
115	120	125
Glu Val Cys Asn Gln Val Thr Ser Pro Gln Ser Val Arg Gly Leu Leu		
130	135	140
Pro Cys Thr Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln		
145	150	155
Leu Pro Ala Leu Pro Pro Thr Pro Gln His Gln Pro Pro Leu Asn Asn		
165	170	175
His Met Ile Ser Gln Ala Glu Asp Leu Ser Asn Pro Phe Gly Gln Met		
180	185	190
Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala Asp Pro Ser Ser Ala		
195	200	205
Leu Phe Gln Pro Pro Leu Ile Ser Gln His Pro Gln Gln Ala Ser Phe		
210	215	220
Ile Met Ala Ser Ala Gly Gln Pro Leu Pro Thr Ser Asn Tyr Ser Thr		
225	230	235
Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu Pro Pro Gln Gly Tyr		
245	250	255

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 275 280 285
 Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln Ala Ser Gln Gln Pro
 290 295 300
 Gly Leu Gln Pro Met Met Ser Asn Gln Gln Gln Thr Ala Tyr Gln Gly
 305 310 315 320
 Met Leu Gly Val Gln Gln Pro Gln Asn Gln Gly Leu Leu Ser Asn Gln
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 Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val Gln Tyr Thr
 340 345 350
 Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser Gln Asn Val
 355 360 365
 Val Gln Pro Ser Phe Gln Gln Pro Met Leu Val Pro Ala Ser Gln Ser
 370 375 380
 Val Gln Gly Gly Leu Pro Thr Gly Gly Val Pro Val Tyr Tyr Ser Met
 385 390 395 400
 Ile Pro Pro Ala Gln Gln Asn Gly Thr Ser Pro Ser Val Gly Phe Leu
 405 410 415
 Gln Pro Pro Gly Ser Glu Gln Tyr Gln Met Pro Gln Ser Pro Ser Pro
 420 425 430
 Cys Ser Pro Pro Gln Met Ser Gln Gln Tyr Ser Gly Val Ser Pro Ser
 435 440 445
 Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn Gly Pro Gln
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 Ala Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys Lys Tyr Tyr

465 470 475 480
 Ser Val Glu Gln Arg Gly Gln Lys Pro Gly Asp Leu Tyr Ser Pro Asp
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 Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu Ser Asn Val
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 Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Pro Phe Pro Arg Pro
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 Gly Gly Pro Ala Gln Gly Asp Gly Arg Tyr Ser Leu Leu Gly Gln Pro
 545 550 555 560
 Leu Gln Tyr Asn Leu Ser Ile Cys Pro Pro Leu Leu His Gly Gln Ser
 565 570 575
 Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu Lys His Gly Asn Arg
 580 585 590
 Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr Asp Leu Gly Thr Ala
 595 600 605
 Asp Val Val Leu Gly Arg Val Leu Glu Val Thr Asp Leu Pro Glu Gly
 610 615 620
 Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr Gln Leu Ala Met Ser
 625 630 635 640
 Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln Gly Leu Pro Gly Ala
 645 650 655
 Gly Gly Gly Asp Asn Ser Gly Thr Ala Glu Asn Gly Arg His Pro Asp
 660 665 670
 Leu Ala Ala Leu Tyr Thr Ile Val Ala Val Phe Pro Ser Pro Leu Ala
 675 680 685

Ala Gln Asn Ala Ser Leu Arg Leu Asn Asn Ser Val Ser Arg Phe Lys
690 695 700
Leu Arg Val Ala Lys Lys Asn Tyr Asp Leu Arg Ile Leu Glu Arg Ala
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Ser Ser Gln

<210> 31

<211> 4331

<212> DNA

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agaagcgcg cgccgcccgg cgctgggggc gagccgcagc cgagcggccg tgggccccgg 240
cggcggggcg agacgtgggc gccctccccg ccaaggcccc tgcgagaggt tagacttggt 300
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ccatagaggc cactgtattc tattgaagaa catgtctaac agtaacacta ctcaagagac 420
cctggaaata atgaaagaat cagaaaaaaaa aactggtgga agaattctgta aacaaaaaca 480
agtttatatc taagactcca agtaaggaag aaattgagaa agaattgtgaa gataccagtt 540
tgcgtcagga gacacagagg cggacatcta accatggtca tgccaggaaa agagccaagt 600
ctaattccaa gctaaagttg gtgcgtagcc tggcagtgtg tgaggagtcc tccaccccat 660
ttgctgatgg gccattagaa acccaggata taattcaatt gcacatcagt tgcccttctg 720
acaaggagga agaaaagtcc acaaaagatg tctctgaaaa ggaagacaag gacaaaaaca 780

aagaaaagat cccaaggaag atg ctg tcc aga gac tcc agc cag gaa tat acg 833

Met Leu Ser Arg Asp Ser Ser Gln Glu Tyr Thr

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10

gac tcc act gga ata gac cta cat gaa ttt ctt gta aat aca ctg aaa 881

Asp Ser Thr Gly Ile Asp Leu His Glu Phe Leu Val Asn Thr Leu Lys

15

20

25

aag aac cca agg gac aga atg atg ctg cta aaa tta gaa cag gag att 929

Lys Asn Pro Arg Asp Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile

30

35

40

ctg gaa ttt att aat gac aac aat aat cag ttc aag aag ttc cct cag 977

Leu Glu Phe Ile Asn Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln

45

50

55

atg acc tca tat cac cgg atg cta tta cac cgg gta gct gcc tat ttt 1025

Met Thr Ser Tyr His Arg Met Leu Leu His Arg Val Ala Ala Tyr Phe

60

65

70

75

ggg atg gac cac aat gtt gat caa act ggg aaa gct gtc atc atc aac 1073

Gly Met Asp His Asn Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn

80

85

90

aaa act agt aac aca aga atc cct gaa cag agg ttc tca gaa cat ata 1121

Lys Thr Ser Asn Thr Arg Ile Pro Glu Gln Arg Phe Ser Glu His Ile

95

100

105

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Lys Asp Glu Lys Asn Thr Glu Phe Gln Gln Arg Phe Ile Leu Lys Arg

110

115

120

gat gat gcc agt atg gac cga gat gat aac cag act ggc cag aac gga 1217

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125

130

135

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cac aag aga agg cag att ttt agg ggg aac cgt gaa gga ctg agc cgc	1313
His Lys Arg Arg Gln Ile Phe Arg Gly Asn Arg Glu Gly Leu Ser Arg	
160 165 170	
acc tca agc agc cgc cag agc agc aca gac agc gaa ctc aaa tcc ctg	1361
Thr Ser Ser Ser Arg Gln Ser Ser Thr Asp Ser Glu Leu Lys Ser Leu	
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gag cca cgc cct tgg agc agc aca gac tct gat ggc tct gtc cgg agc	1409
Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly Ser Val Arg Ser	
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atg cga ccc cct gtc acc aaa gct agc agc ttc agt gga atc tct atc	1457
Met Arg Pro Pro Val Thr Lys Ala Ser Ser Phe Ser Gly Ile Ser Ile	
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Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly Gly Ser Ala Gly	
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Arg Ile Ser Arg Pro Gly Met Ala Leu Gly Ala Pro Glu Val Cys Asn	
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Gln Val Thr Ser Ser Gln Ser Val Arg Gly Leu Leu Pro Cys Thr Ala	
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cag cag caa cag cag cag cag cag cag caa ctt cct gct ctc cca ccc	1649
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Pro Ala Leu Pro Pro	
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 285 290 295
 gat gac ctc agc aac ccc ttt gga caa atg agc ctt agt cgc caa ggt 1745
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 Ile Ser Gln His Pro Gln Gln Thr Ser Phe Ile Met Ala Ser Thr Gly
 335 340 345
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 Gln Pro Leu Pro Thr Ser Asn Tyr Ser Thr Ser Ser His Ala Pro Pro
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 Thr Gln Gln Val Leu Pro Pro Gln Gly Tyr Met Gln Pro Pro Gln Gln
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 atc cag gtt tct tac tat ccc cct gga caa tat cct aac tcc aac cag 1985
 Ile Gln Val Ser Tyr Tyr Pro Pro Gly Gln Tyr Pro Asn Ser Asn Gln
 380 385 390 395
 caa tat cga cct ctc tct cac ccg gtg gcc tat agc ccc caa cgt ggt 2033
 Gln Tyr Arg Pro Leu Ser His Pro Val Ala Tyr Ser Pro Gln Arg Gly
 400 405 410
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 Gln Gln Leu Pro Gln Pro Ser Gln Gln Pro Gly Leu Gln Pro Met Met
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 Pro Asn Gln Gln Gln Ala Ala Tyr Gln Gly Met Ile Gly Val Gln Gln
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 Pro Gln Asn Gln Gly Leu Leu Ser Ser Gln Arg Ser Ser Met Gly Gly
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 Gln Met Gln Gly Leu Val Val Gln Tyr Thr Pro Leu Pro Ser Tyr Gln
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 Gln Lys Pro Gly Asp Leu Tyr Ser Pro Asp Ser Ser Pro Gln Ala Asn
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 655 660 665
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 Gly Gln Ser Gly Leu Lys His Gly Asn Arg Gly Lys Arg Gln Ala Leu
 700 705 710 715

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 Gly Thr Ala Glu Asn Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr
 780 785 790 795
 att gtg gct gtg ttc ccc agc ccc ctg gct gcc caa aat gcc tcc ctt 3233
 Ile Val Ala Val Phe Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu
 800 805 810
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<211> 840

<212> PRT

<213> Homo sapiens

<400> 32

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20 25 30

Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile Leu Glu Phe Ile Asn

35 40 45

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Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn Lys Thr Ser Asn Thr			
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Arg Ile Pro Glu Gln Arg Phe Ser Glu His Ile Lys Asp Glu Lys Asn			
	100	105	110
Thr Glu Phe Gln Gln Arg Phe Ile Leu Lys Arg Asp Asp Ala Ser Met			
	115	120	125
Asp Arg Asp Asp Asn Gln Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile			
	130	135	140
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145	150	155	160
Ile Phe Arg Gly Asn Arg Glu Gly Leu Ser Arg Thr Ser Ser Ser Arg			
	165	170	175
Gln Ser Ser Thr Asp Ser Glu Leu Lys Ser Leu Glu Pro Arg Pro Trp			
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Ser Ser Thr Asp Ser Asp Gly Ser Val Arg Ser Met Arg Pro Pro Val			
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Thr Lys Ala Ser Ser Phe Ser Gly Ile Ser Ile Leu Thr Arg Gly Asp			
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Gln Ser Val Arg Gly Leu Leu Pro Cys Thr Ala Gln Gln Gln Gln			

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275	280	285
Pro Pro Leu Asn Asn His Met Ile Ser Gln Ala Asp Asp Leu Ser Asn		
290	295	300
Pro Phe Gly Gln Met Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala		
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Asp Pro Ser Ala Ala Leu Phe Gln Thr Pro Leu Ile Ser Gln His Pro		
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Gln Gln Thr Ser Phe Ile Met Ala Ser Thr Gly Gln Pro Leu Pro Thr		
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Ser Asn Tyr Ser Thr Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu		
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Pro Pro Gln Gly Tyr Met Gln Pro Pro Gln Gln Ile Gln Val Ser Tyr		
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Tyr Pro Pro Gly Gln Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu		
385	390	395
Ser His Pro Val Ala Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln		
405	410	415
Pro Ser Gln Gln Pro Gly Leu Gln Pro Met Met Pro Asn Gln Gln Gln		
420	425	430
Ala Ala Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln Asn Gln Gly		
435	440	445
Leu Leu Ser Ser Gln Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu		
450	455	460
Val Val Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser		
465	470	475
		480

Asp	Ser	Gln	Asn	Val	Val	Gln	Pro	Pro	Phe	Gln	Gln	Pro	Met	Leu	Val
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				500				505					510		
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Gln	Ser	Pro	Ser	Pro	Cys	Ser	Pro	Pro	Gln	Met	Pro	Gln	Gln	Tyr	Ser
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Pro	Asn	Gly	Pro	Gln	Pro	Pro	Gln	Asn	Pro	Ser	Met	Val	Gln	Trp	Ser
				580				585						590	
His	Cys	Lys	Tyr	Tyr	Ser	Met	Asp	Gln	Arg	Gly	Gln	Lys	Pro	Gly	Asp
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Ser	Pro	Val	Thr	Ser	Pro	Thr	Gln	Ser	Pro	Ala	Pro	Ser	Pro	Val	Thr
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Ser	Leu	Ser	Ser	Val	Cys	Thr	Gly	Leu	Ser	Pro	Leu	Pro	Val	Leu	Thr
					645					650				655	
Gln	Phe	Pro	Arg	Pro	Gly	Gly	Pro	Ala	Gln	Gly	Asp	Gly	Arg	Tyr	Ser
				660				665						670	
Leu	Leu	Gly	Gln	Pro	Leu	Gln	Tyr	Asn	Leu	Ser	Ile	Cys	Pro	Pro	Leu
				675				680						685	

Leu His Gly Gln Ser Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu
 690 695 700
 Lys His Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr
 705 710 715 720
 Asp Leu Gly Thr Ala Asp Val Val Leu Gly Arg Val Leu Glu Val Thr
 725 730 735
 Asp Leu Pro Glu Gly Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr
 740 745 750
 Gln Leu Ala Met Ser Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln
 755 760 765
 Gly Leu Pro Gly Gly Gly Gly Gly Asp Asn Ser Gly Thr Ala Glu Asn
 770 775 780
 Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr Ile Val Ala Val Phe
 785 790 795 800
 Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu Arg Leu Asn Asn Ser
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 ttgctgatgg gccattagaa acccaggata taattcaatt gcacatcagt tgcccttctg 720
 acaaggagga agaaaagtcc acaaaagatg tctctgaaaa ggaagacaag gacaaaaaca 780
 aagaaaagat cccaaggaag atg ctg tcc aga gac tcc agc cag gaa tat acg 833

Met Leu Ser Arg Asp Ser Ser Gln Glu Tyr Thr

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10

gac tcc act gga ata gac cta cat gaa ttt ctt gta aat aca ctg aaa 881

Asp Ser Thr Gly Ile Asp Leu His Glu Phe Leu Val Asn Thr Leu Lys

15

20

25

aag aac cca agg gac aga atg atg ctg cta aaa tta gaa cag gag att 929

Lys Asn Pro Arg Asp Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile

30

35

40

ctg gaa ttt att aat gac aac aat aat cag ttc aag aag ttc cct cag 977

Leu Glu Phe Ile Asn Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln

45

50

55

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 ggg atg gac cac aat gtt gat caa act ggg aaa gct gtc atc atc aac 1073
 Gly Met Asp His Asn Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn
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 aaa act agt aac aca aga atc cct gaa cag agg ttc tca gaa cat ata 1121
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 Tyr Leu Asn Asp Ile Arg Gly Asn Arg Glu Gly Leu Ser Arg Thr Ser
 175 180 185
 agc agc cgc cag agc agc aca gac agc gaa ctc aaa tcc ctg gag cca 1409
 Ser Ser Arg Gln Ser Ser Thr Asp Ser Glu Leu Lys Ser Leu Glu Pro
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 Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly Ser Val Arg Ser Met Arg
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 ccc cct gtc acc aaa gct agc agc ttc agt gga atc tct atc ctt acc 1505
 Pro Pro Val Thr Lys Ala Ser Ser Phe Ser Gly Ile Ser Ile Leu Thr
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 cga ggt gac agc atc ggc agc agt aaa ggc ggc agt gcg gga agg atc 1553
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 tcc agg cca ggt atg gca cta ggt gcc cca gaa gtg tgc aac cag gtc 1601
 Ser Arg Pro Gly Met Ala Leu Gly Ala Pro Glu Val Cys Asn Gln Val
 255 260 265
 acc tca tcc cag tct gtc cgg ggg ctt ctc cct tgt act gcc cag cag 1649
 Thr Ser Ser Gln Ser Val Arg Gly Leu Leu Pro Cys Thr Ala Gln Gln
 270 275 280
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 Gln Gln Gln Gln Gln Gln Gln Gln Leu Pro Ala Leu Pro Pro Thr Pro
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 Gln Gln Gln Pro Pro Leu Asn Asn His Met Ile Ser Gln Ala Asp Asp
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 Glu Ala Ala Asp Pro Ser Ala Ala Leu Phe Gln Thr Pro Leu Ile Ser
 335 340 345

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 Gln His Pro Gln Gln Thr Ser Phe Ile Met Ala Ser Thr Gly Gln Pro
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 Gln Val Leu Pro Pro Gln Gly Tyr Met Gln Pro Pro Gln Gln Ile Gln
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 cga cct ctc tct cac ccg gtg gcc tat agc ccc caa cgt ggt cag cag 2081
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 Leu Pro Gln Pro Ser Gln Gln Pro Gly Leu Gln Pro Met Met Pro Asn
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 Gln Gln Gln Ala Ala Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln
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 aac cag ggc ctg ctc agc agc cag agg agc agc atg ggg ggc cag atg 2225
 Asn Gln Gly Leu Leu Ser Ser Gln Arg Ser Ser Met Gly Gly Gln Met
 460 465 470 475
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 Gln Gly Leu Val Val Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro
 480 485 490

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atg ctg gtc cct gtg agc cag tct gtg caa gga ggc ctc cca gca gcg	2369
Met Leu Val Pro Val Ser Gln Ser Val Gln Gly Gly Leu Pro Ala Ala	
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Gly Val Pro Val Tyr Tyr Ser Met Ile Pro Pro Ala Gln Gln Asn Gly	
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Thr Ser Pro Ser Val Gly Phe Leu Gln Pro Pro Gly Ser Glu Gln Tyr	
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Gln Met Pro Gln Ser Pro Ser Pro Cys Ser Pro Pro Gln Met Pro Gln	
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Gln Tyr Ser Gly Val Ser Pro Ser Gly Pro Gly Val Val Val Met Gln	
575 580 585	
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Leu Asn Val Pro Asn Gly Pro Gln Pro Pro Gln Asn Pro Ser Met Val	
590 595 600	
cag tgg agt cat tgt aaa tac tac agc atg gac cag cgg ggg cag aag	2657
Gln Trp Ser His Cys Lys Tyr Tyr Ser Met Asp Gln Arg Gly Gln Lys	
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cct gga gac ctg tac agt cct gac agc agc ccc cag gcc aac aca caa	2705
Pro Gly Asp Leu Tyr Ser Pro Asp Ser Ser Pro Gln Ala Asn Thr Gln	
620 625 630 635	

atg agc agc agc cct gtc aca tct cct acc cag tct cca gca ccc tct	2753
Met Ser Ser Ser Pro Val Thr Ser Pro Thr Gln Ser Pro Ala Pro Ser	
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cct gtc acc agc ctc agc agt gtc tgc aca gga ctc agt ccc ctg cct	2801
Pro Val Thr Ser Leu Ser Ser Val Cys Thr Gly Leu Ser Pro Leu Pro	
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gtc ctc aca cag ttc ccc cgg cct ggg ggt cca gca cag ggt gat ggg	2849
Val Leu Thr Gln Phe Pro Arg Pro Gly Gly Pro Ala Gln Gly Asp Gly	
670	675
cgc tac tcc ctt ttg ggc cag cca tta cag tac aat ctg tcc atc tgc	2897
Arg Tyr Ser Leu Leu Gly Gln Pro Leu Gln Tyr Asn Leu Ser Ile Cys	
685	690
cct ccc ttg ctc cat ggc cag tca act tac acg gtg cac cag gga cag	2945
Pro Pro Leu Leu His Gly Gln Ser Thr Tyr Thr Val His Gln Gly Gln	
700	705
agt gga ctg aag cat gga aac cgg ggc aag aga caa gca ctc aaa tct	2993
Ser Gly Leu Lys His Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser	
720	725
gcc tcc act gac ctg ggg aca gca gat gtt gtc ctg ggg cgg gtg ctg	3041
Ala Ser Thr Asp Leu Gly Thr Ala Asp Val Val Leu Gly Arg Val Leu	
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gag gtg aca gat ctc cct gag ggc atc acc cgt act gag gcg gac aaa	3089
Glu Val Thr Asp Leu Pro Glu Gly Ile Thr Arg Thr Glu Ala Asp Lys	
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ctc ttc acg cag ctc gcc atg tct ggc gcc aag atc cag tgg ctc aag	3137
Leu Phe Thr Gln Leu Ala Met Ser Gly Ala Lys Ile Gln Trp Leu Lys	
765	770
	775

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780 785 790 795
gct gag aat ggc cgc cac tcg gac ctc gct gcc ttg tac acc att gtg 3233
Ala Glu Asn Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr Ile Val
800 805 810
gct gtg ttc ccc agc ccc ctg gct gcc caa aat gcc tcc ctt cgt ctc 3281
Ala Val Phe Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu Arg Leu
815 820 825
aac aac tcc gtg agt cgc ttc aaa ctt cga atg gcc aaa aag aac tat 3329
Asn Asn Ser Val Ser Arg Phe Lys Leu Arg Met Ala Lys Lys Asn Tyr
830 835 840
gac ctg agg atc ctg gag cga gcc agc tcc caa taaatggagg aggggaaagg 3382
Asp Leu Arg Ile Leu Glu Arg Ala Ser Ser Gln
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<211> 854

<212> PRT

<213> Homo sapiens

<400> 34

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Arg	Met	Met	Leu	Leu	Lys	Leu	Glu	Gln	Glu	Ile	Leu	Glu	Phe	Ile	Asn
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Arg	Met	Leu	Leu	His	Arg	Val	Ala	Ala	Tyr	Phe	Gly	Met	Asp	His	Asn
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Thr	Glu	Phe	Gln	Gln	Arg	Phe	Ile	Leu	Lys	Arg	Asp	Asp	Ala	Ser	Met
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 Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr Gln Arg Val Arg Glu
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 Arg Gly Asn Arg Glu Gly Leu Ser Arg Thr Ser Ser Ser Arg Gln Ser
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 Ser Thr Asp Ser Glu Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser
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 225 230 235 240
 Gly Ser Ser Lys Gly Gly Ser Ala Gly Arg Ile Ser Arg Pro Gly Met
 245 250 255
 Ala Leu Gly Ala Pro Glu Val Cys Asn Gln Val Thr Ser Ser Gln Ser
 260 265 270
 Val Arg Gly Leu Leu Pro Cys Thr Ala Gln Gln Gln Gln Gln Gln
 275 280 285
 Gln Gln Gln Leu Pro Ala Leu Pro Pro Thr Pro Gln Gln Gln Pro Pro
 290 295 300
 Leu Asn Asn His Met Ile Ser Gln Ala Asp Asp Leu Ser Asn Pro Phe
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 Gly Gln Met Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala Asp Pro
 325 330 335
 Ser Ala Ala Leu Phe Gln Thr Pro Leu Ile Ser Gln His Pro Gln Gln

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Tyr Ser Thr Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu Pro Pro		
370	375	380
Gln Gly Tyr Met Gln Pro Pro Gln Gln Ile Gln Val Ser Tyr Tyr Pro		
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Pro Gly Gln Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu Ser His		
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Pro Val Ala Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln Pro Ser		
420	425	430
Gln Gln Pro Gly Leu Gln Pro Met Met Pro Asn Gln Gln Gln Ala Ala		
435	440	445
Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln Asn Gln Gly Leu Leu		
450	455	460
Ser Ser Gln Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val		
465	470	475
Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser		
485	490	495
Gln Asn Val Val Gln Pro Pro Phe Gln Gln Pro Met Leu Val Pro Val		
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Ser Gln Ser Val Gln Gly Gly Leu Pro Ala Ala Gly Val Pro Val Tyr		
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Tyr Ser Met Ile Pro Pro Ala Gln Gln Asn Gly Thr Ser Pro Ser Val		
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Gly Phe Leu Gln Pro Pro Gly Ser Glu Gln Tyr Gln Met Pro Gln Ser		
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		560

Pro Ser Pro Cys Ser Pro Pro Gln Met Pro Gln Gln Tyr Ser Gly Val
 565 570 575
 Ser Pro Ser Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn
 580 585 590
 Gly Pro Gln Pro Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys
 595 600 605
 Lys Tyr Tyr Ser Met Asp Gln Arg Gly Gln Lys Pro Gly Asp Leu Tyr
 610 615 620
 Ser Pro Asp Ser Ser Pro Gln Ala Asn Thr Gln Met Ser Ser Ser Pro
 625 630 635 640
 Val Thr Ser Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu
 645 650 655
 Ser Ser Val Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Gln Phe
 660 665 670
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 Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr Asp Leu
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<211> 1674

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<222> (104).. (658)

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Met Val Lys Leu

1

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5

10

15

20

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Gln Phe Pro Pro Pro Asp Lys Val Val Val Lys Thr Lys Thr Glu Tyr	
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gaa cct gat cgc aaa aaa gga aaa gca cgt cct ccc aag ata gcc gag	307
Glu Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro Lys Ile Ala Glu	
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ttc acc gtc agc atc acc gag ggt gtc acc gag agg ttt aag gtc tcc	355
Phe Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg Phe Lys Val Ser	
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Val Leu Val Leu Phe Ala Leu Ala Phe Leu Thr Cys Val Val Phe Leu	
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Val Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys Pro Asp Gly Phe	
105 110 115	
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Val Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu Glu Ser Tyr Tyr	
120 125 130	
acg gag caa gac tcc agt gcc cgg gag aaa ttt tac act gtc ata aac	547
Thr Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr Thr Val Ile Asn	
135 140 145	
cac tac aac gtg gcc aag cag agc atc acc cgc tcc gtg tcg cca tgg	595
His Tyr Asn Val Ala Lys Gln Ser Ile Thr Arg Ser Val Ser Pro Trp	
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Met Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln Glu Thr Glu Ala

165

170

175

180

gca gag aag tca gct tagcgagcag ggcagggtcc ttacgatgtg tcaacttgaag 698

Ala Glu Lys Ser Ala

185

gcaacaaggg gactttgagg gacatttcat taaatataat taccgataat ttagagatta 758

ctcattttacg gtgcaattgc ttctgtttgc taatgctgct ttgcaaatta aacttgctgc 818

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aatagaatat ctaagtccac aatctttgta agaaaagtat gtttatgttt caatctgaat 1598

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<210> 36

<211> 185

<212> PRT

<213> Mus musculus

<400> 36

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35 40 45
Lys Thr Glu Tyr Glu Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro
50 55 60
Lys Ile Ala Glu Phe Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg
65 70 75 80
Phe Lys Val Ser Val Leu Val Leu Phe Ala Leu Ala Phe Leu Thr Cys
85 90 95
Val Val Phe Leu Val Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys
100 105 110
Pro Asp Gly Phe Val Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu
115 120 125
Glu Ser Tyr Tyr Thr Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr
130 135 140
Thr Val Ile Asn His Tyr Asn Val Ala Lys Gln Ser Ile Thr Arg Ser
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Val Ser Pro Trp Met Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln
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Glu Thr Glu Ala Ala Glu Lys Ser Ala
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<210> 37

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (162)..(716)

<400> 37

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cggagccggg cgtgggctgc agcctcggag ctcccgaac g atg gtg aag ttg ggg 176
                                     Met Val Lys Leu Gly
                                     1           5
aac aat ttc gca gag aag ggc acc aag cag ccg ctg ctg gag gat ggc 224
Asn Asn Phe Ala Glu Lys Gly Thr Lys Gln Pro Leu Leu Glu Asp Gly
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ttc gac acc att ccc ctg atg acg ccc ctc gat gtc aat cag ctg cag 272
Phe Asp Thr Ile Pro Leu Met Thr Pro Leu Asp Val Asn Gln Leu Gln
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ttc ccg ccc ccg gat aag gtg gtc gtg aaa act aag acc gag tat gaa 320
Phe Pro Pro Pro Asp Lys Val Val Val Lys Thr Lys Thr Glu Tyr Glu
          40           45           50
cct gac cgc aag aaa ggg aaa gca cgt cct ccc caa att gct gag ttc 368
Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro Gln Ile Ala Glu Phe
          55           60           65
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Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg Phe Lys Val Ser Val

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Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys Pro Asp Gly Phe Val				
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ctc aag aac acc cag tgc atc cca gaa ggc ttg gag agc tac tac gcg	560			
Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu Glu Ser Tyr Tyr Ala				
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gag caa gac tcc agt gcc cgg gag aaa ttt tac aca gtc ata aac cac	608			
Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr Thr Val Ile Asn His				
135	140	145		
tac aac ctg gcc aag cag agc atc acg cgc tcc gta tcg ccc tgg atg	656			
Tyr Asn Leu Ala Lys Gln Ser Ile Thr Arg Ser Val Ser Pro Trp Met				
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tca gtt ctg tca gaa gag aag ctg tcc gag cag gag act gaa gcg gct	704			
Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln Glu Thr Glu Ala Ala				
170	175	180		
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Glu Lys Ser Ala				
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cgaccaccca cgggcataaa atcaagtgca tttcagcatt gcctaaagag ctctgacacc	936			
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<210> 38

<211> 185

<212> PRT

<213> Homo sapiens

<400> 38

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				20				25						30	
Val	Asn	Gln	Leu	Gln	Phe	Pro	Pro	Pro	Asp	Lys	Val	Val	Val	Lys	Thr
				35				40						45	
Lys	Thr	Glu	Tyr	Glu	Pro	Asp	Arg	Lys	Lys	Gly	Lys	Ala	Arg	Pro	Pro
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Gln	Ile	Ala	Glu	Phe	Thr	Val	Ser	Ile	Thr	Glu	Gly	Val	Thr	Glu	Arg
				65				70				75			80
Phe	Lys	Val	Ser	Val	Leu	Val	Leu	Phe	Ala	Leu	Ala	Phe	Leu	Thr	Cys
				85				90						95	
Val	Val	Phe	Leu	Val	Val	Tyr	Lys	Val	Tyr	Lys	Tyr	Asp	Arg	Ala	Cys

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Glu Ser Tyr Tyr Ala Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr			
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Thr Val Ile Asn His Tyr Asn Leu Ala Lys Gln Ser Ile Thr Arg Ser			
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Glu Thr Glu Ala Ala Glu Lys Ser Ala			
180	185		

<210> 39

<211> 2676

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (35).. (2488)

<400> 39

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gcg gcc gat tct gcg ggt ccg gcc ccg ggt gtc ccg gcc acg ccg gcg 103

Ala Ala Asp Ser Ala Gly Pro Ala Pro Gly Val Pro Ala Thr Pro Ala

10

15

20

agc acg cgg gga gcc gct gcc gcc tct agc ccg tgg agg ccg ccc gag 151

Ser Thr Arg Gly Ala Ala Ala Ala Ser Ser Pro Trp Arg Pro Pro Glu
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 Ser Arg Leu Gln Gly Ser Arg Pro Arg Pro Ala Arg Ala Arg Ala Ala
 40 45 50 55
 gcc ccg gtg cca ccg gcc cgg gag ctg atc cag ccg act gtg agc gag 247
 Ala Pro Val Pro Pro Ala Arg Glu Leu Ile Gln Pro Thr Val Ser Glu
 60 65 70
 ctg tcc cgg gct gtg cgc acc aat att ctg tgc acc gtg cgc ggc tgc 295
 Leu Ser Arg Ala Val Arg Thr Asn Ile Leu Cys Thr Val Arg Gly Cys
 75 80 85
 ggc aag atc ctg ccc aac agc cct gcg ctc aac atg cac ctc gtc aag 343
 Gly Lys Ile Leu Pro Asn Ser Pro Ala Leu Asn Met His Leu Val Lys
 90 95 100
 agc cac cga ctg cag gat ggc ata gta aac ccg aca ata agg aaa gac 391
 Ser His Arg Leu Gln Asp Gly Ile Val Asn Pro Thr Ile Arg Lys Asp
 105 110 115
 ttg aca act gca ccg aaa ttc tac tgt tgt cca atc aaa gga tgt cct 439
 Leu Thr Thr Ala Pro Lys Phe Tyr Cys Cys Pro Ile Lys Gly Cys Pro
 120 125 130 135
 cga ggc ccc gac cga ccg ttt tct cag ttt tct ctg gtt aaa cag cac 487
 Arg Gly Pro Asp Arg Pro Phe Ser Gln Phe Ser Leu Val Lys Gln His
 140 145 150
 ttt atg aaa atg cat gca gag aag aag cac aaa tgc agt aag tgc agt 535
 Phe Met Lys Met His Ala Glu Lys Lys His Lys Cys Ser Lys Cys Ser
 155 160 165
 aat tcc tac ggc acc gag tgg gac ctg aaa aga cac gag gag gat tgt 583

Asn Ser Tyr Gly Thr Glu Trp Asp Leu Lys Arg His Glu Glu Asp Cys	
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Gly Lys Thr Phe Gln Cys Thr Cys Gly Cys Pro Tyr Ala Ser Arg Thr	
185 190 195	
gca ctg cag tct cac atc tac cga act ggc cac gag atc cct gca gag	679
Ala Leu Gln Ser His Ile Tyr Arg Thr Gly His Glu Ile Pro Ala Glu	
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cac aga gac cca cct agt aaa aaa agg aaa atg gaa agc tac ctg caa	727
His Arg Asp Pro Pro Ser Lys Lys Arg Lys Met Glu Ser Tyr Leu Gln	
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aac caa aag ttg tcc agt aaa acc act gaa cca ctg agc gac caa gca	775
Asn Gln Lys Leu Ser Ser Lys Thr Thr Glu Pro Leu Ser Asp Gln Ala	
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Ala Pro Arg Gln Asp Ala Ala Glu Pro Asp Ala Pro Glu Val Lys Pro	
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Ala Ala Ser Leu Glu Asp Ser Cys Ser Ala His Thr Lys Lys Gln Ser	
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Val Ala Thr Pro Pro Arg Cys Pro Gln Lys Leu Leu Leu Pro Lys Pro	
280 285 290 295	
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Lys Val Ala Leu Val Lys Leu Pro Val Met Gln Phe Ser Pro Val Pro	
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Val Phe Val Pro Thr Ala Glu Ser Ser Ala Gln Pro Val Val Leu Gly
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 Val Asp His Ser Ser Ala Ala Gly Thr Val His Leu Val Pro Leu Ser
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 Val Gly Ala Leu Ile Leu Ser Leu Asp Ser Glu Ala Cys Ser Leu Lys
 345 350 355
 gag agc cta ccc ctc tca aaa att atc agt cct gtt gtt gag cca atg 1159
 Glu Ser Leu Pro Leu Ser Lys Ile Ile Ser Pro Val Val Glu Pro Met
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 aat aca ggt gtt caa gtg aac ttg ggt aaa agc ctg tgt agt cct tta 1207
 Asn Thr Gly Val Gln Val Asn Leu Gly Lys Ser Leu Cys Ser Pro Leu
 380 385 390
 caa gag gta ggg agt gtg tgt cag agg acc agc att tcc tca agc aac 1255
 Gln Glu Val Gly Ser Val Cys Gln Arg Thr Ser Ile Ser Ser Ser Asn
 395 400 405
 gtg cag aca gat ctg acc tat gcc tca gcc aac ttg ata ccc tct gct 1303
 Val Gln Thr Asp Leu Thr Tyr Ala Ser Ala Asn Leu Ile Pro Ser Ala
 410 415 420
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 Gln Trp Leu Gly Pro Asp Ser Ser Val Ser Ser Cys Ser Gln Thr Asp
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 ctg tcg ttt gat tct caa gtg tcc ctt cct gtt agt gtc cac acc cag 1399
 Leu Ser Phe Asp Ser Gln Val Ser Leu Pro Val Ser Val His Thr Gln
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gat	gca	ttt	ata	gac	gcc	tgt	ttc	cag	cct	ggg	ggg	gtc	tcc	agg	gaa	1495
Asp	Ala	Phe	Ile	Asp	Ala	Cys	Phe	Gln	Pro	Gly	Gly	Val	Ser	Arg	Glu	
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Thr	Gln	Thr	Ser	Arg	Met	Gln	Asn	Arg	Thr	Asn	Asp	Ser	Val	Pro	Val	
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Gly	His	Thr	Gly	Leu	Cys	Gly	Asp	Ile	Phe	Glu	Ser	Val	His	Ala	Ser	
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tac	agt	gtg	cct	act	gac	acc	atc	atg	agt	agc	agc	tta	gtt	gca	gag	1639
Tyr	Ser	Val	Pro	Thr	Asp	Thr	Ile	Met	Ser	Ser	Ser	Leu	Val	Ala	Glu	
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Thr	Gly	Thr	His	Gly	Leu	Pro	Pro	Gln	Ser	Asp	Pro	Lys	Ile	Leu	Gly	
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caa	gtc	atg	gaa	aag	tct	gca	ccc	gtg	tta	aac	ttc	agc	acc	cag	aac	1735
Gln	Val	Met	Glu	Lys	Ser	Ala	Pro	Val	Leu	Asn	Phe	Ser	Thr	Gln	Asn	
				555				560				565				
ggc	ttg	ctt	cct	gca	cac	acc	atg	aca	gat	aat	cag	acc	caa	acc	ata	1783
Gly	Leu	Leu	Pro	Ala	His	Thr	Met	Thr	Asp	Asn	Gln	Thr	Gln	Thr	Ile	
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gat	ctg	ctg	agc	gac	ttg	gaa	aac	atc	ttg	tca	agt	aac	ctg	cca	ggg	1831
Asp	Leu	Leu	Ser	Asp	Leu	Glu	Asn	Ile	Leu	Ser	Ser	Asn	Leu	Pro	Gly	
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caa	aca	ctg	gat	aac	cgg	ggg	ctc	ttg	tcc	gac	acc	aac	ccc	gga	cct	1879

Gln Thr Leu Asp Asn Arg Gly Leu Leu Ser Asp Thr Asn Pro Gly Pro
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 Asp Ala Gln Leu Pro Ala Gly Ser Ala Gln Asn Ser Gly Ile Asp Phe
 620 625 630
 gat att gaa gag ttc ctc tca gcc tcc aat atc cag act cag act gag 1975
 Asp Ile Glu Glu Phe Leu Ser Ala Ser Asn Ile Gln Thr Gln Thr Glu
 635 640 645
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 Glu Ser Glu Leu Ser Ser Met Ser Thr Glu Pro Val Leu Glu Ser Leu
 650 655 660
 gac atc gag acg cag acc gac gtc ctc ctc tca gat ccc tcc aca cag 2071
 Asp Ile Glu Thr Gln Thr Asp Val Leu Leu Ser Asp Pro Ser Thr Gln
 665 670 675
 ccc tat ggc ttc aga gcg ggg tca ggc ttc ctg ggc ctt gag atg ttc 2119
 Pro Tyr Gly Phe Arg Ala Gly Ser Gly Phe Leu Gly Leu Glu Met Phe
 680 685 690 695
 gac aca cag aca caa aca gac tta aac ttc ttc tta gac agt agt cct 2167
 Asp Thr Gln Thr Gln Thr Asp Leu Asn Phe Phe Leu Asp Ser Ser Pro
 700 705 710
 cac ctg ccc ctg ggc agc atc ctg aaa cac tcc agc ttc tcc atg agt 2215
 His Leu Pro Leu Gly Ser Ile Leu Lys His Ser Ser Phe Ser Met Ser
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 cgg cac ctg cct gct ctg gag agc aag gtc cag ttg agc agc aca gaa 2311

Arg His Leu Pro Ala Leu Glu Ser Lys Val Gln Leu Ser Ser Thr Glu
 745 750 755
 aca caa acc atg agt tct ggc ttc gag ccc ctg ggg aac ttg ttc etc 2359
 Thr Gln Thr Met Ser Ser Gly Phe Glu Pro Leu Gly Asn Leu Phe Leu
 760 765 770 775
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 ctg gcc tgg aat acg atg gag tcc cag ttc agc tcc gtg gaa acc cag 2455
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 795 800 805
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 Thr Cys Ala Glu Leu His Ala Val Ser Ser Phe
 810 815
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<210> 40

<211> 818

<212> PRT

<213> Mus musculus

<400> 40

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 Pro Ala Arg Ala Arg Ala Ala Ala Pro Val Pro Pro Ala Arg Glu Leu
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 Ile Gln Pro Thr Val Ser Glu Leu Ser Arg Ala Val Arg Thr Asn Ile
 65 70 75 80
 Leu Cys Thr Val Arg Gly Cys Gly Lys Ile Leu Pro Asn Ser Pro Ala
 85 90 95
 Leu Asn Met His Leu Val Lys Ser His Arg Leu Gln Asp Gly Ile Val
 100 105 110
 Asn Pro Thr Ile Arg Lys Asp Leu Thr Thr Ala Pro Lys Phe Tyr Cys
 115 120 125
 Cys Pro Ile Lys Gly Cys Pro Arg Gly Pro Asp Arg Pro Phe Ser Gln
 130 135 140
 Phe Ser Leu Val Lys Gln His Phe Met Lys Met His Ala Glu Lys Lys
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 His Lys Cys Ser Lys Cys Ser Asn Ser Tyr Gly Thr Glu Trp Asp Leu
 165 170 175
 Lys Arg His Glu Glu Asp Cys Gly Lys Thr Phe Gln Cys Thr Cys Gly
 180 185 190
 Cys Pro Tyr Ala Ser Arg Thr Ala Leu Gln Ser His Ile Tyr Arg Thr
 195 200 205
 Gly His Glu Ile Pro Ala Glu His Arg Asp Pro Pro Ser Lys Lys Arg
 210 215 220
 Lys Met Glu Ser Tyr Leu Gln Asn Gln Lys Leu Ser Ser Lys Thr Thr
 225 230 235 240
 Glu Pro Leu Ser Asp Gln Ala Ala Pro Arg Gln Asp Ala Ala Glu Pro

245 250 255
Asp Ala Pro Glu Val Lys Pro Ala Ala Ser Leu Glu Asp Ser Cys Ser
260 265 270
Ala His Thr Lys Lys Gln Ser Val Ala Thr Pro Pro Arg Cys Pro Gln
275 280 285
Lys Leu Leu Leu Pro Lys Pro Lys Val Ala Leu Val Lys Leu Pro Val
290 295 300
Met Gln Phe Ser Pro Val Pro Val Phe Val Pro Thr Ala Glu Ser Ser
305 310 315 320
Ala Gln Pro Val Val Leu Gly Val Asp His Ser Ser Ala Ala Gly Thr
325 330 335
Val His Leu Val Pro Leu Ser Val Gly Ala Leu Ile Leu Ser Leu Asp
340 345 350
Ser Glu Ala Cys Ser Leu Lys Glu Ser Leu Pro Leu Ser Lys Ile Ile
355 360 365
Ser Pro Val Val Glu Pro Met Asn Thr Gly Val Gln Val Asn Leu Gly
370 375 380
Lys Ser Leu Cys Ser Pro Leu Gln Glu Val Gly Ser Val Cys Gln Arg
385 390 395 400
Thr Ser Ile Ser Ser Ser Asn Val Gln Thr Asp Leu Thr Tyr Ala Ser
405 410 415
Ala Asn Leu Ile Pro Ser Ala Gln Trp Leu Gly Pro Asp Ser Ser Val
420 425 430
Ser Ser Cys Ser Gln Thr Asp Leu Ser Phe Asp Ser Gln Val Ser Leu
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Pro Val Ser Val His Thr Gln Thr Leu Val Pro Ser Ser Lys Val Thr
450 455 460

Ser Ser Ile Ala Ala Gln Thr Asp Ala Phe Ile Asp Ala Cys Phe Gln
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 Pro Gly Gly Val Ser Arg Glu Thr Gln Thr Ser Arg Met Gln Asn Arg
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 500 505 510
 Phe Glu Ser Val His Ala Ser Tyr Ser Val Pro Thr Asp Thr Ile Met
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 Ser Asp Pro Lys Ile Leu Gly Gln Val Met Glu Lys Ser Ala Pro Val
 545 550 555 560
 Leu Asn Phe Ser Thr Gln Asn Gly Leu Leu Pro Ala His Thr Met Thr
 565 570 575
 Asp Asn Gln Thr Gln Thr Ile Asp Leu Leu Ser Asp Leu Glu Asn Ile
 580 585 590
 Leu Ser Ser Asn Leu Pro Gly Gln Thr Leu Asp Asn Arg Gly Leu Leu
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 Ser Asp Thr Asn Pro Gly Pro Asp Ala Gln Leu Pro Ala Gly Ser Ala
 610 615 620
 Gln Asn Ser Gly Ile Asp Phe Asp Ile Glu Glu Phe Leu Ser Ala Ser
 625 630 635 640
 Asn Ile Gln Thr Gln Thr Glu Glu Ser Glu Leu Ser Ser Met Ser Thr
 645 650 655
 Glu Pro Val Leu Glu Ser Leu Asp Ile Glu Thr Gln Thr Asp Val Leu
 660 665 670
 Leu Ser Asp Pro Ser Thr Gln Pro Tyr Gly Phe Arg Ala Gly Ser Gly

675 680 685
 Phe Leu Gly Leu Glu Met Phe Asp Thr Gln Thr Gln Thr Asp Leu Asn
 690 695 700
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 740 745 750
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 770 775 780
 Asp Asp Phe Leu Leu Ala Asp Leu Ala Trp Asn Thr Met Glu Ser Gln
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<210> 41

<211> 2700

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25).. (2493)

<400> 41

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 Ala Gly Ser Ala Ala Leu Ala Ala Gly Ala Arg Ala Val Pro Ala Ala
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 Thr Thr Gly Ala Ala Ala Ala Ala Ser Gly Pro Trp Val Pro Pro Gly
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 Pro Arg Leu Arg Gly Ser Arg Pro Arg Pro Ala Gly Ala Thr Gln Gln
 45 50 55
 ccc gct gtc ccc gcg ccg ccg gcg ggg gag ctg atc cag ccg tcg gtg 243
 Pro Ala Val Pro Ala Pro Pro Ala Gly Glu Leu Ile Gln Pro Ser Val
 60 65 70
 agc gag ctg tcc cgg gcc gtg cgg acc aac atc ctg tgc acc gtg cgc 291
 Ser Glu Leu Ser Arg Ala Val Arg Thr Asn Ile Leu Cys Thr Val Arg
 75 80 85
 ggc tgc ggc aag atc ctg ccc aac agc ccc gcg ctc aac atg cac cta 339
 Gly Cys Gly Lys Ile Leu Pro Asn Ser Pro Ala Leu Asn Met His Leu
 90 95 100 105
 gtc aag agc cac cgc ctg cag gat ggc ata gtc aat cca aca ata aga 387
 Val Lys Ser His Arg Leu Gln Asp Gly Ile Val Asn Pro Thr Ile Arg
 110 115 120
 aaa gat ttg aaa act gga ccg aaa ttc tac tgc tgt cca att gaa ggc 435
 Lys Asp Leu Lys Thr Gly Pro Lys Phe Tyr Cys Cys Pro Ile Glu Gly
 125 130 135

tgc ccc aga ggc cct gag aga ccg ttt tct cag ttt tct ctc gta aaa	483
Cys Pro Arg Gly Pro Glu Arg Pro Phe Ser Gln Phe Ser Leu Val Lys	
140 145 150	
cag cac ttt atg aaa atg cat gct gag aag aag cac aaa tgt agt aag	531
Gln His Phe Met Lys Met His Ala Glu Lys Lys His Lys Cys Ser Lys	
155 160 165	
tgc agc aat tcg tac ggt aca gaa tgg gac ctg aaa aga cat gca gag	579
Cys Ser Asn Ser Tyr Gly Thr Glu Trp Asp Leu Lys Arg His Ala Glu	
170 175 180 185	
gac tgt ggc aag acc ttc cgg tgc aca tgc ggc tgt ccc tac gcc agt	627
Asp Cys Gly Lys Thr Phe Arg Cys Thr Cys Gly Cys Pro Tyr Ala Ser	
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aga aca gca ctg cag tct cac atc tac cga act ggg cac gag ata cct	675
Arg Thr Ala Leu Gln Ser His Ile Tyr Arg Thr Gly His Glu Ile Pro	
205 210 215	
gca gaa cac agg gac cca cct agt aag aaa agg aaa atg gaa aac tgt	723
Ala Glu His Arg Asp Pro Pro Ser Lys Lys Arg Lys Met Glu Asn Cys	
220 225 230	
gca caa aac cag aag tta tcc aac aag acc att gaa tca ttg aac aac	771
Ala Gln Asn Gln Lys Leu Ser Asn Lys Thr Ile Glu Ser Leu Asn Asn	
235 240 245	
caa cca atc cct aga cca gac act caa gaa cta gaa gct tca gaa ata	819
Gln Pro Ile Pro Arg Pro Asp Thr Gln Glu Leu Glu Ala Ser Glu Ile	
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Lys Leu Glu Pro Ser Phe Glu Asp Ser Cys Gly Ser Asn Thr Asp Lys	
270 275 280	

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 aag ccc aaa gtg gct ttg gtt aaa cta ccc gtg atg cag ttt tct gtc 963
 Lys Pro Lys Val Ala Leu Val Lys Leu Pro Val Met Gln Phe Ser Val
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 atg cct gtc ttt gtg cct aca gcc gac tcc tca gcc cag cct gtg gtg 1011
 Met Pro Val Phe Val Pro Thr Ala Asp Ser Ser Ala Gln Pro Val Val
 315 320 325
 tta ggt gtt gat cag ggc tct gcc aca ggg gct gtg cac tta atg ccc 1059
 Leu Gly Val Asp Gln Gly Ser Ala Thr Gly Ala Val His Leu Met Pro
 330 335 340 345
 ttg tca gta gga acc ctg atc ctc ggc cta gat tca gag gct tgc tct 1107
 Leu Ser Val Gly Thr Leu Ile Leu Gly Leu Asp Ser Glu Ala Cys Ser
 350 355 360
 ctt aag gag agc cta cct ctt ttc aaa att gct aat cct att gct ggt 1155
 Leu Lys Glu Ser Leu Pro Leu Phe Lys Ile Ala Asn Pro Ile Ala Gly
 365 370 375
 gag cca ata agt act ggt gtt caa gtg aac ttt ggt aaa agt cca tct 1203
 Glu Pro Ile Ser Thr Gly Val Gln Val Asn Phe Gly Lys Ser Pro Ser
 380 385 390
 aat cct tta caa gaa cta ggg aac acg tgt caa aag aat agc att tct 1251
 Asn Pro Leu Gln Glu Leu Gly Asn Thr Cys Gln Lys Asn Ser Ile Ser
 395 400 405
 tca atc aac gtg cag aca gat ctg tct tat gcc tca caa aac ttt ata 1299
 Ser Ile Asn Val Gln Thr Asp Leu Ser Tyr Ala Ser Gln Asn Phe Ile
 410 415 420 425

cct tct gca cag tgg gcc act gct gat tcc tct gtg tgg tct tgt tct	1347
Pro Ser Ala Gln Trp Ala Thr Ala Asp Ser Ser Val Ser Ser Cys Ser	
430 435 440	
caa act gat ttg tgg ttt gat tct caa gtg tct ctt ccc att agt gtt	1395
Gln Thr Asp Leu Ser Phe Asp Ser Gln Val Ser Leu Pro Ile Ser Val	
445 450 455	
cac act cag aca ttt ttg ccc agc tct aag gta act tca tct ata gct	1443
His Thr Gln Thr Phe Leu Pro Ser Ser Lys Val Thr Ser Ser Ile Ala	
460 465 470	
gct cag act gat gca ttt atg gac acc tgt ttc cag tca ggt ggg gtc	1491
Ala Gln Thr Asp Ala Phe Met Asp Thr Cys Phe Gln Ser Gly Gly Val	
475 480 485	
tcc aga gaa act caa acc agt ggg ata gaa agt cca acg gat gac cat	1539
Ser Arg Glu Thr Gln Thr Ser Gly Ile Glu Ser Pro Thr Asp Asp His	
490 495 500 505	
gta cag atg gac caa gct gga atg tgc gga gac att ttt gag agt gtt	1587
Val Gln Met Asp Gln Ala Gly Met Cys Gly Asp Ile Phe Glu Ser Val	
510 515 520	
cat tca tca tat aat gtt gct aca ggt aac att ata agc aac agt tta	1635
His Ser Ser Tyr Asn Val Ala Thr Gly Asn Ile Ile Ser Asn Ser Leu	
525 530 535	
gta gca gag aca gta act cat agt ttg tta cct cag aat gag cct aag	1683
Val Ala Glu Thr Val Thr His Ser Leu Leu Pro Gln Asn Glu Pro Lys	
540 545 550	
act tta aat caa gat att gag aaa tct gca cca att ata aat ttc agt	1731
Thr Leu Asn Gln Asp Ile Glu Lys Ser Ala Pro Ile Ile Asn Phe Ser	
555 560 565	

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 Ala Gln Asn Ser Met Leu Pro Ser Gln Asn Met Thr Asp Asn Gln Thr
 570 575 580 585
 caa acc ata gat tta tta agt gat ttg gaa aac atc ttg tca agt aat 1827
 Gln Thr Ile Asp Leu Leu Ser Asp Leu Glu Asn Ile Leu Ser Ser Asn
 590 595 600
 ctg cct gcc cag aca ttg gat cat cgt agt ctt ttg tct gac aca aat 1875
 Leu Pro Ala Gln Thr Leu Asp His Arg Ser Leu Leu Ser Asp Thr Asn
 605 610 615
 cct gga cct gac acc cag ctc cca tct ggc cca gcc cag aac ccc gga 1923
 Pro Gly Pro Asp Thr Gln Leu Pro Ser Gly Pro Ala Gln Asn Pro Gly
 620 625 630
 atc gat ttt gat atc gaa gag ttc ttt tcg gcc tca aat atc cag act 1971
 Ile Asp Phe Asp Ile Glu Glu Phe Phe Ser Ala Ser Asn Ile Gln Thr
 635 640 645
 caa act gaa gag agt gaa ctt agc acc atg acc acc gag cca gtc ttg 2019
 Gln Thr Glu Glu Ser Glu Leu Ser Thr Met Thr Thr Glu Pro Val Leu
 650 655 660 665
 gag tca ctg gac ata gag act caa acg gac ttc tta ctc gca gat acc 2067
 Glu Ser Leu Asp Ile Glu Thr Gln Thr Asp Phe Leu Leu Ala Asp Thr
 670 675 680
 tct gct cag tcc tat ggg tgt agg gga aat tct aac ttc tta ggc ctt 2115
 Ser Ala Gln Ser Tyr Gly Cys Arg Gly Asn Ser Asn Phe Leu Gly Leu
 685 690 695
 gag atg ttt gac aca cag aca cag aca gac tta aac ttt ttc tta gac 2163
 Glu Met Phe Asp Thr Gln Thr Gln Thr Asp Leu Asn Phe Phe Leu Asp
 700 705 710

agt agc cct cat ctg cct ctg gga agt att ctg aaa cac tcc agc ttt 2211
 Ser Ser Pro His Leu Pro Leu Gly Ser Ile Leu Lys His Ser Ser Phe
 715 720 725
 tcc gtg agt act gat tca tct gac aca gag acc caa act gaa gga gtc 2259
 Ser Val Ser Thr Asp Ser Ser Asp Thr Glu Thr Gln Thr Glu Gly Val
 730 735 740 745
 tcc act gct aaa aat ata cct gct cta gaa agc aaa gtt cag ttg aac 2307
 Ser Thr Ala Lys Asn Ile Pro Ala Leu Glu Ser Lys Val Gln Leu Asn
 750 755 760
 agt aca gaa aca cag acc atg agt tct ggg ttt gaa acc ctg ggg agc 2355
 Ser Thr Glu Thr Gln Thr Met Ser Ser Gly Phe Glu Thr Leu Gly Ser
 765 770 775
 ttg ttc ttc acc agc aac gaa act cag aca gca atg gat gac ttt ctt 2403
 Leu Phe Phe Thr Ser Asn Glu Thr Gln Thr Ala Met Asp Asp Phe Leu
 780 785 790
 ctg gct gat ctg gcc tgg aac acg atg gag tct cag ttc agc tct gta 2451
 Leu Ala Asp Leu Ala Trp Asn Thr Met Glu Ser Gln Phe Ser Ser Val
 795 800 805
 gaa acc cag act tct gcg gaa cca cac aca gtc tcc aac ttc 2493
 Glu Thr Gln Thr Ser Ala Glu Pro His Thr Val Ser Asn Phe
 810 815 820
 taaaactaac ggtggagtcc atgtgtgaaa tggcatctac catttcctct ggattaaaac 2553
 tacggactgg ggacaacagt attaattcga ttgaatgtgg ctgatgatgc agttgcttag 2613
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<210> 42

<211> 823

<212> PRT

<213> Homo sapiens

<400> 42

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Ala Ser Gly Pro Trp Val Pro Pro Gly Pro Arg Leu Arg Gly Ser Arg
35 40 45
Pro Arg Pro Ala Gly Ala Thr Gln Gln Pro Ala Val Pro Ala Pro Pro
50 55 60
Ala Gly Glu Leu Ile Gln Pro Ser Val Ser Glu Leu Ser Arg Ala Val
65 70 75 80
Arg Thr Asn Ile Leu Cys Thr Val Arg Gly Cys Gly Lys Ile Leu Pro
85 90 95
Asn Ser Pro Ala Leu Asn Met His Leu Val Lys Ser His Arg Leu Gln
100 105 110
Asp Gly Ile Val Asn Pro Thr Ile Arg Lys Asp Leu Lys Thr Gly Pro
115 120 125
Lys Phe Tyr Cys Cys Pro Ile Glu Gly Cys Pro Arg Gly Pro Glu Arg
130 135 140
Pro Phe Ser Gln Phe Ser Leu Val Lys Gln His Phe Met Lys Met His
145 150 155 160
Ala Glu Lys Lys His Lys Cys Ser Lys Cys Ser Asn Ser Tyr Gly Thr
165 170 175
Glu Trp Asp Leu Lys Arg His Ala Glu Asp Cys Gly Lys Thr Phe Arg

180	185	190
Cys Thr Cys Gly Cys Pro Tyr Ala Ser Arg Thr Ala Leu Gln Ser His		
195	200	205
Ile Tyr Arg Thr Gly His Glu Ile Pro Ala Glu His Arg Asp Pro Pro		
210	215	220
Ser Lys Lys Arg Lys Met Glu Asn Cys Ala Gln Asn Gln Lys Leu Ser		
225	230	235
Asn Lys Thr Ile Glu Ser Leu Asn Asn Gln Pro Ile Pro Arg Pro Asp		
245	250	255
Thr Gln Glu Leu Glu Ala Ser Glu Ile Lys Leu Glu Pro Ser Phe Glu		
260	265	270
Asp Ser Cys Gly Ser Asn Thr Asp Lys Gln Thr Leu Thr Thr Pro Pro		
275	280	285
Arg Tyr Pro Gln Lys Leu Leu Leu Pro Lys Pro Lys Val Ala Leu Val		
290	295	300
Lys Leu Pro Val Met Gln Phe Ser Val Met Pro Val Phe Val Pro Thr		
305	310	315
Ala Asp Ser Ser Ala Gln Pro Val Val Leu Gly Val Asp Gln Gly Ser		
325	330	335
Ala Thr Gly Ala Val His Leu Met Pro Leu Ser Val Gly Thr Leu Ile		
340	345	350
Leu Gly Leu Asp Ser Glu Ala Cys Ser Leu Lys Glu Ser Leu Pro Leu		
355	360	365
Phe Lys Ile Ala Asn Pro Ile Ala Gly Glu Pro Ile Ser Thr Gly Val		
370	375	380
Gln Val Asn Phe Gly Lys Ser Pro Ser Asn Pro Leu Gln Glu Leu Gly		

385	390	395	400
Asn Thr Cys Gln Lys Asn Ser Ile Ser Ser Ile Asn Val Gln Thr Asp			
405	410	415	
Leu Ser Tyr Ala Ser Gln Asn Phe Ile Pro Ser Ala Gln Trp Ala Thr			
420	425	430	
Ala Asp Ser Ser Val Ser Ser Cys Ser Gln Thr Asp Leu Ser Phe Asp			
435	440	445	
Ser Gln Val Ser Leu Pro Ile Ser Val His Thr Gln Thr Phe Leu Pro			
450	455	460	
Ser Ser Lys Val Thr Ser Ser Ile Ala Ala Gln Thr Asp Ala Phe Met			
465	470	475	480
Asp Thr Cys Phe Gln Ser Gly Gly Val Ser Arg Glu Thr Gln Thr Ser			
485	490	495	
Gly Ile Glu Ser Pro Thr Asp Asp His Val Gln Met Asp Gln Ala Gly			
500	505	510	
Met Cys Gly Asp Ile Phe Glu Ser Val His Ser Ser Tyr Asn Val Ala			
515	520	525	
Thr Gly Asn Ile Ile Ser Asn Ser Leu Val Ala Glu Thr Val Thr His			
530	535	540	
Ser Leu Leu Pro Gln Asn Glu Pro Lys Thr Leu Asn Gln Asp Ile Glu			
545	550	555	560
Lys Ser Ala Pro Ile Ile Asn Phe Ser Ala Gln Asn Ser Met Leu Pro			
565	570	575	
Ser Gln Asn Met Thr Asp Asn Gln Thr Gln Thr Ile Asp Leu Leu Ser			
580	585	590	
Asp Leu Glu Asn Ile Leu Ser Ser Asn Leu Pro Ala Gln Thr Leu Asp			
595	600	605	

His Arg Ser Leu Leu Ser Asp Thr Asn Pro Gly Pro Asp Thr Gln Leu
610 615 620
Pro Ser Gly Pro Ala Gln Asn Pro Gly Ile Asp Phe Asp Ile Glu Glu
625 630 635 640
Phe Phe Ser Ala Ser Asn Ile Gln Thr Gln Thr Glu Glu Ser Glu Leu
645 650 655
Ser Thr Met Thr Thr Glu Pro Val Leu Glu Ser Leu Asp Ile Glu Thr
660 665 670
Gln Thr Asp Phe Leu Leu Ala Asp Thr Ser Ala Gln Ser Tyr Gly Cys
675 680 685
Arg Gly Asn Ser Asn Phe Leu Gly Leu Glu Met Phe Asp Thr Gln Thr
690 695 700
Gln Thr Asp Leu Asn Phe Phe Leu Asp Ser Ser Pro His Leu Pro Leu
705 710 715 720
Gly Ser Ile Leu Lys His Ser Ser Phe Ser Val Ser Thr Asp Ser Ser
725 730 735
Asp Thr Glu Thr Gln Thr Glu Gly Val Ser Thr Ala Lys Asn Ile Pro
740 745 750
Ala Leu Glu Ser Lys Val Gln Leu Asn Ser Thr Glu Thr Gln Thr Met
755 760 765
Ser Ser Gly Phe Glu Thr Leu Gly Ser Leu Phe Phe Thr Ser Asn Glu
770 775 780
Thr Gln Thr Ala Met Asp Asp Phe Leu Leu Ala Asp Leu Ala Trp Asn
785 790 795 800
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<210> 43

<211> 2845

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (101).. (1609)

<400> 43

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accctgccag ggtccgagtc actccagaag ctgagcagcc atg aca ttt gct gag 115
                                     Met Thr Phe Ala Glu
                                     1           5
gac aag acc tat aag tat atc cga gac aac cac agc aag ttt tgc tgt 163
Asp Lys Thr Tyr Lys Tyr Ile Arg Asp Asn His Ser Lys Phe Cys Cys
                10           15           20
gtt gac gtt ctg gag atc ctg cct tac ctg tcc tgc ctc aca gct agt 211
Val Asp Val Leu Glu Ile Leu Pro Tyr Leu Ser Cys Leu Thr Ala Ser
                25           30           35
gac cag gat cga ctg cgg gct tcc tac agg cag atc ggg aac cgg gac 259
Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln Ile Gly Asn Arg Asp
                40           45           50
aca ctc tgg gga ctc ttc aat aat ctc cag cgc cgg cct ggc tgg gtg 307
Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg Arg Pro Gly Trp Val
                55           60           65
gag gtc ttc atc cgg gca ctg cag atc tgt gag ctg cct ggg ctg tct 355

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Ala Thr Tyr Gly Pro Val Ser Pro Thr Val Ser Phe Gln Pro Leu Pro
 215 220 225
 cgt act gcc ctg agg aca aac ctc ttg tct ggg gtc aca gta tca gcc 835
 Arg Thr Ala Leu Arg Thr Asn Leu Leu Ser Gly Val Thr Val Ser Ala
 230 235 240 245
 cta tct gct gat acc tct ttg tcc tcc tcg tcc act gga tca gct ttt 883
 Leu Ser Ala Asp Thr Ser Leu Ser Ser Ser Ser Thr Gly Ser Ala Phe
 250 255 260
 gca aag gga gct ggt gac cag gcc aaa gct gcc acc tgt ttc agt act 931
 Ala Lys Gly Ala Gly Asp Gln Ala Lys Ala Ala Thr Cys Phe Ser Thr
 265 270 275
 aca ctc acc aat tct gtg act acc agc tca gcg cct tct ccc aga ttg 979
 Thr Leu Thr Asn Ser Val Thr Thr Ser Ser Ala Pro Ser Pro Arg Leu
 280 285 290
 gtc cca gta aaa acc atg tct tcc aag ttg ccc ctc agt tca aag tcc 1027
 Val Pro Val Lys Thr Met Ser Ser Lys Leu Pro Leu Ser Ser Lys Ser
 295 300 305
 act gct gcg atg acg tct act gtg ctc acc aat aca gcg cca tca aaa 1075
 Thr Ala Ala Met Thr Ser Thr Val Leu Thr Asn Thr Ala Pro Ser Lys
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 Leu Pro Ser Asn Ser Val Tyr Ala Gly Thr Val Pro Ser Arg Val Pro
 330 335 340
 gct agt gtg gcc aaa gca cct gcc aac aca ata cca cct gag agg aac 1171
 Ala Ser Val Ala Lys Ala Pro Ala Asn Thr Ile Pro Pro Glu Arg Asn
 345 350 355
 agc aag caa gcc aag gag acc ccg gag ggt cca gca acc aaa gtc acc 1219

Ser Lys Gln Ala Lys Glu Thr Pro Glu Gly Pro Ala Thr Lys Val Thr
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 act gga ggc aac cag act gga cca aat agc agt atc agg agc ttg cac 1267
 Thr Gly Gly Asn Gln Thr Gly Pro Asn Ser Ser Ile Arg Ser Leu His
 375 380 385
 tct gga cca gag atg agc aag cca ggt gtg ctg gta tcc cag ttg gac 1315
 Ser Gly Pro Glu Met Ser Lys Pro Gly Val Leu Val Ser Gln Leu Asp
 390 395 400 405
 gag cca ttc tca gcc tgc tct gtg gac ctt gcc att agc cct agc agc 1363
 Glu Pro Phe Ser Ala Cys Ser Val Asp Leu Ala Ile Ser Pro Ser Ser
 410 415 420
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 Ser Leu Val Ser Glu Pro Asn His Gly Pro Glu Glu Asn Glu Tyr Ser
 425 430 435
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 Ser Pro Glu Pro Leu Ala Thr Gln Gln Pro Gln Glu Glu Glu Glu His
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 Cys Ala Ser Ser Met Pro Trp Ala Lys Trp Leu Gly Ala Thr Ser Ala
 470 475 480 485
 ctc ttg gct gta ttc ctg gca gtg atg ctg tac cgt agt agg cgc ctg 1603
 Leu Leu Ala Val Phe Leu Ala Val Met Leu Tyr Arg Ser Arg Arg Leu
 490 495 500
 gcc cag tgaagcctca gctgtatgct gttctcttgc tcagttctgc caagcatggt 1659

Ala Gln

ctctaggctt gggctagtag aggctgagtc agagaaactt aaatatggca aggtccactg 1719
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 aatatattct agttttatca ggataattaa aagagtttat ctgtgc 2845

<210> 44

<211> 503

<212> PRT

<213> Mus musculus

<400> 44

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 Cys Leu Thr Ala Ser Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln
 35 40 45
 Ile Gly Asn Arg Asp Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg
 50 55 60
 Arg Pro Gly Trp Val Glu Val Phe Ile Arg Ala Leu Gln Ile Cys Glu
 65 70 75 80
 Leu Pro Gly Leu Ser Asp Gln Val Thr Arg Val Tyr Gln Ser Tyr Leu
 85 90 95
 Pro Pro Gly Thr Ser Leu Arg Ser Leu Glu Pro Leu Gln Leu Pro Asp
 100 105 110
 Phe Pro Ala Ala Val Ser Gly Pro Ser Ala Phe Ala Pro Gly His Asn
 115 120 125
 Ile Pro Gly His Gly Leu Arg Glu Thr Pro Ser Cys Pro Lys Pro Val
 130 135 140
 Gln Asp Thr Gln Pro Pro Glu Ser Pro Val Glu Asn Ser Glu Gln Leu
 145 150 155 160
 Leu Gln Thr Asn Ser Gly Ala Val Ala Arg Met Ser Gly Gly Ser Leu
 165 170 175
 Ile Pro Ser Pro Asn Gln Gln Ala Leu Ser Pro Gln Pro Ser Arg Glu
 180 185 190
 His Gln Glu Gln Glu Pro Glu Leu Gly Gly Ala His Ala Ala Asn Val
 195 200 205
 Ala Ser Val Pro Ile Ala Thr Tyr Gly Pro Val Ser Pro Thr Val Ser

210	215	220	
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225	230	235	240
Val Thr Val Ser Ala Leu Ser Ala Asp Thr Ser Leu Ser Ser Ser Ser			
	245	250	255
Thr Gly Ser Ala Phe Ala Lys Gly Ala Gly Asp Gln Ala Lys Ala Ala			
	260	265	270
Thr Cys Phe Ser Thr Thr Leu Thr Asn Ser Val Thr Thr Ser Ser Ala			
	275	280	285
Pro Ser Pro Arg Leu Val Pro Val Lys Thr Met Ser Ser Lys Leu Pro			
	290	295	300
Leu Ser Ser Lys Ser Thr Ala Ala Met Thr Ser Thr Val Leu Thr Asn			
305	310	315	320
Thr Ala Pro Ser Lys Leu Pro Ser Asn Ser Val Tyr Ala Gly Thr Val			
	325	330	335
Pro Ser Arg Val Pro Ala Ser Val Ala Lys Ala Pro Ala Asn Thr Ile			
	340	345	350
Pro Pro Glu Arg Asn Ser Lys Gln Ala Lys Glu Thr Pro Glu Gly Pro			
	355	360	365
Ala Thr Lys Val Thr Thr Gly Gly Asn Gln Thr Gly Pro Asn Ser Ser			
	370	375	380
Ile Arg Ser Leu His Ser Gly Pro Glu Met Ser Lys Pro Gly Val Leu			
385	390	395	400
Val Ser Gln Leu Asp Glu Pro Phe Ser Ala Cys Ser Val Asp Leu Ala			
	405	410	415
Ile Ser Pro Ser Ser Ser Leu Val Ser Glu Pro Asn His Gly Pro Glu			
	420	425	430

Glu Asn Glu Tyr Ser Ser Phe Arg Ile Gln Val Asp Glu Ser Pro Ser
 435 440 445
 Ala Asp Leu Leu Gly Ser Pro Glu Pro Leu Ala Thr Gln Gln Pro Gln
 450 455 460
 Glu Glu Glu Glu His Cys Ala Ser Ser Met Pro Trp Ala Lys Trp Leu
 465 470 475 480
 Gly Ala Thr Ser Ala Leu Leu Ala Val Phe Leu Ala Val Met Leu Tyr
 485 490 495
 Arg Ser Arg Arg Leu Ala Gln
 500

<210> 45

<211> 3929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129).. (1748)

<400> 45

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 gagcagca atg ccg ttt gct gaa gac aag acc tat aag tat atc tgc cgc 170
 Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg
 1 5 10
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 Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr
 15 20 25 30

ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc acc tgc	266
Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys	
35 40 45	
aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat acc ctt	314
Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu	
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cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg agg ggc	362
Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly	
65 70 75	
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Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser	
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Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro	
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tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg gcc cac	506
Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His	
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agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac ccc atg	554
Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met	
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cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat tca gag	602
Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu	
145 150 155	
caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat cca gat	650
Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp	
160 165 170	

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 Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His
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 Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser
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 Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser
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 Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe
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 Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys
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 cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc agt ggg 986
 Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly
 275 280 285
 gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc acc ttg 1034
 Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu
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 atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca gca tct 1082
 Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser
 305 310 315

gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc cct ggt 1130
 Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly
 320 325 330
 gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa ttg ccc 1178
 Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro
 335 340 345 350
 atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct act agc 1226
 Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser
 355 360 365
 atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac ggg agc 1274
 Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser
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 Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu
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 ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta gac agc 1418
 Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser
 415 420 425 430
 ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc acc tcc 1466
 Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser
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 ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat aag tcc 1514
 Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser
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gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc cag ctc 1562
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 Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg
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 Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg
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 Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu
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 gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1748
 Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
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<211> 540

<212> PRT

<213> Homo sapiens

<400> 46

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35 40 45
Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60
Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80
Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
85 90 95
Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110
Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125
Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140
Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160
Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175
Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser

180	185	190
Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala		
195	200	205
Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser		
210	215	220
Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu		
225	230	235
Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser		
245	250	255
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly		
260	265	270
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu		
275	280	285
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro		
290	295	300
Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser		
305	310	315
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val		
325	330	335
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn		
340	345	350
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val		
355	360	365
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg		
370	375	380
Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly		
385	390	395
		400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
405 410 415
Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430
Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445
Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460
Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480
Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495
Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
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Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
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<210> 47

<211> 3173

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (144).. (2108)

<400> 47

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Met Ala Ala Ala Ala Ala Ala Ser His Leu

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aac ctg gat gcc ctc cgg gaa gtg cta gaa tgt ccc atc tgc atg gag				221
Asn Leu Asp Ala Leu Arg Glu Val Leu Glu Cys Pro Ile Cys Met Glu				
	15	20	25	
tcc ttc act gaa gag cag ctg cga ccc aag ctg ctg cac tgt ggc cat				269
Ser Phe Thr Glu Glu Gln Leu Arg Pro Lys Leu Leu His Cys Gly His				
	30	35	40	
acc atc tgc cgc cag tgt ctg gag aag ctc ctg gcc agc agc atc aat				317
Thr Ile Cys Arg Gln Cys Leu Glu Lys Leu Leu Ala Ser Ser Ile Asn				
	45	50	55	
ggc gtc cgc tgc ccc ttt tgc agc aag att act cgc atc acc agc ctg				365
Gly Val Arg Cys Pro Phe Cys Ser Lys Ile Thr Arg Ile Thr Ser Leu				
	60	65	70	
acc cag ctg acc gac aac ctg acg gtg ctg aag atc att gac aca gct				413
Thr Gln Leu Thr Asp Asn Leu Thr Val Leu Lys Ile Ile Asp Thr Ala				
	75	80	85	90
ggg ctc agt gag gcc gtc ggc ctg ctc atg tgc cga ggc tgt ggc cgg				461
Gly Leu Ser Glu Ala Val Gly Leu Leu Met Cys Arg Gly Cys Gly Arg				
	95	100	105	
cgg ctg cct cgg cag ttc tgc cga agc tgt ggt gtg gtg ttg tgt gaa				509
Arg Leu Pro Arg Gln Phe Cys Arg Ser Cys Gly Val Val Leu Cys Glu				
	110	115	120	
ccc tgc cgg gag gca gat cac caa ccc cct ggc cac tgc aca ctt ccg				557

Pro Cys Arg Glu Ala Asp His Gln Pro Pro Gly His Cys Thr Leu Pro
 125 130 135
 gtc aag gag gca gct gag gag cgg cgg agg gac ttc ggg gag aag ttg 605
 Val Lys Glu Ala Ala Glu Glu Arg Arg Arg Asp Phe Gly Glu Lys Leu
 140 145 150
 act cgt cta agg gaa ctt act gga gag ctg cag agg agg aag gca gcc 653
 Thr Arg Leu Arg Glu Leu Thr Gly Glu Leu Gln Arg Arg Lys Ala Ala
 155 160 165 170
 ttg gag ggc gtc tcc agg gat ctt cag gca agg tat aag gct gtt ctt 701
 Leu Glu Gly Val Ser Arg Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu
 175 180 185
 caa gaa tat ggc cat gag gaa cgc cgc atc cag gaa gag cta gcc cgc 749
 Gln Glu Tyr Gly His Glu Glu Arg Arg Ile Gln Glu Glu Leu Ala Arg
 190 195 200
 tct cgg aag ttc ttc aca ggc tcc ttg gct gag gtt gag aag tcc aac 797
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 Ser Gln Val Val Glu Glu Gln Ser Tyr Leu Leu Asn Ile Ala Glu Val
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 cag gcc gtg tct cgc tgt gac tac ttt cta gcg aag atc aag caa gct 893
 Gln Ala Val Ser Arg Cys Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala
 235 240 245 250
 gat gta gcc ctc ctg gag gag gca gcg gat gag gag gag ccc gag ctc 941
 Asp Val Ala Leu Leu Glu Glu Ala Ala Asp Glu Glu Glu Pro Glu Leu
 255 260 265
 act gcc agc cta ccc cgg gag ctt acc ctg caa gat gtg gag ctc ctt 989

Thr Ala Ser Leu Pro Arg Glu Leu Thr Leu Gln Asp Val Glu Leu Leu
 270 275 280
 aag gta gga cac gtt ggt cct ctg caa att ggc cag gct gtt aag aag 1037
 Lys Val Gly His Val Gly Pro Leu Gln Ile Gly Gln Ala Val Lys Lys
 285 290 295
 ccc cgg aca gtt aac atg gaa gat tcc tgg gca ggg gag gag gga gca 1085
 Pro Arg Thr Val Asn Met Glu Asp Ser Trp Ala Gly Glu Glu Gly Ala
 300 305 310
 gca tct tct gcc tca gcc tcg gta acc ttt aga gag atg gac atg agc 1133
 Ala Ser Ser Ala Ser Ala Ser Val Thr Phe Arg Glu Met Asp Met Ser
 315 320 325 330
 cct gag gaa gta gct ccc agc cct agg gct tcc ccc gcg aaa cag cgg 1181
 Pro Glu Glu Val Ala Pro Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg
 335 340 345
 agt tct gag gca gct tcc ggt atc cag cag tgt ctg ttt ctc aag aag 1229
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 Met Gly Ala Lys Gly Ser Thr Pro Gly Met Phe Asn Leu Pro Val Ser
 365 370 375
 ctc tat gtg acc agt cag agt gag gtg ctg gtt gcc gac cgg ggc aac 1325
 Leu Tyr Val Thr Ser Gln Ser Glu Val Leu Val Ala Asp Arg Gly Asn
 380 385 390
 tat cgt atc caa gtg ttc aac cgc aaa ggc ttt ttg aag gag atc cgc 1373
 Tyr Arg Ile Gln Val Phe Asn Arg Lys Gly Phe Leu Lys Glu Ile Arg
 395 400 405 410
 cgc agc ccc agc ggc att gat agc ttc gtg cta agc ttc ctt gga gcc 1421

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 Asp Leu Pro Asn Leu Thr Pro Leu Ser Val Ala Met Asn Cys His Gly
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 ctg att ggt gtc act gat agc tac gac aac tcc ctt aaa gtc tat acc 1517
 Leu Ile Gly Val Thr Asp Ser Tyr Asp Asn Ser Leu Lys Val Tyr Thr
 445 450 455
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 Met Asp Gly His Cys Val Ala Cys His Arg Ser Gln Leu Ser Lys Pro
 460 465 470
 tgg ggc atc aca gcc cta cca tct ggc cag ttt gtg gtg act gac gtg 1613
 Trp Gly Ile Thr Ala Leu Pro Ser Gly Gln Phe Val Val Thr Asp Val
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 Glu Gly Gly Lys Leu Trp Cys Phe Thr Val Asp Arg Gly Ala Gly Val
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 gtc aaa tac agc tgc ctc tgc agt gct gtg agg ccc aag ttt gtc acc 1709
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 510 515 520
 tgt gat gct gaa ggc aca gtc tac ttc acc caa ggc ttg ggg ctc aat 1757
 Cys Asp Ala Glu Gly Thr Val Tyr Phe Thr Gln Gly Leu Gly Leu Asn
 525 530 535
 gtg gaa aac cga cag aat gaa cac cac ctg gag ggt ggc ttc tcc atc 1805
 Val Glu Asn Arg Gln Asn Glu His His Leu Glu Gly Gly Phe Ser Ile
 540 545 550
 ggt tct gtt ggc ccc gat ggg cag ctg ggc cgg caa atc agc cac ttc 1853

Gly Ser Val Gly Pro Asp Gly Gln Leu Gly Arg Gln Ile Ser His Phe
 555 560 565 570
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 Phe Ser Glu Asn Glu Asp Phe Arg Cys Ile Ala Gly Met Cys Val Asp
 575 580 585
 gct cgg ggc gac ctc att gtg gca gat agc agc cgc aag gaa att ctc 1949
 Ala Arg Gly Asp Leu Ile Val Ala Asp Ser Ser Arg Lys Glu Ile Leu
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 His Phe Pro Lys Gly Gly Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu
 605 610 615
 acc tgt cca gtg ggc atc gcc ctc aca ccc aag ggg cag ctg ctg gtc 2045
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 620 625 630
 ttg gac tgt tgg gat cac tgc gtc aag atc tac agc tat cat ctg aga 2093
 Leu Asp Cys Trp Asp His Cys Val Lys Ile Tyr Ser Tyr His Leu Arg
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 Arg Tyr Ser Thr Pro
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 tcatc 3173

<210> 48

<211> 655

<212> PRT

<213> Mus musculus

<400> 48

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				20						25				30	
Leu	Arg	Pro	Lys	Leu	Leu	His	Cys	Gly	His	Thr	Ile	Cys	Arg	Gln	Cys
				35						40				45	
Leu	Glu	Lys	Leu	Leu	Ala	Ser	Ser	Ile	Asn	Gly	Val	Arg	Cys	Pro	Phe
				50						55				60	
Cys	Ser	Lys	Ile	Thr	Arg	Ile	Thr	Ser	Leu	Thr	Gln	Leu	Thr	Asp	Asn
65					70					75				80	

Leu Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu Ala Val
 85 90 95
 Gly Leu Leu Met Cys Arg Gly Cys Gly Arg Arg Leu Pro Arg Gln Phe
 100 105 110
 Cys Arg Ser Cys Gly Val Val Leu Cys Glu Pro Cys Arg Glu Ala Asp
 115 120 125
 His Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala Ala Glu
 130 135 140
 Glu Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg Glu Leu
 145 150 155 160
 Thr Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val Ser Arg
 165 170 175
 Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly His Glu
 180 185 190
 Glu Arg Arg Ile Gln Glu Glu Leu Ala Arg Ser Arg Lys Phe Phe Thr
 195 200 205
 Gly Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val Glu Glu
 210 215 220
 Gln Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser Arg Cys
 225 230 235 240
 Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu Leu Glu
 245 250 255
 Glu Ala Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu Pro Arg
 260 265 270
 Glu Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His Val Gly
 275 280 285
 Pro Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val Asn Met

290	295	300	
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305	310	315	320
Ser Val Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Ala Pro			
325	330	335	
Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg Ser Ser Glu Ala Ala Ser			
340	345	350	
Gly Ile Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly Ser			
355	360	365	
Thr Pro Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser Gln			
370	375	380	
Ser Glu Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val Phe			
385	390	395	400
Asn Arg Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly Ile			
405	410	415	
Asp Ser Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu Thr			
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Pro Leu Ser Val Ala Met Asn Cys His Gly Leu Ile Gly Val Thr Asp			
435	440	445	
Ser Tyr Asp Asn Ser Leu Lys Val Tyr Thr Met Asp Gly His Cys Val			
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Ala Cys His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala Leu			
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Pro Ser Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu Trp			
485	490	495	
Cys Phe Thr Val Asp Arg Gly Ala Gly Val Val Lys Tyr Ser Cys Leu			
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Cys Ser Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly Thr
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 Val Tyr Phe Thr Gln Gly Leu Gly Leu Asn Val Glu Asn Arg Gln Asn
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 545 550 555 560
 Gly Gln Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu Asp
 565 570 575
 Phe Arg Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu Ile
 580 585 590
 Val Ala Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly Gly
 595 600 605
 Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly Ile
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<213> Homo sapiens

<220>

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<222> (131).. (2089)

<400> 49

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aggaagagca atg gct gca gca gca gct tct cac ctg aac ctg gat gcc 169
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ctc cgg gaa gtg cta gaa tgc ccc atc tgc atg gag tcc ttc aca gaa 217
Leu Arg Glu Val Leu Glu Cys Pro Ile Cys Met Glu Ser Phe Thr Glu
      15              20              25
gag cag ctg cgt ccc aag ctt ctg cac tgt ggc cat acc atc tgc cgc 265
Glu Gln Leu Arg Pro Lys Leu Leu His Cys Gly His Thr Ile Cys Arg
      30              35              40              45
cag tgc ctg gag aag cta ttg gcc agt agc atc aat ggt gtc cgc tgt 313
Gln Cys Leu Glu Lys Leu Leu Ala Ser Ser Ile Asn Gly Val Arg Cys
            50              55              60
ccc ttt tgc agc aag att acc cgc ata acc agc ttg acc cag ctg aca 361
Pro Phe Cys Ser Lys Ile Thr Arg Ile Thr Ser Leu Thr Gln Leu Thr
            65              70              75
gac aat ctg aca gtg cta aag atc att gat aca gct ggg ctc agc gag 409
Asp Asn Leu Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu
            80              85              90
gct gtg ggg ctg ctc atg tgt cgg tcc tgt ggg cgg cgt ctg ccc cgg 457
Ala Val Gly Leu Leu Met Cys Arg Ser Cys Gly Arg Arg Leu Pro Arg
            95              100              105
caa ttc tgc cgg agc tgt ggt ttg gtg tta tgt gag ccc tgc cgg gag 505
Gln Phe Cys Arg Ser Cys Gly Leu Val Leu Cys Glu Pro Cys Arg Glu
110              115              120              125
gca gac cat cag cct cct ggc cac tgt aca ctc cct gtc aaa gaa gca 553

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Glu Leu Met Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val	
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tcc aag gac ctt cag gca agg tat aaa gca gtt ctc cag gag tat ggg	697
Ser Lys Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly	
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His Glu Glu Arg Arg Val Gln Asp Glu Leu Ala Arg Ser Arg Lys Phe	
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Phe Thr Gly Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val	
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Arg Cys Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu	
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Leu Glu Glu Thr Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu	
255	260
265	
cct cgg gag ctc acc ctg caa gat gtg gag ctc ctt aag gta ggt cat	985

Pro Arg Glu Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His	
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gtt ggc ccc ctc caa att gga caa gct gtt aag aag ccc cgg aca gtt	1033
Val Gly Pro Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val	
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aac gtg gaa gat tcc tgg gcc atg gag gcc aca gcg tct gct gcc tct	1081
Asn Val Glu Asp Ser Trp Ala Met Glu Ala Thr Ala Ser Ala Ala Ser	
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acc tct gtt act ttt aga gag atg gac atg agc ccg gag gaa gtg gtt	1129
Thr Ser Val Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Val	
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gcc agc cct agg gcc tca cct gct aaa cag cgg ggt cct gag gca gcc	1177
Ala Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg Gly Pro Glu Ala Ala	
335	340
345	
tcc aat atc cag cag tgc ctc ttt ctc aag aag atg ggg gcc aaa ggc	1225
Ser Asn Ile Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly	
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Ser Thr Pro Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser	
370	375
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caa ggt gaa gta cta gtc gct gac cgt ggt aac tat cgt ata caa gtc	1321
Gln Gly Glu Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val	
385	390
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ttt acc cgc aaa ggc ttt ttg aag gaa atc cgc cgc agc ccc agt ggc	1369
Phe Thr Arg Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly	
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Ile Asp Ser Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu
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 Val Ala Cys His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala
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 ttg cca tct ggc cag ttt gta gta acc gat gtg gaa ggt gga aag ctt 1609
 Leu Pro Ser Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu
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 Trp Cys Phe Thr Val Asp Arg Gly Ser Gly Val Val Lys Tyr Ser Cys
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 cta tgt agt gct gtg cgg ccc aaa ttt gtc acc tgt gat gct gag ggc 1705
 Leu Cys Ser Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly
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 Thr Val Tyr Phe Thr Gln Gly Leu Gly Leu Asn Leu Glu Asn Arg Gln
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 aat gag cac cac ctg gag ggt ggc ttt tcc att ggc tct gta ggc cct 1801
 Asn Glu His His Leu Glu Gly Gly Phe Ser Ile Gly Ser Val Gly Pro
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Asp Gly Gln Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu
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 atc gtg gct gac agt agt cgc aag gaa att ctc cat ttt cct aag ggt 1945
 Ile Val Ala Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly
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 Gly Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly
 610 615 620
 ata gcc cta act cct aag ggg cag ctg ctg gtc ttg gac tgt tgg gat 2041
 Ile Ala Leu Thr Pro Lys Gly Gln Leu Leu Val Leu Asp Cys Trp Asp
 625 630 635
 cat tgc atc aag atc tac agc tac cat ctg aga aga tat tcc acc cca 2089
 His Cys Ile Lys Ile Tyr Ser Tyr His Leu Arg Arg Tyr Ser Thr Pro
 640 645 650
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 gtatgaaagt cattcattta gtgctaccaa aggggataca caagcccttt aggaagcagt 2689

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<210> 50

<211> 653

<212> PRT

<213> Homo sapiens

<400> 50

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20 25 30

Arg Pro Lys Leu Leu His Cys Gly His Thr Ile Cys Arg Gln Cys Leu

35 40 45

Glu Lys Leu Leu Ala Ser Ser Ile Asn Gly Val Arg Cys Pro Phe Cys

50 55 60

Ser Lys Ile Thr Arg Ile Thr Ser Leu Thr Gln Leu Thr Asp Asn Leu

65 70 75 80

Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu Ala Val Gly

85 90 95

Leu Leu Met Cys Arg Ser Cys Gly Arg Arg Leu Pro Arg Gln Phe Cys

100	105	110
Arg Ser Cys Gly Leu Val Leu Cys Glu Pro Cys Arg Glu Ala Asp His		
115	120	125
Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala Ala Glu Glu		
130	135	140
Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg Glu Leu Met		
145	150	155
Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val Ser Lys Asp		
165	170	175
Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly His Glu Glu		
180	185	190
Arg Arg Val Gln Asp Glu Leu Ala Arg Ser Arg Lys Phe Phe Thr Gly		
195	200	205
Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val Glu Glu Gln		
210	215	220
Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser Arg Cys Asp		
225	230	235
Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu Leu Glu Glu		
245	250	255
Thr Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu Pro Arg Glu		
260	265	270
Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His Val Gly Pro		
275	280	285
Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val Asn Val Glu		
290	295	300
Asp Ser Trp Ala Met Glu Ala Thr Ala Ser Ala Ala Ser Thr Ser Val		
305	310	315
		320

Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Val Ala Ser Pro
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 Arg Ala Ser Pro Ala Lys Gln Arg Gly Pro Glu Ala Ala Ser Asn Ile
 340 345 350
 Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly Ser Thr Pro
 355 360 365
 Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser Gln Gly Glu
 370 375 380
 Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val Phe Thr Arg
 385 390 395 400
 Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly Ile Asp Ser
 405 410 415
 Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu Thr Pro Leu
 420 425 430
 Ser Val Ala Met Asn Cys Gln Gly Leu Ile Gly Val Thr Asp Ser Tyr
 435 440 445
 Asp Asn Ser Leu Lys Val Tyr Thr Leu Asp Gly His Cys Val Ala Cys
 450 455 460
 His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala Leu Pro Ser
 465 470 475 480
 Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu Trp Cys Phe
 485 490 495
 Thr Val Asp Arg Gly Ser Gly Val Val Lys Tyr Ser Cys Leu Cys Ser
 500 505 510
 Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly Thr Val Tyr
 515 520 525
 Phe Thr Gln Gly Leu Gly Leu Asn Leu Glu Asn Arg Gln Asn Glu His

530 535 540
 His Leu Glu Gly Gly Phe Ser Ile Gly Ser Val Gly Pro Asp Gly Gln
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 565 570 575
 Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu Ile Val Ala
 580 585 590
 Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly Gly Gly Tyr
 595 600 605
 Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly Ile Ala Leu
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<210> 51

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (357)

<400> 51

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 cctcctcagc cagcc atg ctg gag cat ctg agc tcg ctg ccc acg cag atg 171

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met
1 5 10
gtg agg gcg caa ccc ggg gac ctc tgc acg ccg ttc ttg tgc ctg gca 219
Val Arg Ala Gln Pro Gly Asp Leu Cys Thr Pro Phe Leu Cys Leu Ala
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gct tcg aag ccc atg ttg gag cac cga ccc ggt gct gcg ctg ttc cgg 267
Ala Ser Lys Pro Met Leu Glu His Arg Pro Gly Ala Ala Leu Phe Arg
30 35 40
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Ala Arg Met Val Thr Val His Pro Leu Ser Arg Ile Ala Ser Trp Val
45 50 55 60
ccc ttc tct tct act ccg cga gaa tct cct gtc cat tct cgg 357
Pro Phe Ser Ser Thr Pro Arg Glu Ser Pro Val His Ser Pro
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 cacaagtatg aagtttcttt cagggtgtaaa taatgaaaaa taaatgcctc ataatgata 1977
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<210> 52

<211> 74

<212> PRT

<213> Homo sapiens

<400> 52

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10

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Pro Gly Asp Leu Cys Thr Pro Phe Leu Cys Leu Ala Ala Ser Lys Pro

20

25

30

Met Leu Glu His Arg Pro Gly Ala Ala Leu Phe Arg Ala Arg Met Val

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 Thr Val His Pro Leu Ser Arg Ile Ala Ser Trp Val Pro Phe Ser Ser
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 Thr Pro Arg Glu Ser Pro Val His Ser Pro
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<210> 53

<211> 798

<212> DNA

<213> Homo sapiens

<220>

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<222> (136).. (441)

<400> 53

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 cctcctcagc cagcc atg ctg gag cat ctg agc tcg ctg ccc acg cag atg 171

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met

1

5

10

gat tac aag ggc cag aag cta gct gaa cag atg ttt cag gga att att 219

Asp Tyr Lys Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile

15

20

25

ctt ttt tct gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag 267

Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln

30

35

40

ttc ggg tgg act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt 315

Phe Gly Trp Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys

45 50 55 60
 ttg ctg aca ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag 363
 Leu Leu Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys
 65 70 75
 tgg tta cct gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa 411
 Trp Leu Pro Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu
 80 85 90
 aga aaa att aag agg cat gct aaa aat aat tgaggttttc atgattcagc 461
 Arg Lys Ile Lys Arg His Ala Lys Asn Asn
 95 100
 acctgctttt gtttctgtga gatgagctaa attgctttca taccccagat aagggtctaaa 521
 accacctaatt gctcttatgg cacagctgtg tatagattta gttctcttta tacttcattt 581
 ctagcccagt tgggttttga tttatataag tagtttagac cttctcttca taatcttget 641
 ctgagatggg gaacagaaca cacaagtatg aagtttcttt caggtgtaaa taatgaaaaa 701
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 taaccatttt aatgtttcca attaaacctc atagtgc 798

<210> 54

<211> 102

<212> PRT

<213> Homo sapiens

<400> 54

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 Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr

35	40	45
Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu		
50	55	60
Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val		
65	70	75
Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys		
85	90	95
Arg His Ala Lys Asn Asn		
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<210> 55

<211> 1583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (513).. (1226)

<400> 55

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actttgaagt gatcggaag tgatgtgacg ctccggggat cccaccaggc tcagagacac 180
ccctgggttag ggctccgaca agtcgttccc ctcaaaggct cgccgcggcc gcccttactg 240
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ccgcgcgcga ggccccggag ccagcccgt tgtctggccg cccgcgttcc ctgcacgctg 360
ggccgagcac acttgccctc tagctccgtg gcagccgcgc agccccacta cgcccagcca 420
gcccgcagcg gtaaccgcta gagcgtcgcg ccaagcaggc gccgcggggc agccctgccg 480
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										Met	Glu	Thr	Arg	Gly	Arg	Arg		
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cgg	ccg	ttg	ggc	cgc	gca	agt	act	gtc	aag	gac	agt	ttt	cgg	gac	ggg		581	
Arg	Pro	Leu	Gly	Arg	Ala	Ser	Thr	Val	Lys	Asp	Ser	Phe	Arg	Asp	Gly			
			10				15				20							
gga	cgc	ggc	tcc	agg	cac	cca	aca	gca	ctg	acg	gcg	aac	act	tca	cgg		629	
Gly	Arg	Gly	Ser	Arg	His	Pro	Thr	Ala	Leu	Thr	Ala	Asn	Thr	Ser	Arg			
			25				30				35							
gcg	cgc	gat	gcc	tcg	aca	agg	cgg	ccg	cca	cca	cca	cct	cag	ctg	ccc		677	
Ala	Arg	Asp	Ala	Ser	Thr	Arg	Arg	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Pro			
			40				45				50				55			
tcg	cgg	gca	gca	cgg	cgc	ggc	aaa	agc	gca	cgt	cgc	cta	gcg	atg	gcg		725	
Ser	Arg	Ala	Ala	Arg	Arg	Gly	Lys	Ser	Ala	Arg	Arg	Leu	Ala	Met	Ala			
						60				65				70				
cgg	ggc	ggg	gac	acg	ggc	tgt	acc	ggc	ccg	tcg	gag	act	tcc	gct	tcc		773	
Arg	Gly	Gly	Asp	Thr	Gly	Cys	Thr	Gly	Pro	Ser	Glu	Thr	Ser	Ala	Ser			
			75				80				85							
ggg	gcc	gcc	gcc	atc	gct	ctc	ccg	ggc	tta	gaa	ggc	ccg	gct	act	gac		821	
Gly	Ala	Ala	Ala	Ile	Ala	Leu	Pro	Gly	Leu	Glu	Gly	Pro	Ala	Thr	Asp			
			90				95				100							
gcg	cag	tgc	cag	acc	tta	gcc	ctc	acg	gtc	ctt	aag	tct	cgg	tcg	ccc		869	
Ala	Gln	Cys	Gln	Thr	Leu	Ala	Leu	Thr	Val	Leu	Lys	Ser	Arg	Ser	Pro			
			105				110				115							
tcg	cct	cgc	agc	ctg	cca	ccc	gcg	ctc	agc	tgc	ccg	cct	cct	cag	cca		917	
Ser	Pro	Arg	Ser	Leu	Pro	Pro	Ala	Leu	Ser	Cys	Pro	Pro	Pro	Gln	Pro			
			120				125				130				135			
gcc	atg	ctg	gag	cat	ctg	agc	tcg	ctg	ccc	acg	cag	atg	gat	tac	aag		965	

Ala Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys
 140 145 150
 ggc cag aag cta gct gaa cag atg ttt cag gga att att ctt ttt tct 1013
 Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser
 155 160 165
 gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg 1061
 Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp
 170 175 180
 act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt ttg ctg aca 1109
 Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr
 185 190 195
 ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct 1157
 Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro
 200 205 210 215
 gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att 1205
 Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile
 220 225 230
 aag agg cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt 1256
 Lys Arg His Ala Lys Asn Asn
 235
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<211> 238

<212> PRT

<213> Homo sapiens

<400> 56

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 35 40 45
 Pro Pro Pro Pro Gln Leu Pro Ser Arg Ala Ala Arg Arg Gly Lys Ser
 50 55 60
 Ala Arg Arg Leu Ala Met Ala Arg Gly Gly Asp Thr Gly Cys Thr Gly
 65 70 75 80
 Pro Ser Glu Thr Ser Ala Ser Gly Ala Ala Ala Ile Ala Leu Pro Gly
 85 90 95
 Leu Glu Gly Pro Ala Thr Asp Ala Gln Cys Gln Thr Leu Ala Leu Thr
 100 105 110
 Val Leu Lys Ser Arg Ser Pro Ser Pro Arg Ser Leu Pro Pro Ala Leu
 115 120 125
 Ser Cys Pro Pro Pro Gln Pro Ala Met Leu Glu His Leu Ser Ser Leu
 130 135 140
 Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Glu Gln Met Phe
 145 150 155 160
 Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr Gly Tyr
 165 170 175

Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala Gly Phe

180

185

190

Ala Phe Ser Cys Leu Leu Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg

195

200

205

His Pro Leu Lys Trp Leu Pro Val Gln Glu Ser Ser Thr Asp Asp Lys

210

215

220

Lys Pro Gly Glu Arg Lys Ile Lys Arg His Ala Lys Asn Asn

225

230

235

<210> 57

<211> 782

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110).. (421)

<400> 57

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gcctcgcagc ctgccaccgc cgtcagctg cccgcctcct cagccagcc atg ctg gag 118

Met Leu Glu

1

cat ctg agc tcg ctg ccc acg cag atg gat tac aag ggc cag aag cta 166

His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu

5

10

15

gct gaa cag atg ttt cag gga att att ctt ttt tct gca ata gtt gga 214

Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly

20

25

30

35

ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg act gtc tat ata 262
 Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile
 40 45 50
 gtt atg gcc gga ttt gct ttt tca tgt ttg gcc cag ctg aca ctt cct 310
 Val Met Ala Gly Phe Ala Phe Ser Cys Leu Ala Gln Leu Thr Leu Pro
 55 60 65
 cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct gtt caa 358
 Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val Gln
 70 75 80
 gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att aag agg 406
 Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys Arg
 85 90 95
 cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt gtttctgtga 461
 His Ala Lys Asn Asn
 100
 gatgagctaa attgctttca taccacagat aagagctaaa accacctaata gctcttatgg 521
 cacagctgtg tatagattta gttctcttta tacttcattt ctagcccagt tgggttttga 581
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<210> 58

<211> 104

<212> PRT

<213> Homo sapiens

<400> 58

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 Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
 35 40 45
 Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Ala Gln Leu
 50 55 60
 Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu
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 Pro Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys
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 Ile Lys Arg His Ala Lys Asn Asn
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<210> 59

<211> 2402

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(450)

<400> 59

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Ala Glu Leu Pro Pro Gln Pro Ala Ala Gly Gln Tyr Gly Pro Gly Asp
 15 20 25
 tcg gca gat gca ccc aac ccc tgg tcg agg gag ccg cgt gac cga tca 147
 Ser Ala Asp Ala Pro Asn Pro Trp Ser Arg Glu Pro Arg Asp Arg Ser
 30 35 40
 ggg cat ctg tcc caa aca cca aga agc cct gaa gct ctt ctg cga ggt 195
 Gly His Leu Ser Gln Thr Pro Arg Ser Pro Glu Ala Leu Leu Arg Gly
 45 50 55
 aga cga aga ggc cat ctg tgt ggt gtg ccg aga atc cag gag cca caa 243
 Arg Arg Arg Gly His Leu Cys Gly Val Pro Arg Ile Gln Glu Pro Gln
 60 65 70
 aca gca cag cgt ggt gcc att gga gga ggt ggt gca gga gta caa ggc 291
 Thr Ala Gln Arg Gly Ala Ile Gly Gly Gly Gly Ala Gly Val Gln Gly
 75 80 85 90
 caa act gca ggg gca cgt gga acc act gag gaa gca cct gga ggc agt 339
 Gln Thr Ala Gly Ala Arg Gly Thr Thr Glu Glu Ala Pro Gly Gly Ser
 95 100 105
 gca gaa gat gaa agc caa gga gga gag gcg agt gac aga act gaa gag 387
 Ala Glu Asp Glu Ser Gln Gly Gly Glu Ala Ser Asp Arg Thr Glu Glu
 110 115 120
 cca gat gaa gtc aga gct ggc agc ggt ggc ctc gga gtt tgg gcg act 435
 Pro Asp Glu Val Arg Ala Gly Ser Gly Gly Leu Gly Val Trp Ala Thr
 125 130 135
 gac acg gtt tct ggc tgaagagcag gcagggtgg aacggcgtct cagagagatg 490
 Asp Thr Val Ser Gly
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<210> 60

<211> 143

<212> PRT

<213> Homo sapiens

<400> 60

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Pro	Ala	Ala	Gly	Gln	Tyr	Gly	Pro	Gly	Asp	Ser	Ala	Asp	Ala	Pro	Asn
			20					25					30		
Pro	Trp	Ser	Arg	Glu	Pro	Arg	Asp	Arg	Ser	Gly	His	Leu	Ser	Gln	Thr
			35					40					45		
Pro	Arg	Ser	Pro	Glu	Ala	Leu	Leu	Arg	Gly	Arg	Arg	Arg	Gly	His	Leu
			50					55					60		
Cys	Gly	Val	Pro	Arg	Ile	Gln	Glu	Pro	Gln	Thr	Ala	Gln	Arg	Gly	Ala
			65					70					75		80
Ile	Gly	Gly	Gly	Gly	Ala	Gly	Val	Gln	Gly	Gln	Thr	Ala	Gly	Ala	Arg
					85					90				95	
Gly	Thr	Thr	Glu	Glu	Ala	Pro	Gly	Gly	Ser	Ala	Glu	Asp	Glu	Ser	Gln
			100					105					110		
Gly	Gly	Glu	Ala	Ser	Asp	Arg	Thr	Glu	Glu	Pro	Asp	Glu	Val	Arg	Ala
			115					120					125		
Gly	Ser	Gly	Gly	Leu	Gly	Val	Trp	Ala	Thr	Asp	Thr	Val	Ser	Gly	

130

135

140

<210> 61

<211> 2402

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86).. (1366)

<400> 61

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ccgcccccaac ctgcagctgg ccaat atg gtc cag gtg att cgg cag atg cac 112
                                Met Val Gln Val Ile Arg Gln Met His
                                1             5
cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc tgt ccc 160
Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro
    10             15             20             25
aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa gag gcc 208
Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala
                30             35             40
atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac agc gtg 256
Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val
                45             50             55
gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg cag ggg 304
Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly
                60             65             70
cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag atg aaa 352

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His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys
 75 80 85
 gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg aag tca 400
 Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser
 90 95 100 105
 gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg ttt ctg 448
 Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu
 110 115 120
 gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg cat gaa 496
 Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu
 125 130 135
 gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca gaa cag 544
 Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln
 140 145 150
 gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg agc cag 592
 Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln
 155 160 165
 cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc aat agg 640
 Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg
 170 175 180 185
 tgt gaa gag gta cag ctg cag ccc cca gag gtc tgg tcc cct gac ccg 688
 Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro
 190 195 200
 tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg agg aaa 736
 Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys
 205 210 215
 atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg ctg gac 784

Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp
 220 225 230
 cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc cgg ggg 832
 Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly
 235 240 245
 gtc cgc ctg gca gag cgg cgg cag gag gtt gct gac cat ccc aag cgc 880
 Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg
 250 255 260 265
 ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag ggc ttc cgc tcc ggc 928
 Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly
 270 275 280
 cgg cac tac tgg gag gta gag gtg ggc ggg cgg cgg ggc tgg gcg gtg 976
 Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp Ala Val
 285 290 295
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 Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly Pro Gly
 300 305 310
 ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc tcg cgc cat cac cat 1072
 Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His His His
 315 320 325
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 Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln Arg Glu
 330 335 340 345
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 Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln Ser Ser
 350 355 360
 aca gaa cag acg ctg ctg agc ccc agt gag aaa cca agg cgc ttt ggt 1216

Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg Phe Gly
 365 370 375
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 Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn Ala Glu
 380 385 390
 act cta gcc cac gtg cac acc ttc tcg gct gcc ttc ctg ggc gag cgt 1312
 Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly Glu Arg
 395 400 405
 gtc ttt cct ttc ttc cgg gtg ctc tcc aag ggc acc cgc atc aag ctc 1360
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 410 415 420 425
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218/861

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 Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu
 165 170 175
 Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln
 180 185 190
 Pro Pro Glu Val Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp
 195 200 205
 Phe Leu Thr Asp Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln
 210 215 220
 Ala Ala Arg Val Asp Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala
 225 230 235 240
 Leu Met Leu Ser Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg
 245 250 255
 Gln Glu Val Ala Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val
 260 265 270
 Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu
 275 280 285
 Val Gly Gly Arg Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr
 290 295 300
 His His Lys Glu Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly
 305 310 315 320
 Asp Ala Ser Ser Ser Arg His His His Arg Arg Arg Arg Leu His Leu
 325 330 335
 Pro Gln Gln Pro Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn
 340 345 350
 Gly Lys Arg Tyr Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser

355	360	365
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370	375	380
Gly Arg Leu Gly Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr		
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Leu Ser Lys Gly Thr Arg Ile Lys Leu Cys Pro		
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<210> 63

<211> 2691

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (711).. (2264)

<400> 63

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 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly
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 Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg
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 gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag gac ctg agg 1148
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 Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln
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 atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc 1388
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 Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu
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 gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac 1484
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Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu
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 Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met
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 Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg
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 ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg 1724
 Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met
 325 330 335
 cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca 1772
 His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala
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 gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg 1820
 Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg
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 Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe
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 Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro
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 gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg 1964

Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val
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 agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg 2012
 Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr
 420 425 430
 ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc 2060
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 Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro
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 Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg
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 tcc ggc cgg cac tac tgg gag gag cct aaa gaa ccc tcc tgg cct cca 2204
 Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp Pro Pro
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 gct cag cct tct ctc acc tac tat gtc tgt cca aca gac cgg cca gaa 2252
 Ala Gln Pro Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp Arg Pro Glu
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 ttt agc ttc act tgagagagat ctggaatggt cgccatgatt gaaaccacgc 2304
 Phe Ser Phe Thr
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<210> 64

<211> 518

<212> PRT

<213> Homo sapiens

<400> 64

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			20					25					30		
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
			35					40					45		
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
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	65				70					75				80	
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Ser	Arg	Ser	Ser	Trp	Asp	Asn	Met	Asp	Tyr	Val	Trp	Glu	Glu	Glu	Asp
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Glu	Glu	Glu	Asp	Leu	Asp	Tyr	Tyr	Leu	Gly	Asp	Met	Glu	Glu	Glu	Asp
				130						135				140	

Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val
145 150 155 160
Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala
165 170 175
Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg
180 185 190
Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile
195 200 205
Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln
210 215 220
Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val
225 230 235 240
Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
245 250 255
Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala
260 265 270
Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val
275 280 285
Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser
290 295 300
Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu
305 310 315 320
Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg
325 330 335
Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg
340 345 350
Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln

355 360 365
 Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu
 370 375 380
 Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp
 385 390 395 400
 Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala
 405 410 415
 Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp
 420 425 430
 Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro
 435 440 445
 Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp
 450 455 460
 His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly
 465 470 475 480
 Phe Arg Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp
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 Pro Glu Phe Ser Phe Thr
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<210> 65

<211> 1749

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (24).. (1322)

<400> 65

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Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15 20 25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu

30 35 40

gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag 197

Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu

45 50 55

gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag 245

Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu

60 65 70

gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca 293

Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro

75 80 85 90

gcc cct cgg agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct 341

Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro

95 100 105

cgg cgg agc ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg 389

Arg Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val

110 115 120

att cgg cag atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat 437
 Ile Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp
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 cag ggc atc tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag 485
 Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu
 140 145 150
 gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac 533
 Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His
 155 160 165 170
 aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag 581
 Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys
 175 180 185
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala
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 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys
 205 210 215
 agc cag atg aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga 725
 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg
 220 225 230
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu
 235 240 245 250
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser
 255 260 265

cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869
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 270 275 280
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 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys
 285 290 295
 gag act ttc aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc 965
 Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val
 300 305 310
 tgg tcc cct gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat 1013
 Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp
 315 320 325 330
 gcc atc gtg agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg 1061
 Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val
 335 340 345
 gac ctg acg ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc 1109
 Asp Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser
 350 355 360
 cct gac cgc cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct 1157
 Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala
 365 370 375
 gac cat ccc aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag 1205
 Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln
 380 385 390
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 Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser
 395 400 405 410

tgg cct cca gct cag cct tct ctc acc tac tat gtc tgt cca aca gac 1301
 Trp Pro Pro Ala Gln Pro Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp

415

420

425

cgg cca gaa ttt agc ttc act tgagagagat ctggaatggt cgccatgatt 1352
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430

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<210> 66

<211> 433

<212> PRT

<213> Homo sapiens

<400> 66

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 35 40 45
 Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg Gly Glu Asp
 50 55 60

232/861

275 280 285
Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys
290 295 300
Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro Cys
305 310 315 320
Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys Met
325 330 335
Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp Pro
340 345 350
Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly Val
355 360 365
Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg Phe
370 375 380
Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg
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His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp Pro Pro Ala Gln Pro
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<210> 67

<211> 2694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24).. (1658)

<400> 67

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1

5

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Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15

20

25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu

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35

40

gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag 197

Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu

45

50

55

gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag 245

Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu

60

65

70

gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca 293

Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro

75

80

85

90

gcc cct cgg agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct 341

Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro

95

100

105

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110

115

120

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 Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu
 140 145 150
 gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac 533
 Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His
 155 160 165 170
 aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag 581
 Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys
 175 180 185
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala
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 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys
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 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg
 220 225 230
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu
 235 240 245 250
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser
 255 260 265
 cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869

Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala
 270 275 280
 cag gag cgg agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag 917
 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys
 285 290 295
 gag act ttc aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc 965
 Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val
 300 305 310
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 Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp
 315 320 325 330
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 Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val
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 gac ctg acg ctg gac cct gac acg gct cac cgg gcc ctg atg ctg tcc 1109
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 cct gac cgc cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct 1157
 Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala
 365 370 375
 gac cat ccc aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag 1205
 Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln
 380 385 390
 ggc ttc cgc tcc ggc cgg cac tac tgg gag gta gag gtg ggc ggg cgg 1253
 Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg
 395 400 405 410
 cgg ggc tgg gcg gtg ggt gct gcc cgt gaa tca acc cat cat aag gaa 1301

Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu
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 aag gtg ggc cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc 1349
 Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser
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 tcg cgc cat cac cat cgc cgc cgc cgg ctc cac ctg ccc cag cag ccc 1397
 Ser Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro
 445 450 455
 ctg ctc cag cgg gaa gtg tgg tgc gtg ggc acc aac ggc aaa cgc tat 1445
 Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr
 460 465 470
 cag gcc cag agc tcc aca gaa cag acg ctg ctg agc ccc agt gag aaa 1493
 Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys
 475 480 485 490
 cca agg cgc ttt ggt gtg tac ctg gac tat gaa gct ggg cgc ctg ggc 1541
 Pro Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly
 495 500 505
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 Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala
 510 515 520
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 Phe Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly
 525 530 535
 acc cgc atc aag ctc tgc cct tgattatcct gccaccgca ggggcccctc 1688
 Thr Arg Ile Lys Leu Cys Pro
 540 545
 tgtcagcact tggggggtgg gtggtggagg gtggcccgta agtttgaggg ctcaaaggct 1748

cttcccactg cttgttactg tgttgettcc cactccccct tgaccccagg cccctgcttc 1808
 tccctctagg agcctaaaga accctcctgg cctccagctc agccttctct cacctactat 1868
 gtctgtccaa caggtctgca tgggtccctg ataatgagaa cagctgcctg gtcttctctc 1928
 ccagtctgcc tagcccagcc ctgggactgg aatttgagta ggggatgagg ggaaattgta 1988
 atttcattcc ttaacttcct tttccccacc cctgctcttc aacctcttta tcagttctga 2048
 ggctggaggg tttgggcaag gcaacatccc cattccaatt ccattttctg atgcagattt 2108
 tagctgaggg atttggaagc catttgggga ggcaggtctg gccaaagggt agagctgggt 2168
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 ggtttgggtc ccaggagga ggccttggg tataatctat ttttctagga gcctcttgcc 2588
 ttgtcacttg cagctttgc cctctgcttt gatggctgag gtgaactcat gttctttggg 2648
 aaaagggaag gcgtgctgtg gaaataaaat gtttatttgc ttctct 2694

<210> 68

<211> 545

<212> PRT

<213> Homo sapiens

<400> 68

Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu Val Glu Glu

1 5 10 15

Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg Ser Ser Trp

20 25 30

Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu Glu Asp Leu

35	40	45	
Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg Gly Glu Asp			
50	55	60	
Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu Glu Asp Leu			
65	70	75	80
Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg Arg Cys Phe			
85	90	95	
Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser Phe Arg Pro			
100	105	110	
Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln Met His Pro			
115	120	125	
Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro Lys			
130	135	140	
His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala Ile			
145	150	155	160
Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val Val			
165	170	175	
Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly His			
180	185	190	
Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys Ala			
195	200	205	
Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser Glu			
210	215	220	
Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu Ala			
225	230	235	240
Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu Ala			
245	250	255	

Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala
260 265 270
Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln
275 280 285
Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys
290 295 300
Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro Cys
305 310 315 320
Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys Met
325 330 335
Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp Pro
340 345 350
Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly Val
355 360 365
Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg Phe
370 375 380
Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg
385 390 395 400
His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp Ala Val Gly
405 410 415
Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly Pro Gly Gly
420 425 430
Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His His His Arg
435 440 445
Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln Arg Glu Val
450 455 460
Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln Ser Ser Thr

465 470 475 480
 Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg Phe Gly Val
 485 490 495
 Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn Ala Glu Thr
 500 505 510
 Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly Glu Arg Val
 515 520 525
 Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr Arg Ile Lys Leu Cys
 530 535 540

Pro

545

<210> 69

<211> 3636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (711).. (2600)

<400> 69

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 tttctcccca gcggcggggg atgggggtag gcggttcctc tggttctttct gcgttccccg 180
 cggcctctta ccacagagac gcgggcctcc accgtcctag ccctcccgcc ctgttctcta 240
 gtgcggacta gagcgtctcc tcgccatttc ctgtcgccct ggggccccgc ggggaaaaag 300
 ggggagtagc aggacagcgg agggaagtcg cgagcttagg tggtgtgtag acgccggaag 360
 tggttggaag gaggccggaa gctaggggcg gggccaggaa gtgaggaggg gcgggggttt 420

atgaggagtc caagggagca ttggggcaga cttgcactca gagccacctg agggacttgg 480
 cgggtggcgcc cagcactgtc ccctccctc gtagagacac ggttgtcgtt tgggagtagg 540
 gaacactgtg ttgggggtggg ttgtcggcag gacatctctc tggctgctct tggggcgagg 600
 tgtggagggg cagggctggg ggtggagccg ggtcgccagg gcgtcggtag ggaagacccc 660
 cgcccctcgc cccccaccg aacctctaca ctggctggct ggacactaag atg gct 716

Met Ala

1

gcc gtt gcc atg aca ccc aac cct gtg cag acc ctt cag gag gag gcg 764
 Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu Glu Ala

5

10

15

gtg tgc gcc atc tgc ctc gat tac ttc acg gac ccc gtg tcc atc ggc 812
 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly

20

25

30

tgc ggg cac aac ttc tgc cga gtt tgt gta acc cag ttg tgg ggt ggg 860
 Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp Gly Gly

35

40

45

50

gag gat gag gag gac aga gat gag tta gat cgg gag gag gag gag gag 908
 Glu Asp Glu Glu Asp Arg Asp Glu Leu Asp Arg Glu Glu Glu Glu Glu

55

60

65

gac gga gag gag gag gaa gtg gag gct gtg ggg gct ggc gcg ggg tgg 956
 Asp Gly Glu Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala Gly Trp

70

75

80

gac acc ccc atg cgg gat gaa gac tac gag ggt gac atg gag gag gag 1004
 Asp Thr Pro Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu

85

90

95

gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc atg agc agg 1052
 Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg

100	105	110	
tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag gac gag gag			1100
Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu			
115	120	125	130
gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag gac ctg agg			1148
Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg			
	135	140	145
ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag gtt gag gaa			1196
Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu			
	150	155	160
gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca gcc cct cgg			1244
Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg			
	165	170	175
agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct cgg cgg agc			1292
Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser			
	180	185	190
ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg att cgg cag			1340
Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln			
195	200	205	210
atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc			1388
Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile			
	215	220	225
tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa			1436
Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu			
	230	235	240
gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac			1484
Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His			

245	250	255	
agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg			1532
Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu			
260	265	270	
cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag			1580
Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys			
275	280	285	290
atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg			1628
Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met			
	295	300	305
aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg			1676
Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg			
	310	315	320
ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg			1724
Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met			
	325	330	335
cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca			1772
His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala			
	340	345	350
gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg			1820
Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg			
	355	360	365
agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc			1868
Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe			
	375	380	385
aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc tgg tcc cct			1916
Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro			

390	395	400	
gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg			1964
Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val			
405	410	415	
agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg			2012
Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr			
420	425	430	
ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc			2060
Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg			
435	440	445	450
cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct gac cat ccc			2108
Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro			
455	460	465	
aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag ggc ttc cgc			2156
Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg			
470	475	480	
tcc ggc cgg cac tac tgg gag gta gag gtg ggc ggg cgg cgg ggc tgg			2204
Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp			
485	490	495	
gcg gtg ggt gct gcc cgt gaa tca acc cat cat aag gaa aag gtg ggc			2252
Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly			
500	505	510	
cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc tcg cgc cat			2300
Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His			
515	520	525	530
cac cat cgc cgc cgc cgg ctc cac ctg ccc cag cag ccc ctg ctc cag			2348
His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln			

535	540	545	
cgg gaa gtg tgg tgc gtg ggc acc aac ggc aaa cgc tat cag gcc cag			2396
Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln			
550	555	560	
agc tcc aca gaa cag acg ctg ctg agc ccc agt gag aaa cca agg cgc			2444
Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg			
565	570	575	
ttt ggt gtg tac ctg gac tat gaa gct ggg cgc ctg ggc ttc tac aac			2492
Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn			
580	585	590	
gca gag act cta gcc cac gtg cac acc ttc tcg gct gcc ttc ctg ggc			2540
Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly			
595	600	605	610
gag cgt gtc ttt cct ttc ttc cgg gtg ctc tcc aag ggc acc cgc atc			2588
Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr Arg Ile			
615	620	625	
aag ctc tgc cct tgattatcct gccaccgca ggggccctc tgtcagcact			2640
Lys Leu Cys Pro			
630			
tggggggtgg gtggtggagg gtggcccgta agtttgagg ctcaaaggct cttccactg			2700
cttggttactg tggtgcttcc cactccccct tgaccccgagg cccctgcttc tccctctagg			2760
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<210> 70

<211> 630

<212> PRT

<213> Homo sapiens

<400> 70

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Glu	Ala	Val	Cys	Ala	Ile	Cys	Leu	Asp	Tyr	Phe	Thr	Asp	Pro	Val	Ser
				20					25					30	
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
				35					40					45	
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
				50					55					60	
Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Val	Glu	Ala	Val	Gly	Ala	Gly	Ala
				65					70					75	
Gly	Trp	Asp	Thr	Pro	Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu
				85					90					95	

Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met
 100 105 110
 Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp
 115 120 125
 Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp
 130 135 140
 Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val
 145 150 155 160
 Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala
 165 170 175
 Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg
 180 185 190
 Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile
 195 200 205
 Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln
 210 215 220
 Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val
 225 230 235 240
 Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
 245 250 255
 Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala
 260 265 270
 Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val
 275 280 285
 Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser
 290 295 300
 Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu

305 310 315 320
 Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg
 325 330 335
 Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg
 340 345 350
 Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln
 355 360 365
 Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu
 370 375 380
 Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp
 385 390 395 400
 Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala
 405 410 415
 Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp
 420 425 430
 Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro
 435 440 445
 Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp
 450 455 460
 His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly
 465 470 475 480
 Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg
 485 490 495
 Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys
 500 505 510
 Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser
 515 520 525

Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu
 530 535 540
 Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln
 545 550 555 560
 Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro
 565 570 575
 Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe
 580 585 590
 Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe
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 Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr
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<210> 71

<211> 3833

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (711)..(1898)

<400> 71

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 gaacactgtg ttgggggtggg ttgtcggcag gacatctctc tggctgctct tggggcgagg 600
 tgtggagggg cagggtggg ggtggagccg ggtcgccagg gcgtcggtag ggaagacccc 660
 cgcccctcgc cccccaccg aacctctaca ctggctggct ggacactaag atg gct 716

Met Ala

1

gcc gtt gcc atg aca ccc aac cct gtg cag acc ctt cag gag gag gcg 764
 Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu Glu Ala

5

10

15

gtg tgc gcc atc tgc ctc gat tac ttc acg gac ccc gtg tcc atc ggc 812
 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly

20

25

30

tgc ggg cac aac ttc tgc cga gtt tgt gta acc cag ttg tgg ggt ggg 860
 Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp Gly Gly

35

40

45

50

gag gat gag gag gac aga gat gag tta gat cgg gag gag gag gag gag 908
 Glu Asp Glu Glu Asp Arg Asp Glu Leu Asp Arg Glu Glu Glu Glu Glu

55

60

65

gac gga gag gag gag gaa gtg gag gct gtg ggg gct ggc gcg ggg tgg 956
 Asp Gly Glu Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala Gly Trp

70

75

80

gac acc ccc atg cgg gat gaa gac tac gag ggt gac atg gag gag gag 1004
 Asp Thr Pro Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu

85	90	95	
gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc atg agc agg	1052		
Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg			
100	105	110	
tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag gac gag gag	1100		
Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu			
115	120	125	130
gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag gac ctg agg	1148		
Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg			
	135	140	145
ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag gtt gag gaa	1196		
Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu			
	150	155	160
gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca gcc cct cgg	1244		
Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg			
	165	170	175
agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct cgg cgg agc	1292		
Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser			
180	185	190	
ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg att cgg cag	1340		
Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln			
195	200	205	210
atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc	1388		
Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile			
	215	220	225
tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa	1436		
Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu			

230	235	240	
gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac			1484
Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His			
245	250	255	
agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg			1532
Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu			
260	265	270	
cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag			1580
Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys			
275	280	285	290
atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg			1628
Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met			
295	300	305	
aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg			1676
Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg			
310	315	320	
ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg			1724
Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met			
325	330	335	
cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca			1772
His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala			
340	345	350	
gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg			1820
Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg			
355	360	365	370
agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc			1868
Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe			

375	380	385	
aat agg tgt gtt ccc agt ctt tgc cct tcg tgacccagtg gcatctggtt			1918
Asn Arg Cys Val Pro Ser Leu Cys Pro Ser			
390	395		
ccctgtccct gcttctcttc ggtatccctc tctctctctt ccttccccag gacctgagtt			1978
tccatctcct ggaccctcct ctcttcccc tcagcttttg cttttccctc tgggaatatc			2038
gtggtcccac cccctgcccc gtcccccttc tccaggtgtg aagaggtaca gctgcagccc			2098
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ctccacctgc ccagcagcc cctgctccag cgggaagtgt ggtgcgtggg caccaacggc			2578
aaacgctatc aggcccagag ctccacagaa cagacgtgc tgagccccag tgagaaacca			2638
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<210> 72

<211> 396

<212> PRT

<213> Homo sapiens

<400> 72

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Glu	Ala	Val	Cys	Ala	Ile	Cys	Leu	Asp	Tyr	Phe	Thr	Asp	Pro	Val	Ser
				20					25					30	
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
				35					40					45	
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
				50					55					60	
Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Val	Glu	Ala	Val	Gly	Ala	Gly	Ala
				65					70					75	
Gly	Trp	Asp	Thr	Pro	Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu
				85					90					95	

Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met
 100 105 110
 Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp
 115 120 125
 Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp
 130 135 140
 Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val
 145 150 155 160
 Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala
 165 170 175
 Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg
 180 185 190
 Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile
 195 200 205
 Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln
 210 215 220
 Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val
 225 230 235 240
 Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
 245 250 255
 Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala
 260 265 270
 Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val
 275 280 285
 Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser
 290 295 300
 Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu

305	310	315	320
Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg			
	325	330	335
Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg			
	340	345	350
Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln			
	355	360	365
Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu			
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Thr Phe Asn Arg Cys Val Pro Ser Leu Cys Pro Ser			
385	390	395	

<210> 73

<211> 2891

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24).. (956)

<400> 73

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gag gag gag gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc 101

Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15 20 25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu
 30 35 40
 gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag 197
 Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu
 45 50 55
 gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag 245
 Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu
 60 65 70
 gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca 293
 Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro
 75 80 85 90
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 Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro
 95 100 105
 cgg cgg agc ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg 389
 Arg Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val
 110 115 120
 att cgg cag atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat 437
 Ile Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp
 125 130 135
 cag ggc atc tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag 485
 Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu
 140 145 150
 gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac 533
 Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His
 155 160 165 170
 aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag 581

Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys
 175 180 185
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala
 190 195 200
 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys
 205 210 215
 agc cag atg aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga 725
 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg
 220 225 230
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu
 235 240 245 250
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser
 255 260 265
 cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869
 Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala
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 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys
 285 290 295
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 Glu Thr Phe Asn Arg Cys Val Pro Ser Leu Cys Pro Ser
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<210> 74

<211> 311

<212> PRT

<213> Homo sapiens

<400> 74

Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu	Glu	Glu	Val	Glu	Glu
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Glu	Glu	Glu	Gly	Val	Phe	Trp	Thr	Ser	Gly	Met	Ser	Arg	Ser	Ser	Trp
				20				25					30		
Asp	Asn	Met	Asp	Tyr	Val	Trp	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Leu
				35				40					45		
Asp	Tyr	Tyr	Leu	Gly	Asp	Met	Glu	Glu	Glu	Asp	Leu	Arg	Gly	Glu	Asp
				50				55					60		
Glu	Glu	Asp	Glu	Glu	Glu	Val	Leu	Glu	Glu	Val	Glu	Glu	Glu	Asp	Leu
				65			70			75				80	
Asp	Pro	Val	Thr	Pro	Leu	Pro	Pro	Pro	Pro	Ala	Pro	Arg	Arg	Cys	Phe
				85				90					95		
Thr	Cys	Pro	Gln	Cys	Arg	Lys	Ser	Phe	Pro	Arg	Arg	Ser	Phe	Arg	Pro
				100				105					110		
Asn	Leu	Gln	Leu	Ala	Asn	Met	Val	Gln	Val	Ile	Arg	Gln	Met	His	Pro
				115				120					125		

Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro Lys
130 135 140
His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala Ile
145 150 155 160
Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val Val
165 170 175
Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly His
180 185 190
Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys Ala
195 200 205
Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser Glu
210 215 220
Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu Ala
225 230 235 240
Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu Ala
245 250 255
Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala
260 265 270
Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln
275 280 285
Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys
290 295 300
Val Pro Ser Leu Cys Pro Ser
305 310

<210> 75

<211> 3070

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (267).. (1295)

<400> 75

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 ctgccagacc aggggacctc ggagaggcaa ggacagaggt tcaggatctt cctctccctc 180
 gggacccaag gccacaaagg agagctccgt ggagagaaga aaatcatttg actcctgggg 240
 acacagattt gctgccacag aggctg atg gac aac cag gcg gag aga gaa agt 293

Met Asp Asn Gln Ala Glu Arg Glu Ser

1

5

gag gct ggt gtt ggt ttg caa agg gat gag gat gac gct cct ctg tgt 341
 Glu Ala Gly Val Gly Leu Gln Arg Asp Glu Asp Asp Ala Pro Leu Cys

10

15

20

25

gaa gac gtg gag cta caa gac gga gat ctg tcc ccc gaa gaa aaa ata 389
 Glu Asp Val Glu Leu Gln Asp Gly Asp Leu Ser Pro Glu Glu Lys Ile

30

35

40

ttt ttg aga gaa ttt ccc aga ttg aaa gaa gat ctg aaa ggg aac att 437
 Phe Leu Arg Glu Phe Pro Arg Leu Lys Glu Asp Leu Lys Gly Asn Ile

45

50

55

gac aag ctc cgt gcc ctc gca gac gat att gac aaa acc cac aag aaa 485
 Asp Lys Leu Arg Ala Leu Ala Asp Asp Ile Asp Lys Thr His Lys Lys

60

65

70

ttc acc aag gct aac atg gtg gcc acc tct act gct gtc atc tct gga 533
 Phe Thr Lys Ala Asn Met Val Ala Thr Ser Thr Ala Val Ile Ser Gly

75	80	85	
gtg atg agc ctc ctg ggt tta gcc ctt gcc cca gca aca gga gga gga	581		
Val Met Ser Leu Leu Gly Leu Ala Leu Ala Pro Ala Thr Gly Gly Gly			
90	95	100	105
agc ctg ctg ctc tcc acc gct ggt caa ggt ttg gca aca gca gct ggg	629		
Ser Leu Leu Leu Ser Thr Ala Gly Gln Gly Leu Ala Thr Ala Ala Gly			
110	115	120	
gtc acc agc atc gtg agt ggt acg ttg gaa cgc tcc aaa aat aaa gaa	677		
Val Thr Ser Ile Val Ser Gly Thr Leu Glu Arg Ser Lys Asn Lys Glu			
125	130	135	
gcc caa gca cgg gcg gaa gac ata ctg ccc acc tac gac caa gag gac	725		
Ala Gln Ala Arg Ala Glu Asp Ile Leu Pro Thr Tyr Asp Gln Glu Asp			
140	145	150	
agg gag gat gag gaa gag aag gca gac tat gtc aca gct gct gga aag	773		
Arg Glu Asp Glu Glu Glu Lys Ala Asp Tyr Val Thr Ala Ala Gly Lys			
155	160	165	
att atc tat aat ctt aga aac acc ttg aag tat gcc aag aaa aac gtc	821		
Ile Ile Tyr Asn Leu Arg Asn Thr Leu Lys Tyr Ala Lys Lys Asn Val			
170	175	180	185
cgt gca ttt tgg aaa ctc aga gcc aac cca cgc ttg gcc aat gct acc	869		
Arg Ala Phe Trp Lys Leu Arg Ala Asn Pro Arg Leu Ala Asn Ala Thr			
190	195	200	
aag cgt ctt ctg acc act ggc caa gtc tcc tcc cgg agc cgc gtg cag	917		
Lys Arg Leu Leu Thr Thr Gly Gln Val Ser Ser Arg Ser Arg Val Gln			
205	210	215	
gtg caa aag gcc ttt gcg gga aca aca ctg gcg atg acc aaa aat gct	965		
Val Gln Lys Ala Phe Ala Gly Thr Thr Leu Ala Met Thr Lys Asn Ala			

220	225	230	
cgc gtg ctg gga ggt gtg atg tcc gcc ttc tcc ctt ggc tat gac ttg			1013
Arg Val Leu Gly Gly Val Met Ser Ala Phe Ser Leu Gly Tyr Asp Leu			
235	240	245	
gcc act ctc tca aag gaa tgg aag cac ctg aag gaa gga gca agg aca			1061
Ala Thr Leu Ser Lys Glu Trp Lys His Leu Lys Glu Gly Ala Arg Thr			
250	255	260	265
aag ttt gcg gaa gag ttg aga gcc aag gcc ttg gag ctg gag agg aaa			1109
Lys Phe Ala Glu Glu Leu Arg Ala Lys Ala Leu Glu Leu Glu Arg Lys			
270	275	280	
ctc aca gaa ctc acc cag ctc tac aag agc ttg cag cag aaa gtg agg			1157
Leu Thr Glu Leu Thr Gln Leu Tyr Lys Ser Leu Gln Gln Lys Val Arg			
285	290	295	
tca agg gcc aga ggg gtg ggg aag gat tta act ggg acc tgc gaa acc			1205
Ser Arg Ala Arg Gly Val Gly Lys Asp Leu Thr Gly Thr Cys Glu Thr			
300	305	310	
gag gct tac tgg aag gag tta agg gag cat gtg tgg atg tgg ctg tgg			1253
Glu Ala Tyr Trp Lys Glu Leu Arg Glu His Val Trp Met Trp Leu Trp			
315	320	325	
ctg tgt gtg tgt ctg tgt gtc tgt gtg tat gta cag ttt aca			1295
Leu Cys Val Cys Leu Cys Val Cys Val Tyr Val Gln Phe Thr			
330	335	340	
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<211> 343

<212> PRT

<213> Homo sapiens

<400> 76

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35 40 45

Leu Lys Glu Asp Leu Lys Gly Asn Ile Asp Lys Leu Arg Ala Leu Ala

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Asp Asp Ile Asp Lys Thr His Lys Lys Phe Thr Lys Ala Asn Met Val

65 70 75 80

Ala Thr Ser Thr Ala Val Ile Ser Gly Val Met Ser Leu Leu Gly Leu

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Ala Leu Ala Pro Ala Thr Gly Gly Gly Ser Leu Leu Leu Ser Thr Ala

100 105 110

Gly Gln Gly Leu Ala Thr Ala Ala Gly Val Thr Ser Ile Val Ser Gly

115 120 125

Thr Leu Glu Arg Ser Lys Asn Lys Glu Ala Gln Ala Arg Ala Glu Asp

130 135 140

Ile Leu Pro Thr Tyr Asp Gln Glu Asp Arg Glu Asp Glu Glu Glu Lys

145 150 155 160

Ala Asp Tyr Val Thr Ala Ala Gly Lys Ile Ile Tyr Asn Leu Arg Asn

165 170 175

Thr Leu Lys Tyr Ala Lys Lys Asn Val Arg Ala Phe Trp Lys Leu Arg

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Ala Asn Pro Arg Leu Ala Asn Ala Thr Lys Arg Leu Leu Thr Thr Gly					
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Gln Val Ser Ser Arg Ser Arg Val Gln Val Gln Lys Ala Phe Ala Gly					
210		215		220	
Thr Thr Leu Ala Met Thr Lys Asn Ala Arg Val Leu Gly Gly Val Met					
225		230		235	240
Ser Ala Phe Ser Leu Gly Tyr Asp Leu Ala Thr Leu Ser Lys Glu Trp					
	245		250		255
Lys His Leu Lys Glu Gly Ala Arg Thr Lys Phe Ala Glu Glu Leu Arg					
	260		265		270
Ala Lys Ala Leu Glu Leu Glu Arg Lys Leu Thr Glu Leu Thr Gln Leu					
	275		280		285
Tyr Lys Ser Leu Gln Gln Lys Val Arg Ser Arg Ala Arg Gly Val Gly					
	290		295		300
Lys Asp Leu Thr Gly Thr Cys Glu Thr Glu Ala Tyr Trp Lys Glu Leu					
305		310		315	320
Arg Glu His Val Trp Met Trp Leu Trp Leu Cys Val Cys Leu Cys Val					
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Cys Val Tyr Val Gln Phe Thr					
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<210> 77

<211> 2506

<212> DNA

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<220>

<221> CDS

<222> (108).. (1607)

<400> 77

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cgc gtc ttt ctc gca ttc tgt gtc tgg ctg act ctg ccg gga gct gaa 164
Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu
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acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 212
Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser
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Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Gly Ser Phe
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Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp
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Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly Tyr Glu Pro
              85              90              95

gtt tct ggg gca aaa aca ttc aag aat gag agc gag aac acc tgt caa 452
Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn Thr Cys Gln

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Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly				
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ttc aag ttc ata cct gag gat ccg aag gtc tgc aca gat gtg gac gag				596
Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp Val Asp Glu				
	150	155	160	
tgc agc tcc ggg cag cat cag tgt gac agc tcc acc gag ggc tgc cag				644
Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu Gly Cys Gln				
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gtg ctg ggc agc aag aac ggc agc acc acc tgc caa tgc agc cac ctg				692
Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu				
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Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys				
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Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu				
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Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser				
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Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser				

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Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu			
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cgc tgc cgc ctg gtg gcc ggg ctg ctg cac tac tgt ttc ctg gcc gcc	980		
Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala			
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ttc tgc tgg atg agc ctc gaa ggc ctg gag ctc tac ttt ctt gtg gtg	1028		
Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val			
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cgc gtg ttc caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc	1076		
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325	330	335	
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Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln			
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ggc ttc ctc tgg agc ttc ttg gga cct gtg acc ttc atc att ttg tgc	1220		
Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys			
360	365	370	
aat gct gtc att ttc gtg act acc gtc tgg aag ctc act cag aag ttt	1268		
Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe			
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Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu			

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<210> 78

<211> 500

<212> PRT

<213> Homo sapiens

<400> 78

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				20					25					30	
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Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp			
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Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu			
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Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys			
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Ser His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu			
	195	200	205
Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu			
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Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile			
225	230	235	240
Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe			
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Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln			
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Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe			
	275	280	285
Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe			
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Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala
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Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser
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<210> 79

<211> 2506

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108)..(1607)

<400> 79

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Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu
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acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 212
Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser
      20              25              30              35

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Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe
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tct gag atc atc acc acc ccg acg gag act tgt gac gac atc aac gag 308
Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp Ile Asn Glu
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tgt gca aca ccg tcg aaa gtg tca tgc gga aaa ttc tcg gac tgc tgg 356
Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp
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Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn Thr Cys Gln
100              105              110              115
gat gtg gac gaa tgt cag cag aac cca agg ctc tgt aaa agc tac ggc 500
Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly
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Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly
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Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu Gly Cys Gln
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Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu
180              185              190              195
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Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys
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ctg acc ctg atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg 788
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cgc acc acc ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc	884
Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser	
245 250 255	
acc atc ttc ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg	932
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Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala	
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Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val	
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Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr	
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Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln	
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 Ile
 500

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<210> 80

<211> 500

<212> PRT

<213> Homo sapiens

<400> 80

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25

30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe

35

40

45

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 Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys
 180 185 190
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 195 200 205
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 Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile
 225 230 235 240
 Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe
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260	265	270
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275	280	285
Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe		
290	295	300
Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu		
305	310	315
Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala		
325	330	335
Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp		
340	345	350
Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile		
355	360	365
Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr		
370	375	380
Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala		
385	390	395
Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys		
405	410	415
Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu		
420	425	430
Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr		
435	440	445
Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys		
450	455	460
Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser		
465	470	475
		480

Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser

485

490

495

Glu Ser Gly Ile

500

<210> 81

<211> 2917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (2314)

<400> 81

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cctgccgctc ctgccggcag ctccaacc atg gga ggc cgc gtc ttt ctc gca 112

Met Gly Gly Arg Val Phe Leu Ala

1

5

ttc tgt gtc tgg ctg act ctg ccg gga gct gaa acc cag gac tcc agg 160
Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu Thr Gln Asp Ser Arg

10

15

20

ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg tgt gtc aat gcc acc 208
Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser Cys Val Asn Ala Thr

25

30

35

40

gcc tgt cgc tgc aat cca ggg ttc agc tct ttt tct gag atc atc acc 256
Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe Ser Glu Ile Ile Thr

45

50

55

acc ccg acg gag act tgt gac gac atc aac gag tgt gca aca ccg tcg 304

Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp	Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser	
60				65				70								
aaa	gtg	tca	tgc	gga	aaa	ttc	tcg	gac	tgc	tgg	aac	aca	gag	ggg	agc	352
Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser	Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser	
75				80				85								
tac	gac	tgc	gtg	tgc	agc	ccg	gga	tat	gag	cct	gtt	tct	ggg	gca	aaa	400
Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly	Tyr	Glu	Pro	Val	Ser	Gly	Ala	Lys	
90				95				100								
aca	ttc	aag	aat	gag	agc	gag	aac	acc	tgt	caa	gat	gtg	gac	gag	tgc	448
Thr	Phe	Lys	Asn	Glu	Ser	Glu	Asn	Thr	Cys	Gln	Asp	Val	Asp	Glu	Cys	
105				110				115				120				
agc	tcc	ggg	cag	cat	cag	tgt	gac	agc	tcc	acc	gtc	tgc	ttc	aac	acc	496
Ser	Ser	Gly	Gln	His	Gln	Cys	Asp	Ser	Ser	Thr	Val	Cys	Phe	Asn	Thr	
125				130				135								
gtg	ggt	tca	tac	agc	tgc	cgc	tgc	cgc	cca	ggc	tgg	aag	ccc	aga	cac	544
Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro	Gly	Trp	Lys	Pro	Arg	His	
140				145				150								
gga	atc	ccg	aat	aac	caa	aag	gac	act	gtc	tgt	gaa	gat	atg	act	ttc	592
Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val	Cys	Glu	Asp	Met	Thr	Phe	
155				160				165								
tcc	acc	tgg	acc	ccg	ccc	cct	gga	gtc	cac	agc	cag	acg	ctt	tcc	cga	640
Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His	Ser	Gln	Thr	Leu	Ser	Arg	
170				175				180								
ttc	ttc	gac	aaa	gtc	cag	gac	ctg	ggc	aga	gac	tcc	aag	aca	agc	tca	688
Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg	Asp	Ser	Lys	Thr	Ser	Ser	
185				190				195				200				
gcc	gag	gtc	acc	atc	cag	aat	gtc	atc	aaa	ttg	gtg	gat	gaa	ctg	atg	736

Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu Val Asp Glu Leu Met	
205	210
gaa gct cct gga gac gta gag gcc ctg gcg cca cct gtc cgg cac ctc	784
Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro Pro Val Arg His Leu	
220	225
ata gcc acc cag ctg ctc tca aac ctt gaa gat atc atg agg atc ctg	832
Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp Ile Met Arg Ile Leu	
235	240
gcc aag agc ctg cct aaa ggc ccc ttc acc tac att tcc cct tcg aac	880
Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr Tyr Ile Ser Pro Ser Asn	
250	255
aca gag ctg acc ctg atg atc cag gag cgg ggg gac aag aac gtc act	928
Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly Asp Lys Asn Val Thr	
265	270
atg ggt cag agc agc gca cgc atg aag ctg aat tgg gct gtg gca gct	976
Met Gly Gln Ser Ser Ala Arg Met Lys Leu Asn Trp Ala Val Ala Ala	
285	290
gga gcc gag gat cca ggc ccc gcc gtg gcg ggc atc ctc tcc atc cag	1024
Gly Ala Glu Asp Pro Gly Pro Ala Val Ala Gly Ile Leu Ser Ile Gln	
300	305
aac atg acg aca ttg ctg gcc aat gcc tcc ttg aac ctg cat tcc aag	1072
Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu Asn Leu His Ser Lys	
315	320
aag caa gcc gaa ctg gag gag ata tat gaa agc agc atc cgt ggt gtc	1120
Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser Ser Ile Arg Gly Val	
330	335
caa ctc aga cgc ctc tct gcc gtc aac tcc atc ttt ctg agc cac aac	1168

Gln Leu Arg Arg Leu Ser Ala Val Asn Ser Ile Phe Leu Ser His Asn
 345 350 355 360
 aac acc aag gaa ctc aac tcc ccc atc ctt ttc gcc ttc tcc cac ctt 1216
 Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe Ala Phe Ser His Leu
 365 370 375
 gag tcc tcc gat ggg gag gcg gga aga gac cct cct gcc aag gac gtg 1264
 Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro Pro Ala Lys Asp Val
 380 385 390
 atg cct ggg cca cgg cag gag ctg ctc tgt gcc ttc tgg aag agt gac 1312
 Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala Phe Trp Lys Ser Asp
 395 400 405
 agc gac agg gga ggg cac tgg gcc acc gag ggc tgc cag gtg ctg ggc 1360
 Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly Cys Gln Val Leu Gly
 410 415 420
 agc aag aac ggc agc acc acc tgc caa tgc agc cac ctg agc agc ttt 1408
 Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu Ser Ser Phe
 425 430 435 440
 gcg atc ctt atg gct cat tat gac gtg gag gac tgg aag ctg acc ctg 1456
 Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys Leu Thr Leu
 445 450 455
 atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg ctg ctg tgc 1504
 Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu Leu Leu Cys
 460 465 470
 atc ctc act ttc ctg ctg gtg cgg ccc atc cag ggc tcg cgc acc acc 1552
 Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser Arg Thr Thr
 475 480 485
 ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc acc atc ttc 1600

Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser Thr Ile Phe
 490 495 500
 ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg cgc tgc cgc 1648
 Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu Arg Cys Arg
 505 510 515 520
 ctg gtg gcc ggg ctg ctg cac tac tgt ttc ctg gcc gcc ttc tgc tgg 1696
 Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala Phe Cys Trp
 525 530 535
 atg agc ctc gaa ggc ctg gag ctc tac ttt ctt gtg gtg cgc gtg ttc 1744
 Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val Arg Val Phe
 540 545 550
 caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc ggc tat ggc 1792
 Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile Gly Tyr Gly
 555 560 565
 gtg ccc ctg ctc atc gtg ggc gtc tcg gct gcc atc tac agc aag ggc 1840
 Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr Ser Lys Gly
 570 575 580
 tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag ggc ttc ctc 1888
 Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln Gly Phe Leu
 585 590 595 600
 tgg agc ttc ttg gga cct gtg acc ttc atc att ttg tgc aat gct gtc 1936
 Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys Asn Ala Val
 605 610 615
 att ttc gtg act acc gtc tgg aag ctc act cag aag ttt tct gaa atc 1984
 Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe Ser Glu Ile
 620 625 630
 aat cca gac atg aag aaa tta aag aag gcg agg gcg ctg acc atc acg 2032

Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu Thr Ile Thr
 635 640 645
 gcc atc gcg cag ctc ttc ctg ttg ggc tgc acc tgg gtc ttt ggc ctg 2080
 Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr Trp Val Phe Gly Leu
 650 655 660
 ttc atc ttc gac gat cgg agc ttg gtg ctg acc tat gtg ttt acc atc 2128
 Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val Phe Thr Ile
 665 670 675 680
 ctc aac tgc ctg cag ggc gcc ttc ctc tac ctg ctg cac tgc ctg ctc 2176
 Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu Leu His Cys Leu Leu
 685 690 695
 aac aag aag gtt cgg gaa gaa tac cgg aag tgg gcc tgc cta gtt gct 2224
 Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys Leu Val Ala
 700 705 710
 ggg ggg agc aag tac tca gaa ttc acc tcc acc acg tct ggc act ggc 2272
 Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr Thr Ser Gly Thr Gly
 715 720 725
 cac aat cag acc cgg gcc ctc agg gca tca gag tcc ggc ata 2314
 His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly Ile
 730 735 740
 tgaaggcgca tggttctgga cggcccagca gctcctgtgg ccacagcagc tttgtacacg 2374
 aagaccatcc atcctccctt cgtccaccac tctactccct ccaccctccc tccctgatcc 2434
 cgtgtgccac caggagggag tggcagctat agtctggcac caaagtccag gacaccagct 2494
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atgtcagagg ccccatggcg aggccccttg gggccactgc ctgaggetca cggtagacagag 2794
gcctgccctg cctggccggg caggagggttc tcaactgttgt gaaggttgta gacgttgtgt 2854
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cag 2917

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<211> 742

<212> PRT

<213> Homo sapiens

<400> 82

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Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln
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35 40 45
Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
50 55 60
Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
65 70 75 80
Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
85 90 95
Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn
100 105 110
Thr Cys Gln Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp
115 120 125
Ser Ser Thr Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys

130	135	140	
Arg Pro Gly Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp			
145	150	155	160
Thr Val Cys Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly			
	165	170	175
Val His Ser Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu			
	180	185	190
Gly Arg Asp Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val			
	195	200	205
Ile Lys Leu Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala			
	210	215	220
Leu Ala Pro Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn			
225	230	235	240
Leu Glu Asp Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro			
	245	250	255
Phe Thr Tyr Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln			
	260	265	270
Glu Arg Gly Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met			
	275	280	285
Lys Leu Asn Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala			
	290	295	300
Val Ala Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn			
305	310	315	320
Ala Ser Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile			
	325	330	335
Tyr Glu Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val			
	340	345	350

Asn Ser Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro
 355 360 365
 Ile Leu Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly
 370 375 380
 Arg Asp Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu
 385 390 395 400
 Leu Cys Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala
 405 410 415
 Thr Glu Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys
 420 425 430
 Gln Cys Ser His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp
 435 440 445
 Val Glu Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu
 450 455 460
 Ser Leu Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg
 465 470 475 480
 Pro Ile Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys
 485 490 495
 Leu Phe Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly
 500 505 510
 Gly Gln Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr
 515 520 525
 Cys Phe Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu
 530 535 540
 Tyr Phe Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg
 545 550 555 560
 Trp Leu Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val

565 570 575
Ser Ala Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp
580 585 590
Leu Asp Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr
595 600 605
Phe Ile Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys
610 615 620
Leu Thr Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys
625 630 635 640
Lys Ala Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu
645 650 655
Gly Cys Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu
660 665 670
Val Leu Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe
675 680 685
Leu Tyr Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr
690 695 700
Arg Lys Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe
705 710 715 720
Thr Ser Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg
725 730 735
Ala Ser Glu Ser Gly Ile
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<210> 83

<211> 3156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(2553)

<400> 83

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Met Gly Gly
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Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu
5 10 15

acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 153
Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser
20 25 30 35

tgt gtc aat gcc acc gcc tgt cgc tgc aat cca ggg ttc agc tct ttt 201
Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe
40 45 50

tct gag atc atc acc acc ccg acg gag act tgt gac gac atc aac gag 249
Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp Ile Asn Glu
55 60 65

tgt gca aca ccg tcg aaa gtg tca tgc gga aaa ttc tcg gac tgc tgg 297
Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp
70 75 80

aac aca gag ggg agc tac gac tgc gtg tgc agc ccg gga tat gag cct 345
Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly Tyr Glu Pro
85 90 95

gtt tct ggg gca aaa aca ttc aag aat gag agc gag aac acc tgt caa 393
 Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn Thr Cys Gln

100 105 110 115
 gat gtg gac gaa tgt cag cag aac cca agg ctc tgt aaa agc tac ggc 441
 Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly

120 125 130
 acc tgc gtc aac acc ctt ggc agc tat acc tgc cag tgc ctg cct ggc 489
 Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly

135 140 145
 ttc aag ttc ata cct gag gat ccg aag gtc tgc aca gat gtg aat gaa 537
 Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp Val Asn Glu

150 155 160
 tgc acc tcc gga caa aat ccg tgc cac agc tcc acc cac tgc ctc aac 585
 Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His Cys Leu Asn

165 170 175
 aac gtg ggc agc tat cag tgt cgc tgc cga ccg ggc tgg caa ccg att 633
 Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp Gln Pro Ile

180 185 190 195
 ccg ggg tcc ccc aat ggc cca aac aat acc gtc tgt gaa gat gtg gac 681
 Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu Asp Val Asp

200 205 210
 gag tgc agc tcc ggg cag cat cag tgt gac agc tcc acc gtc tgc ttc 729
 Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Val Cys Phe

215 220 225
 aac acc gtg ggt tca tac agc tgc cgc tgc cgc cca ggc tgg aag ccc 777
 Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly Trp Lys Pro

230	235	240	
aga cac gga atc ccg aat aac caa aag gac act gtc tgt gaa gat atg			825
Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys Glu Asp Met			
245	250	255	
act ttc tcc acc tgg acc ccg ccc cct gga gtc cac agc cag acg ctt			873
Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His Ser Gln Thr Leu			
260	265	270	275
tcc cga ttc ttc gac aaa gtc cag gac ctg ggc aga gac tcc aag aca			921
Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg Asp Ser Lys Thr			
280	285	290	
agc tca gcc gag gtc acc atc cag aat gtc atc aaa ttg gtg gat gaa			969
Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu Val Asp Glu			
295	300	305	
ctg atg gaa gct cct gga gac gta gag gcc ctg gcg cca cct gtc cgg			1017
Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro Pro Val Arg			
310	315	320	
cac ctc ata gcc acc cag ctg ctc tca aac ctt gaa gat atc atg agg			1065
His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp Ile Met Arg			
325	330	335	
atc ctg gcc aag agc ctg cct aaa ggc ccc ttc acc tac att tcc cct			1113
Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr Tyr Ile Ser Pro			
340	345	350	355
tcg aac aca gag ctg acc ctg atg atc cag gag cgg ggg gac aag aac			1161
Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly Asp Lys Asn			
360	365	370	
gtc act atg ggt cag agc agc gca cgc atg aag ctg aat tgg gct gtg			1209
Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu Asn Trp Ala Val			

375	380	385	
gca gct gga gcc gag gat cca ggc ccc gcc gtg gcg ggc atc ctc tcc			1257
Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala Val Ala Gly Ile Leu Ser			
390	395	400	
atc cag aac atg acg aca ttg ctg gcc aat gcc tcc ttg aac ctg cat			1305
Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu Asn Leu His			
405	410	415	
tcc aag aag caa gcc gaa ctg gag gag ata tat gaa agc agc atc cgt			1353
Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser Ser Ile Arg			
420	425	430	435
ggg gtc caa ctc aga cgc ctc tct gcc gtc aac tcc atc ttt ctg agc			1401
Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser Ile Phe Leu Ser			
440	445	450	
cac aac aac acc aag gaa ctc aac tcc ccc atc ctt ttc gcc ttc tcc			1449
His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe Ala Phe Ser			
455	460	465	
cac ctt gag tcc tcc gat ggg gag gcg gga aga gac cct cct gcc aag			1497
His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro Pro Ala Lys			
470	475	480	
gac gtg atg cct ggg cca cgg cag gag ctg ctc tgt gcc ttc tgg aag			1545
Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala Phe Trp Lys			
485	490	495	
agt gac agc gac agg gga ggg cac tgg gcc acc gag ggc tgc cag gtg			1593
Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly Cys Gln Val			
500	505	510	515
ctg ggc agc aag aac ggc agc acc acc tgc caa tgc agc cac ctg agc			1641
Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu Ser			

520	525	530	
agc ttt gcg atc ctt atg gct cat tat gac gtg gag gac tgg aag ctg			1689
Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys Leu			
535	540	545	
acc ctg atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg ctg			1737
Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu Leu			
550	555	560	
ctg tgc atc ctc act ttc ctg ctg gtg cgg ccc atc cag ggc tcg cgc			1785
Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser Arg			
565	570	575	
acc acc ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc acc			1833
Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser Thr			
580	585	590	595
atc ttc ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg cgc			1881
Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu Arg			
600	605	610	
tgc cgc ctg gtg gcc ggg ctg ctg cac tac tgt ttc ctg gcc gcc ttc			1929
Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala Phe			
615	620	625	
tgc tgg atg agc ctc gaa ggc ctg gag ctc tac ttt ctt gtg gtg cgc			1977
Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val Arg			
630	635	640	
gtg ttc caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc ggc			2025
Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile Gly			
645	650	655	
tat ggc gtg ccc ctg ctc atc gtg ggc gtc tcg gct gcc atc tac agc			2073
Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr Ser			

660	665	670	675	
aag ggc tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag ggc	2121			
Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln Gly				
	680	685	690	
ttc ctc tgg agc ttc ttg gga cct gtg acc ttc atc att ttg tgc aat	2169			
Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys Asn				
	695	700	705	
gct gtc att ttc gtg act acc gtc tgg aag ctc act cag aag ttt tct	2217			
Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe Ser				
	710	715	720	
gaa atc aat cca gac atg aag aaa tta aag aag gcg agg gcg ctg acc	2265			
Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu Thr				
	725	730	735	
atc acg gcc atc gcg cag ctc ttc ctg ttg ggc tgc acc tgg gtc ttt	2313			
Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr Trp Val Phe				
	740	745	750	755
ggc ctg ttc atc ttc gac gat cgg agc ttg gtg ctg acc tat gtg ttt	2361			
Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val Phe				
	760	765	770	
acc atc ctc aac tgc ctg cag ggc gcc ttc ctc tac ctg ctg cac tgc	2409			
Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu Leu His Cys				
	775	780	785	
ctg ctc aac aag aag gtt cgg gaa gaa tac cgg aag tgg gcc tgc cta	2457			
Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys Leu				
	790	795	800	
gtt gct ggg ggg agc aag tac tca gaa ttc acc tcc acc acg tct ggc	2505			
Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr Thr Ser Gly				

805 810 815
 act ggc cac aat cag acc cgg gcc ctc agg gca tca gag tcc ggc ata 2553
 Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly Ile
 820 825 830 835
 tgaaggcgca tggttctgga cggcccagca gtcctgtgg ccacagcagc tttgtacacg 2613
 aagaccatcc atcctccctt cgtccaccac tctactccct ccaccctccc tccctgatcc 2673
 cgtgtgccac caggagggag tggcagctat agtctggcac caaagtccag gacacccagt 2733
 ggggtggagt cggagccact ggtcctgctg ctggctgcct ctctgctcca ccttgtgacc 2793
 caggggtgggg acaggggctg gcccagggt gcaatgcagc atgttgccct ggcacctgtg 2853
 gccagtactc gggacagact aagggcgctt gtcccatcct ggacttttcc tctcatgtct 2913
 ttgctgcaga actgaagaga ctaggcgctg gggctcagct tccctcttaa gctaagactg 2973
 atgtcagagg ccccatggcg aggccccttg gggccactgc ctgaggctca cggtaacagag 3033
 gcctgccctg cctggccggg caggaggttc tcaactgttg gaaggttgta gacgttgtgt 3093
 aatgtgtttt tatctgttaa aatttttcag tgttgacact taaaattaaa cacatgcata 3153
 cag 3156

<210> 84

<211> 835

<212> PRT

<213> Homo sapiens

<400> 84

Met Gly Gly Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro

1

5

10

15

Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln

20

25

30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe

35

40

45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
 50 55 60
 Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
 65 70 75 80
 Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
 85 90 95
 Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn
 100 105 110
 Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys
 115 120 125
 Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys
 130 135 140
 Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp
 145 150 155 160
 Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His
 165 170 175
 Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp
 180 185 190
 Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu
 195 200 205
 Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr
 210 215 220
 Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly
 225 230 235 240
 Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys
 245 250 255
 Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His Ser

260 265 270
Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg Asp
275 280 285
Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu
290 295 300
Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro
305 310 315 320
Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp
325 330 335
Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr Tyr
340 345 350
Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly
355 360 365
Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu Asn
370 375 380
Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala Val Ala Gly

385 390 395 400
Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu
405 410 415
Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser
420 425 430
Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser Ile
435 440 445
Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe
450 455 460
Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro

465 470 475 480
 Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala
 485 490 495
 Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly
 500 505 510
 Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser
 515 520 525
 His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp
 530 535 540
 Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe
 545 550 555 560
 Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln
 565 570 575
 Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val
 580 585 590
 Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val
 595 600 605
 Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu
 610 615 620
 Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu
 625 630 635 640
 Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys
 645 650 655
 Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala
 660 665 670
 Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe
 675 680 685

Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile
 690 695 700
 Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln
 705 710 715 720
 Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg
 725 730 735
 Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr
 740 745 750
 Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr
 755 760 765
 Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu
 770 775 780
 Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp
 785 790 795 800
 Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr
 805 810 815
 Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu
 820 825 830
 Ser Gly Ile
 835

<210> 85

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (756)

<400> 85

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gtgacc atg gcc agg ctg gcg ttg tct cct gtg ccc agc cac tgg atg      108
      Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met
          1              5              10
gtg gcg ttg ctg ctg ctg ctc tca gca gct gag cca gta cca gca gcc      156
Val Ala Leu Leu Leu Leu Leu Ser Ala Ala Glu Pro Val Pro Ala Ala
      15              20              25              30
aga tcg gag gac cgg tac cgg aat ccc aaa ggt agt gct tgt tcg cgg      204
Arg Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg
          35              40              45
atc tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg gtg      252
Ile Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val
          50              55              60
aaa atg cac tgc tac atg aac agc gcc tcc ggc aat gtg agc tgg ctc      300
Lys Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu
          65              70              75
tgg aag cag gag atg gac gag aat ccc cag cag ctg aag ctg gaa aag      348
Trp Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys
          80              85              90
ggc cgc atg gaa gag tcc cag aac gaa tct ctc gcc acc ctc acc atc      396
Gly Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile
          95              100              105              110
caa ggc atc cgg ttt gag gac aat ggc atc tac ttc tgc cag cag aag      444
Gln Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys
          115              120              125

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tgc aac aac acc tcg gag gtc tac cag ggc tgc ggc aca gag ctg cga 492
 Cys Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg
 130 135 140
 gtc atg gga ttc agc acc ttg gca cag ctg aag cag agg aac acg ctg 540
 Val Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu
 145 150 155
 aag gat ggt atc atc atg atc cag acg ctg ctg atc atc ctc ttc atc 588
 Lys Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile
 160 165 170
 atc gtg cct atc ttc ctg ctg ctg gac aag gat gac agc aag gct ggc 636
 Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly
 175 180 185 190
 atg gag gaa gat cac acc tac gag ggc ctg gac att gac cag aca gcc 684
 Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala
 195 200 205
 acc tat gag gac ata gtg acg ctg cgg aca ggg gaa gtg aag tgg tct 732
 Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser
 210 215 220
 gta ggt gag cac cca ggc cag gag tgagagccag gtcgccccat gacctgggtg 786
 Val Gly Glu His Pro Gly Gln Glu
 225 230
 caggctccct ggcctcagtg actgcttcgg agctgccttg ctcatggccc aacccttttc 846
 ccggaccccc cagctggcct ctgaagctgg ccacacagag ctgccatttg tctccagccc 906
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ccttcccccg tggaataaac ggtgtgtcct gag 1239

<210> 86

<211> 230

<212> PRT

<213> Homo sapiens

<400> 86

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Leu Leu Leu Leu Leu Ser Ala Ala Glu Pro Val Pro Ala Ala Arg Ser

20 25 30

Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp

35 40 45

Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met

50 55 60

His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys

65 70 75 80

Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg

85 90 95

Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly

100 105 110

Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn

115 120 125

Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met

130 135 140

Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp

145 150 155 160
 Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val
 165 170 175
 Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu
 180 185 190
 Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr
 195 200 205
 Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly
 210 215 220
 Glu His Pro Gly Gln Glu
 225 230

<210> 87

<211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (753)

<400> 87

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 Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met
 1 5 10
 gtg gcg ttg ctg ctg ctg ctc tca gct gag cca gta cca gca gcc aga 156
 Val Ala Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg
 15 20 25 30

tcg gag gac cgg tac cgg aat ccc aaa ggt agt gct tgt tcg cgg atc	204
Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile	
35 40 45	
tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg gtg aaa	252
Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys	
50 55 60	
atg cac tgc tac atg aac agc gcc tcc ggc aat gtg agc tgg ctc tgg	300
Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp	
65 70 75	
aag cag gag atg gac gag aat ccc cag cag ctg aag ctg gaa aag ggc	348
Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly	
80 85 90	
cgc atg gaa gag tcc cag aac gaa tct ctc gcc acc ctc acc atc caa	396
Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln	
95 100 105 110	
ggc atc cgg ttt gag gac aat ggc atc tac ttc tgc cag cag aag tgc	444
Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys	
115 120 125	
aac aac acc tcg gag gtc tac cag ggc tgc ggc aca gag ctg cga gtc	492
Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val	
130 135 140	
atg gga ttc agc acc ttg gca cag ctg aag cag agg aac acg ctg aag	540
Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys	
145 150 155	
gat ggt atc atc atg atc cag acg ctg ctg atc atc ctc ttc atc atc	588
Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile	
160 165 170	

gtg cct atc ttc ctg ctg ctg gac aag gat gac agc aag gct ggc atg 636
 Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met
 175 180 185 190
 gag gaa gat cac acc tac gag ggc ctg gac att gac cag aca gcc acc 684
 Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr
 195 200 205
 tat gag gac ata gtg acg ctg cgg aca ggg gaa gtg aag tgg tct gta 732
 Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val
 210 215 220
 ggt gag cac cca ggc cag gag tgagagccag gtcgccccat gacctgggtg 783
 Gly Glu His Pro Gly Gln Glu
 225
 caggctccct ggcctcagt actgcttcgg agctgcctgg ctcatggccc aaccctttc 843
 ccggaccccc cagctggcct ctgaagctgg cccaccagag ctgccatttg tctccagccc 903
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 gagggcctcc cagcagagct tgggaagggc catggaccca actgggcccc agaagagcca 1143
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<210> 88

<211> 229

<212> PRT

<213> Homo sapiens

<400> 88

Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala

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Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu
20 25 30
Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln
35 40 45
Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His
50 55 60
Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln
65 70 75 80
Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met
85 90 95
Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile
100 105 110
Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn
115 120 125
Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly
130 135 140
Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly
145 150 155 160
Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro
165 170 175
Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu
180 185 190
Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu
195 200 205
Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu
210 215 220

His Pro Gly Gln Glu

225

<210> 89

<211> 2137

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (1112)

<400> 89

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 tggattcctc tgctaagacc gctgcc atg cca gtg acg gta acc cgc acc acc 173

Met Pro Val Thr Val Thr Arg Thr Thr

1

5

atc aca acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc 221
 Ile Thr Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile
 10 15 20 25
 gtg ggg tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg 269
 Val Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu
 30 35 40
 ctg cag ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg 317
 Leu Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val
 45 50 55
 ggc gcc tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc 365
 Gly Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys

60	65	70	
ttc tgc ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg	413		
Phe Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly			
75	80	85	
ctc cag gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc	461		
Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe			
90	95	100	105
gcc tgc tat gcg gcc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc	509		
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro			
	110	115	120
acc acc tat gtc cag ttc ctg tcc cac gcc cgt tcg cgg gac cac gcc	557		
Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala			
	125	130	135
atc gcc gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc	605		
Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr			
	140	145	150
gaa gtg gcc tgg acc cgg gcc cgg ccc gcc gag atc act gcc tat atg	653		
Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met			
	155	160	165
gcc acc gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc	701		
Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys			
	170	175	180
atc atc ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg	749		
Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro			
	190	195	200
gcc ctg gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg	797		
Ala Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala			

205	210	215	
gcc atc gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc			845
Ala Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro			
220	225	230	
atc ccc ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc			893
Ile Pro Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu			
235	240	245	
ctc tat gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag			941
Leu Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu			
250	255	260	265
aag tat ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc			989
Lys Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg			
270	275	280	
agc cat gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc			1037
Ser His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala			
285	290	295	
atc ctg acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac			1085
Ile Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His			
300	305	310	
tct gcc cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct			1132
Ser Ala His Leu Val Phe Val Lys Val			
315	320		
cccgttccct ctccaacctc ttgtttcttc ttgcccagagt tttctttatg gagtacttct			1192
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ccttcccaat tccttgcaact ctaaccagtt cttggatgca tcttcttcct tccctttcct			1312
cttgctgttt ccttctgtg ttgttttggt gccacatcc tgttttcacc cctgagctgt			1372
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 ctttcttata tgctgtttt gcaagcacct tctcctgtgt ccttgggagc cctgagactt 1672
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 tagctgggga ttgggccctc tttctccag tggaggaagg tgtgcagtgt acttcccctt 1912
 taaattaaaa aacatatata tatatatatt tggaggtcag taatttcaa tgggcgggag 1972
 gcattaagca ccgaccctgg gtccctaggc cccgcctggc actcagcctt gccagagatt 2032
 ggctccagaa tttttgccag gcttacagaa caccactgc ctagaggcca tcttaaagga 2092
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<210> 90

<211> 322

<212> PRT

<213> Homo sapiens

<400> 90

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Ser
1				5					10				15	
Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	Ala
			20					25					30	Leu
Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	Ser	Thr
			35					40					45	Cys
Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	Thr	Gly	Ser
			50					55					60	Met
Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	Phe	Ser	Val	Thr
														Leu

315/861

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu

290

295

300

Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val

305

310

315

320

Lys Val

<210> 91

<211> 1644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (172).. (639)

<400> 91

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aggccggcag cgcctctcct ccatggctct gtctgtcagc gctgttttgg gagcccgccg 120
gtgaggccgg gccacgtca gacacttcca tcgtcgagtc tgtcactggg c atg gcg 177

Met Ala

1

ggt cag ttc cgc agc tac gtg tgg gac ccg ctg ctg atc ctg tcg cag 225

Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln

5

10

15

atc gtc ctc atg cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg 273

Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu

20

25

30

gcg ctg gtg gac ggg cta gtg cga agc agc ccc tcg ctg gac cag atg 321

Ala Leu Val Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met

35	40	45	50	
ttc gac gcc gag atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc	369			
Phe Asp Ala Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser				
55	60	65		
atg atg tcc ttc atc ctc aac gcc ctc acc tgt gcc ctg ggc ttg ctg	417			
Met Met Ser Phe Ile Leu Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu				
70	75	80		
tac ttc atc cgg cga gga aag cag tgt ctg gat ttc act gtc act gtc	465			
Tyr Phe Ile Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val				
85	90	95		
cat ttc ttt cac ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc	513			
His Phe Phe His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro				
100	105	110		
tcg gcg ctg acc tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg	561			
Ser Ala Leu Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met				
115	120	125	130	
gct gtc atc ggg gag tac ctg tgc atg cgg acg gag ctc aag gag ata	609			
Ala Val Ile Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile				
135	140	145		
ccc ctc aac tca gcc cct aaa tcc aat gtc tagaatcagg ccctttggac	659			
Pro Leu Asn Ser Ala Pro Lys Ser Asn Val				
150	155			
atcctgctga cacttgggcc ccttaacacc ttgggctgct cagaccctcc agatgaggtc	719			
cagcccagat ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag	779			
tgagggcctg tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg	839			
tctgttgaag ccttggtatc tgagaggtca ggaaggggac ctctttgagg gtaataacat	899			
aattggaacc atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga	959			

gaaaaaaaaat caaggatatc tgattggagc aaaccacttc tttagtcac tgtcttacct 1019
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 taaaataca gtattttcca tgggtt 1644

<210> 92

<211> 156

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu

1 5 10 15

Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu

20 25 30

Trp Leu Ala Leu Val Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp

35 40 45

Gln Met Phe Asp Ala Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg

50 55 60

Leu Ser Met Met Ser Phe Ile Leu Asn Ala Leu Thr Cys Ala Leu Gly

65	70	75	80
Leu Leu Tyr Phe Ile Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val			
	85	90	95
Thr Val His Phe Phe His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg			
	100	105	110
Phe Pro Ser Ala Leu Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala			
	115	120	125
Leu Met Ala Val Ile Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys			
	130	135	140
Glu Ile Pro Leu Asn Ser Ala Pro Lys Ser Asn Val			
145	150	155	

<210> 93

<211> 2608

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1053)

<400> 93

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 ctccccagat acctgaaact gaccacctga gtacgttttc ccattgctga gctgtttccc 120
 tgatatctgg cc atg caa cgg aga tca aga ggg ata aat act gga ctt att 171

Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile

1

5

10

cta ctc ctt tct caa atc ttc cat gtt ggg atc aac aat att cca cct 219
 Leu Leu Leu Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro

15	20	25	
gtc acc cta gca act ttg gcc ctc aac atc tgg ttc ttc ttg aac cct	267		
Val Thr Leu Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro			
30	35	40	45
cag aag cca ctg tat agc tcc tgc ctt agt gtg gag aag tgt tac cag	315		
Gln Lys Pro Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln			
50	55	60	
caa aaa gac tgg cag cgt tta ctg ctc tct ccc ctt cac cat gct gat	363		
Gln Lys Asp Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp			
65	70	75	
gat tgg cat ttg tat ttc aat atg gca tcc atg ctc tgg aaa gga ata	411		
Asp Trp His Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile			
80	85	90	
aat cta gaa aga aga ctg gga agt aga tgg ttt gcc tat gtt atc acc	459		
Asn Leu Glu Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr			
95	100	105	
gca ttt tct gta ctt act gga gtg gta tac ctg ctc ttg caa ttt gct	507		
Ala Phe Ser Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala			
110	115	120	125
gtt gcc gaa ttt atg gat gaa cct gac ttc aaa agg agc tgt gct gta	555		
Val Ala Glu Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val			
130	135	140	
ggt ttc tca gga gtt ttg ttt gct ttg aaa gtt ctt aac aac cat tat	603		
Gly Phe Ser Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr			
145	150	155	
tgc cct gga ggc ttt gtc aac att ttg ggc ttt cct gta ccg aac aga	651		
Cys Pro Gly Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg			

160	165	170	
ttt gct tgt tgg gtc gaa ctt gtg gct att cat tta ttc tca cca ggg	699		
Phe Ala Cys Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly			
175	180	185	
act tcc ttc gct ggg cat ctg gct ggg att ctt gtt gga cta atg tac	747		
Thr Ser Phe Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr			
190	195	200	205
act caa ggg cct ctg aag aaa atc atg gaa gca tgt gca ggc ggt ttt	795		
Thr Gln Gly Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe			
210	215	220	
tcc tcc agt gtt ggt tac cca gga cgg caa tac tac ttt aat agt tca	843		
Ser Ser Ser Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser			
225	230	235	
ggc agc tct gga tat cag gat tat tat ccg cat ggc agg cca gat cac	891		
Gly Ser Ser Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His			
240	245	250	
tat gaa gaa gca ccc agg aac tat gac acg tac aca gca gga ctg agt	939		
Tyr Glu Glu Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser			
255	260	265	
gaa gaa gaa cag ctc gag aga gca tta caa gcc agc ctc tgg gac cga	987		
Glu Glu Glu Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg			
270	275	280	285
gag tgc tgg gat tac agg cgt gag cca ccg tgc cca gcc gtt gtg atc	1035		
Glu Cys Trp Asp Tyr Arg Arg Glu Pro Pro Cys Pro Ala Val Val Ile			
290	295	300	
atc ttg aat tca gaa aac tgaaaactca gaggaaatac cagaaatagc	1083		
Ile Leu Asn Ser Glu Asn			

305

ccaccaccct acgggtttca tctctcacca gaagaaatga ggagacagcg gcttcacaga 1143
 ttcgatagcc agtgaggtag catcttgga agacatggcc tattcgtgta attattgccc 1203
 atttggtca tccccaaagc ccctaattca ttttaattca ttttaaaca aagcagagta 1263
 caccggtatt gctccagatc gctcacatca cctgggacag tcccatggcc cctatgagtc 1323
 aactcacagc ttgcggggag tgggccttct cctggccttg ttcttgctca taaacaggtc 1383
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 gtggagccat ccccgctcc tcttggcga ttgccactgt ggctgtccag gaacaggatg 1623
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 tctctttttt tcatggctgc tagtatttta ttttagaatc acagactctc agcttagaga 2043
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 catctgtttc tctgtctctc ctacagtgct cttgagcagt acgttgctctg gaatgtcaga 2583
 accaataaat acttgtggat tgaaa 2608

<210> 94

<211> 307

<212> PRT

<213> Homo sapiens

<400> 94

Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile Leu Leu Leu
1 5 10 15
Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu
20 25 30
Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro
35 40 45
Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp
50 55 60
Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His
65 70 75 80
Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu
85 90 95
Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser
100 105 110
Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu
115 120 125
Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser
130 135 140
Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly
145 150 155 160
Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys

165 170 175
 Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe
 180 185 190
 Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly
 195 200 205
 Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser
 210 215 220
 Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser
 225 230 235 240
 Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu
 245 250 255
 Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu
 260 265 270
 Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Glu Cys Trp
 275 280 285
 Asp Tyr Arg Arg Glu Pro Pro Cys Pro Ala Val Val Ile Ile Leu Asn
 290 295 300
 Ser Glu Asn
 305

<210> 95

<211> 2423

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (122).. (1066)

<400> 95

gacgtgggga cgcaggcggg tcgtagagag cgttcagccg tctgtatatc tccccagata 60
 cctgaaactg accacctgag tacgttttcc cattgctgag ctgtttccct gatatctggc 120
 c atg caa cgg aga tca aga ggg ata aat act gga ctt att cta ctc ctt 169
 Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile Leu Leu Leu
 1 5 10 15
 tct caa atc ttc cat gtt ggg atc aac aat att cca cct gtc acc cta 217
 Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu
 20 25 30
 gca act ttg gcc ctc aac atc tgg ttc ttc ttg aac cct cag aag cca 265
 Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro
 35 40 45
 ctg tat agc tcc tgc ctt agt gtg gag aag tgt tac cag caa aaa gac 313
 Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp
 50 55 60
 tgg cag cgt tta ctg ctc tct ccc ctt cac cat gct gat gat tgg cat 361
 Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His
 65 70 75 80
 ttg tat ttc aat atg gca tcc atg ctc tgg aaa gga ata aat cta gaa 409
 Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu
 85 90 95
 aga aga ctg gga agt aga tgg ttt gcc tat gtt atc acc gca ttt tct 457
 Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser
 100 105 110
 gta ctt act gga gtg gta tac ctg ctc ttg caa ttt gct gtt gcc gaa 505
 Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu
 115 120 125

ttt atg gat gaa cct gac ttc aaa agg agc tgt gct gta ggt ttc tca 553
 Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser
 130 135 140
 gga gtt ttg ttt gct ttg aaa gtt ctt aac aac cat tat tgc cct gga 601
 Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly
 145 150 155 160
 ggc ttt gtc aac att ttg ggc ttt cct gta ccg aac aga ttt gct tgt 649
 Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys
 165 170 175
 tgg gtc gaa ctt gtg gct att cat tta ttc tca cca ggg act tcc ttc 697
 Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe
 180 185 190
 gct ggg cat ctg gct ggg att ctt gtt gga cta atg tac act caa ggg 745
 Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly
 195 200 205
 cct ctg aag aaa atc atg gaa gca tgt gca ggc ggt ttt tcc tcc agt 793
 Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser
 210 215 220
 gtt ggt tac cca gga cgg caa tac tac ttt aat agt tca ggc agc tct 841
 Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser
 225 230 235 240
 gga tat cag gat tat tat ccg cat ggc agg cca gat cac tat gaa gaa 889
 Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu
 245 250 255
 gca ccc agg aac tat gac acg tac aca gca gga ctg agt gaa gaa gaa 937
 Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu
 260 265 270

cag ctc gag aga gca tta caa gcc agc ctc tgg gac cga gga aat acc 985
 Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Gly Asn Thr
 275 280 285
 aga aat agc cca cca ccc tac ggg ttt cat ctc tca cca gaa gaa atg 1033
 Arg Asn Ser Pro Pro Pro Tyr Gly Phe His Leu Ser Pro Glu Glu Met
 290 295 300
 agg aga cag cgg ctt cac aga ttc gat agc cag tgaggtggca tcttggaag 1086

 Arg Arg Gln Arg Leu His Arg Phe Asp Ser Gln
 305 310 315
 acatggccta ttcgtgtaat tattgcccatt ttggtcatt cccaagccc ctaattcatt 1146
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<210> 96

<211> 315

<212> PRT

<213> Homo sapiens

<400> 96

Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile Leu Leu Leu
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 Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu
 20 25 30
 Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro
 35 40 45
 Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp
 50 55 60
 Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His
 65 70 75 80
 Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu
 85 90 95
 Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser
 100 105 110
 Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu

115 120 125
Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser
130 135 140
Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly
145 150 155 160
Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys
165 170 175
Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe
180 185 190
Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly
195 200 205
Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser
210 215 220
Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser
225 230 235 240
Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu
245 250 255
Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu
260 265 270
Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Gly Asn Thr
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Arg Asn Ser Pro Pro Pro Tyr Gly Phe His Leu Ser Pro Glu Glu Met
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Arg Arg Gln Arg Leu His Arg Phe Asp Ser Gln
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<211> 2207

<212> DNA

<213> Homo sapiens

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<222> (138)..(443)

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 tctgccggtc acagcca atg tac ggc tcg gcc tgg ctg ccc cct ccc cca 170

Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro

1

5

10

gga ttc ccc atc ccc agc ttc tcg ccc tcc ccg cac cgc ccc cac ccc 218

Gly Phe Pro Ile Pro Ser Phe Ser Pro Ser Pro His Arg Pro His Pro

15

20

25

ggg att tcg acc ccc tta agg gct cca ccc cgc tcc ggg atc ccc ttc 266

Gly Ile Ser Thr Pro Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe

30

35

40

tcc cag ctc cta tcc ctt agg act gcc ccg ccc cct aga acc tcc ccg 314

Ser Gln Leu Leu Ser Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro

45

50

55

tca gga tct ccg tcc ctc agc cgc tca cag cct cct ccc agc gcc cat 362

Ser Gly Ser Pro Ser Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His

60

65

70

75

cgc ctt gag ctg ccc act acc tct aga ctg ccc tcc cgg gct ggc gtc 410

Arg Leu Glu Leu Pro Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val

80

85

90

cca cgg agt ctc agc cgc gca ccc ctt ctc cgg tagctcctac ccctgcctgt 463
 Pro Arg Ser Leu Ser Arg Ala Pro Leu Leu Arg

95

100

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<211> 102

<212> PRT

<213> Homo sapiens

<400> 98

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 Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe Ser Gln Leu Leu Ser
 35 40 45
 Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro Ser Gly Ser Pro Ser
 50 55 60
 Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His Arg Leu Glu Leu Pro
 65 70 75 80
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 85 90 95
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<210> 99

<211> 2246

<212> DNA

<213> Homo sapiens

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<222> (138).. (482)

<400> 99

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tctgccggtc acagcca atg tac ggc tcg gcc tgg ctg ccc cct ccc cca 170
      Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro
              1              5              10
gga ttc ccc atc ccc agc ttc tcg ccc tcc ccg cac cgc ccc cac ccc 218
Gly Phe Pro Ile Pro Ser Phe Ser Pro Ser Pro His Arg Pro His Pro
              15              20              25
ggg att tcg acc ccc tta agg gct cca ccc cgc tcc ggg atc ccc ttc 266
Gly Ile Ser Thr Pro Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe
              30              35              40
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Ser Gln Leu Leu Ser Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro
              45              50              55
tca gga tct ccg tcc ctc agc cgc tca cag cct cct ccc agc gcc cat 362
Ser Gly Ser Pro Ser Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His
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cgc ctt gag ctg ccc act acc tct aga ctg ccc tcc cgg gct ggc gtc 410
Arg Leu Glu Leu Pro Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val

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Asp Ser Thr Pro Ser Leu Leu Arg			
110	115		
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<211> 115

<212> PRT

<213> Homo sapiens

<400> 100

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 Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe Ser Gln Leu Leu Ser
 35 40 45
 Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro Ser Gly Ser Pro Ser
 50 55 60
 Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His Arg Leu Glu Leu Pro
 65 70 75 80
 Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val Pro Arg Ser Leu Ser
 85 90 95

Arg Ala Pro Leu Pro Arg Val Thr Leu Leu Pro Asp Ser Thr Pro Ser
 100 105 110

Leu Leu Arg
 115

<210> 101

<211> 3243

<212> DNA

<213> Homo sapiens

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<222> (43).. (1467)

<400> 101

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 Leu Lys Asp Glu Leu Leu Cys Ser Ile Cys Leu Ser Ile Tyr Gln Asp
 5 10 15 20

ccg gtg agc ctg ggc tgc gag cac tac ttc tgc cgc cgc tgc atc acg 150
 Pro Val Ser Leu Gly Cys Glu His Tyr Phe Cys Arg Arg Cys Ile Thr
 25 30 35

gag cac tgg gtg cgg cag gag gcg cag ggc gcc cgc gac tgc ccc gag 198
 Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg Asp Cys Pro Glu
 40 45 50

tgc cgg cgc acg ttc gcc gag ccc gcg ctg gcg ccc agc ctc aag ctg 246
 Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro Ser Leu Lys Leu

55	60	65	
gcc aac atc gtg gag cgc tac agc tcc ttc ccg ctg gac gcc atc ctc			294
Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu Asp Ala Ile Leu			
70	75	80	
aac gcg cgc cgc gcc gcg cga ccc tgc cag gcg cac gac aag gtc aag			342
Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His Asp Lys Val Lys			
85	90	95	100
ctc ttc tgc ctc acg gac cgc gcg ctt ctc tgc ttc ttc tgc gac gag			390
Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe Phe Cys Asp Glu			
	105	110	115
cct gca ctg cac gag cag cat cag gtc acc gcc atc gac gac gcc ttc			438
Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile Asp Asp Ala Phe			
	120	125	130
gac gag ctg cag agg gag ctg aag gac caa ctt cag gcc ctt caa gac			486
Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln Ala Leu Gln Asp			
	135	140	145
agc gag cgg gaa cac acc gaa gcg ctg cag ctg ctc aag cga caa ctg			534
Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu Lys Arg Gln Leu			
	150	155	160
gcg gag acc aag tct tcc acc aag agc ctg cgg acc act atc gcc gag			582
Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr Thr Ile Gly Glu			
165	170	175	180
gcc ttc gag cgg ctg cac cgg ctg ctg cgt gaa cgc cag aag gcc atg			630
Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg Gln Lys Ala Met			
	185	190	195
cta gag gag ctg gag gcg gac acg gcc cgc acg ctg acc gac atc gag			678
Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu Thr Asp Ile Glu			

200	205	210	
cag aaa gtc cag cgc tac agc cag cag ctg cgc aag gtc cag gag gga			726
Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys Val Gln Glu Gly			
215	220	225	
gcc cag atc ctg cag gag cgg ctg gct gaa acc gac cgg cac acc ttc			774
Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp Arg His Thr Phe			
230	235	240	
ctg gct ggg gtg gcc tca ctg tcc gag cgg ctc aag gga aaa atc cat			822
Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys Gly Lys Ile His			
245	250	255	260
gag acc aac ctc aca tat gaa gac ttc ccg acc tcc aag tac aca ggc			870
Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser Lys Tyr Thr Gly			
265	270	275	
ccc ctg cag tac acc atc tgg aag tcc ctg ttc cag gac atc cac cca			918
Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln Asp Ile His Pro			
280	285	290	
gtg cca gcc gcc cta acc ctg gac ccg ggc aca gcc cac cag cgc ctg			966
Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala His Gln Arg Leu			
295	300	305	
atc ctg tcg gac gac tgc acc att gtg gct tac ggc aac ttg cac cca			1014
Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly Asn Leu His Pro			
310	315	320	
cag cca ctg cag gac tcg cca aag cgc ttc gat gtg gag gtg tcg gtg			1062
Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val Glu Val Ser Val			
325	330	335	340
ctg ggt tct gaa gcc ttc agt agt ggc gtc cac tac tgg gag gtg gtg			1110
Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr Trp Glu Val Val			

345	350	355	
gtg gcg gag aag acc cag tgg gtg atc ggg ctg gca cac gaa gcc gca			1158
Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala His Glu Ala Ala			
360	365	370	
agc cgc aag ggc agc atc cag atc cag ccc agc cgc ggc ttc tac tgc			1206
Ser Arg Lys Gly Ser Ile Gln Ile Gln Pro Ser Arg Gly Phe Tyr Cys			
375	380	385	
atc gtg atg cac gat ggc aac cag tac agc gcc tgc acg gag ccc tgg			1254
Ile Val Met His Asp Gly Asn Gln Tyr Ser Ala Cys Thr Glu Pro Trp			
390	395	400	
acg cgg ctt aac gtc cgg gac aag ctt gac aag gtg ggt gtc ttc ctg			1302
Thr Arg Leu Asn Val Arg Asp Lys Leu Asp Lys Val Gly Val Phe Leu			
405	410	415	420
gac tat gac caa ggc ttg ctc atc ttc tac aat gct gat gac atg tcc			1350
Asp Tyr Asp Gln Gly Leu Leu Ile Phe Tyr Asn Ala Asp Asp Met Ser			
425	430	435	
tgg ctc tac acc ttc cgc gag aag ttc cct ggc aag ctc tgc tct tac			1398
Trp Leu Tyr Thr Phe Arg Glu Lys Phe Pro Gly Lys Leu Cys Ser Tyr			
440	445	450	
ttc agc cct ggc cag agc cac gcc aat ggc aag aac gtt cag ccg ctg			1446
Phe Ser Pro Gly Gln Ser His Ala Asn Gly Lys Asn Val Gln Pro Leu			
455	460	465	
cgg atc aac acc gtc cgc atc tagtccaggc agaaggagac cacaacctcc			1497
Arg Ile Asn Thr Val Arg Ile			
470	475		
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3243

<210> 102

<211> 475

<212> PRT

<213> Homo sapiens

<400> 102

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20 25 30

Arg Cys Ile Thr Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg

35 40 45

Asp Cys Pro Glu Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro

50 55 60

Ser Leu Lys Leu Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu

65 70 75 80

Asp Ala Ile Leu Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His

85 90 95

Asp Lys Val Lys Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe

100 105 110

Phe Cys Asp Glu Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile

115 120 125

Asp Asp Ala Phe Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln

130 135 140

Ala Leu Gln Asp Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu

145 150 155 160

Lys Arg Gln Leu Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr
 165 170 175
 Thr Ile Gly Glu Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg
 180 185 190
 Gln Lys Ala Met Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu
 195 200 205
 Thr Asp Ile Glu Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys
 210 215 220
 Val Gln Glu Gly Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp
 225 230 235 240
 Arg His Thr Phe Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys
 245 250 255
 Gly Lys Ile His Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser
 260 265 270
 Lys Tyr Thr Gly Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln
 275 280 285
 Asp Ile His Pro Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala
 290 295 300
 His Gln Arg Leu Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly
 305 310 315 320
 Asn Leu His Pro Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val
 325 330 335
 Glu Val Ser Val Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr
 340 345 350
 Trp Glu Val Val Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala
 355 360 365
 His Glu Ala Ala Ser Arg Lys Gly Ser Ile Gln Ile Gln Pro Ser Arg

370 375 380
 Gly Phe Tyr Cys Ile Val Met His Asp Gly Asn Gln Tyr Ser Ala Cys
 385 390 395 400
 Thr Glu Pro Trp Thr Arg Leu Asn Val Arg Asp Lys Leu Asp Lys Val
 405 410 415
 Gly Val Phe Leu Asp Tyr Asp Gln Gly Leu Leu Ile Phe Tyr Asn Ala
 420 425 430
 Asp Asp Met Ser Trp Leu Tyr Thr Phe Arg Glu Lys Phe Pro Gly Lys
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<211> 788

<212> DNA

<213> Homo sapiens

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 cagcc atg ctg gag cat ctg agc tcg ctg ccc acg çag atg gat tac aag 170

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys

1

5

10

15

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 Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser
 20 25 30
 gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg 266
 Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp
 35 40 45
 act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt ttg ctg aca 314
 Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr
 50 55 60
 ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct 362
 Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro
 65 70 75
 gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att 410
 Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile
 80 85 90 95
 aag agg cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt 461
 Lys Arg His Ala Lys Asn Asn
 100
 gtttctgtga gatgagctaa attgctttca taccacagat aagagctaaa accacctaatt 521
 gctcttatgg cacagctgtg tatagattta gttctcttta tacttcattt ctagcccagt 581
 tgggttttga tttatataag tagtttagac cttctcttca taatcttgct ctgagatggg 641
 gaacagaaca cacaagtatg aagtttcttt caggtgtaaa taatgaaaaa taaatgcctc 701
 ataaatgata gtacaatgta actatcaaag ttttataatt cattatgagt taaccatttt 761
 aatgtttcca attaaacctc atagtgc 788

<210> 104

<211> 102

<212> PRT

<213> Homo sapiens

<400> 104

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly
1 5 10 15
Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
20 25 30
Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
35 40 45
Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu
50 55 60
Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val
65 70 75 80
Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys
85 90 95
Arg His Ala Lys Asn Asn
100

<210> 105

<211> 2189

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (253).. (966)

<400> 105

atcggccccg ggtctgtccg ggcgttgccg gattggggcc tgggaacgct cggcccccg 60

cagccgagaa gcccgtagact gggctgagca gcaccatccc agccctgggg cctgctgact 120
 gccagatccc ggcttcacct gcagcgaacc cggagcgttg ctatcctcca ccgactgtc 180
 aggctctgcg cgccccgcgg aggtcggcgg cgaccagcag cgactgcgga gcgacggcgg 240
 gcggccccgg gc atg tac gcc ccc gga ggc gca ggg ctg ccc ggc ggg cgc 291

Met Tyr Ala Pro Gly Gly Ala Gly Leu Pro Gly Gly Arg

1 5 10

cgg cgg agg agc ccg gga ggc agc gct ctg ccc aag cag ccg gag cgt 339
 Arg Arg Arg Ser Pro Gly Gly Ser Ala Leu Pro Lys Gln Pro Glu Arg

15 20 25

agc ctg gcc tcg gcc ctg cct ggc gcc ctg tct atc acg gcg ctg tgc 387
 Ser Leu Ala Ser Ala Leu Pro Gly Ala Leu Ser Ile Thr Ala Leu Cys

30 35 40 45

act gcc ctc gcc gag ccc gcc tgg ttg cac atc cac gga ggc acc tgt 435
 Thr Ala Leu Ala Glu Pro Ala Trp Leu His Ile His Gly Gly Thr Cys

50 55 60

tcg cgc cag gag ctg ggg gtc tcc gac gtg ttg ggc tat gtg cac ccg 483
 Ser Arg Gln Glu Leu Gly Val Ser Asp Val Leu Gly Tyr Val His Pro

65 70 75

gac ctg ctg aaa gat ttc tgc atg aat ccc cag aca gtg ctg ctc ctg 531
 Asp Leu Leu Lys Asp Phe Cys Met Asn Pro Gln Thr Val Leu Leu Leu

80 85 90

cgg gtc atc gcc gcc ttc tgt ttc ctg ggc atc ctg tgt agt ctc tcc 579
 Arg Val Ile Ala Ala Phe Cys Phe Leu Gly Ile Leu Cys Ser Leu Ser

95 100 105

gct ttc ctt ctg gat gtc ttt ggg ccg aag cat cct gct ctg aag atc 627
 Ala Phe Leu Leu Asp Val Phe Gly Pro Lys His Pro Ala Leu Lys Ile

110 115 120 125

act cgt cgc tat gcc ttc gcc cat atc cta acg gtt ctg cag tgt gcc 675
 Thr Arg Arg Tyr Ala Phe Ala His Ile Leu Thr Val Leu Gln Cys Ala
 130 135 140
 acc gtc att ggc ttt tct tat tgg gct tct gaa ctc atc ttg gcc cag 723
 Thr Val Ile Gly Phe Ser Tyr Trp Ala Ser Glu Leu Ile Leu Ala Gln
 145 150 155
 cag cag cag cat aag aag tac cat gga tcc cag gtc tat gtc acc ttc 771
 Gln Gln Gln His Lys Lys Tyr His Gly Ser Gln Val Tyr Val Thr Phe
 160 165 170
 gcc gtt agc ttc tac ctg gtg gca gga gct ggt gga gcc tca atc ctg 819
 Ala Val Ser Phe Tyr Leu Val Ala Gly Ala Gly Gly Ala Ser Ile Leu
 175 180 185
 gcc acg gca gcc aac ctc ctg cgc cac tac ccc aca gag gaa gag gag 867
 Ala Thr Ala Ala Asn Leu Leu Arg His Tyr Pro Thr Glu Glu Glu Glu
 190 195 200 205
 cag gcg ctg gag ctg ctc tca gag atg gaa gag aac gag ccc tac ccg 915
 Gln Ala Leu Glu Leu Leu Ser Glu Met Glu Glu Asn Glu Pro Tyr Pro
 210 215 220
 gcg gaa tat gag gtc atc aac cag ttc cag cca ccc cct gct tac aca 963
 Ala Glu Tyr Glu Val Ile Asn Gln Phe Gln Pro Pro Pro Ala Tyr Thr
 225 230 235
 ccc taatgccagc cctgggctct cttcctcggc agcccctccc tcaactctgc 1016
 Pro
 agtcctcttc gcacccagag gagctccttt ccccagcagg cctcactggt aggatcctga 1076
 gatggaacct ggcctcagtt taggaacagg ggccacaaca gggcaggaac ccaccaccct 1136
 ccacatagga atacaaccag tggggccaca tcatgtgagg catcagaccc aactgtcag 1196
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gcagcttgcc acgtgccctc tcccctcttg aatgtactct ggtcttgcag tgtgctgctg 1316
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 ctgaaaagga aatggattcc aatctcttcc aacctttaag gtgatagata gtttgagcaa 1556
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 gtctttggcc ttctcttctt ttctctttcc ctctgccatc ctgacactga tagtttgtca 2096
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 aaaaaacca gaaaccacga ataagaatgg aaa 2189

<210> 106

<211> 238

<212> PRT

<213> Homo sapiens

<400> 106

Met Tyr Ala Pro Gly Gly Ala Gly Leu Pro Gly Gly Arg Arg Arg Arg

1

5

10

15

Ser Pro Gly Gly Ser Ala Leu Pro Lys Gln Pro Glu Arg Ser Leu Ala

20

25

30

Ser Ala Leu Pro Gly Ala Leu Ser Ile Thr Ala Leu Cys Thr Ala Leu

35 40 45
Ala Glu Pro Ala Trp Leu His Ile His Gly Gly Thr Cys Ser Arg Gln
50 55 60
Glu Leu Gly Val Ser Asp Val Leu Gly Tyr Val His Pro Asp Leu Leu
65 70 75 80
Lys Asp Phe Cys Met Asn Pro Gln Thr Val Leu Leu Leu Arg Val Ile
85 90 95
Ala Ala Phe Cys Phe Leu Gly Ile Leu Cys Ser Leu Ser Ala Phe Leu
100 105 110
Leu Asp Val Phe Gly Pro Lys His Pro Ala Leu Lys Ile Thr Arg Arg
115 120 125
Tyr Ala Phe Ala His Ile Leu Thr Val Leu Gln Cys Ala Thr Val Ile
130 135 140
Gly Phe Ser Tyr Trp Ala Ser Glu Leu Ile Leu Ala Gln Gln Gln Gln
145 150 155 160
His Lys Lys Tyr His Gly Ser Gln Val Tyr Val Thr Phe Ala Val Ser
165 170 175
Phe Tyr Leu Val Ala Gly Ala Gly Gly Ala Ser Ile Leu Ala Thr Ala
180 185 190
Ala Asn Leu Leu Arg His Tyr Pro Thr Glu Glu Glu Glu Gln Ala Leu
195 200 205
Glu Leu Leu Ser Glu Met Glu Glu Asn Glu Pro Tyr Pro Ala Glu Tyr
210 215 220
Glu Val Ile Asn Gln Phe Gln Pro Pro Pro Ala Tyr Thr Pro
225 230 235

<210> 107

<211> 1195

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1166)

<400> 107

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Met Gly Pro Gly Arg

1

5

tgc ctc ctg acg gcc ttg ttg ctt ctg gcc ctg gcg cca ccg ccg gaa 164

Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu Ala Pro Pro Pro Glu

10

15

20

gcc tcc cag tac tgc ggc cgc ctt gaa tac tgg aac cca gac aac aag 212

Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp Asn Pro Asp Asn Lys

25

30

35

tgc tgc agc agc tgc ctg caa cgc ttc ggg ccg ccc ccc tgc ccg gac 260

Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro Pro Pro Cys Pro Asp

40

45

50

tat gag ttc cgg gaa aac tgc gga ctc aat gac cac ggc gat ttc gta 308

Tyr Glu Phe Arg Glu Asn Cys Gly Leu Asn Asp His Gly Asp Phe Val

55

60

65

acg ccc ccg ttc cga aag tgt tct tct ggg cag tgc aac ccc gac ggc 356

Thr Pro Pro Phe Arg Lys Cys Ser Ser Gly Gln Cys Asn Pro Asp Gly

70

75

80

85

gcg gag cta tgt agc ccc tgc ggc ggc gga gcc gtg acc cct act ccc 404

Ala Glu Leu Cys Ser Pro Cys Gly Gly Gly Ala Val Thr Pro Thr Pro	
90 95 100	
gcc gcg ggc ggg ggc aga acc ccg tgg cgc tgc aga gag agg ccg gtc	452
Ala Ala Gly Gly Gly Arg Thr Pro Trp Arg Cys Arg Glu Arg Pro Val	
105 110 115	
cct gcc aag ggg cac tgc ccc ctc aca cct gga aac cca ggc gcc cct	500
Pro Ala Lys Gly His Cys Pro Leu Thr Pro Gly Asn Pro Gly Ala Pro	
120 125 130	
agc tcc cag gag cgc agc tca ccg gca agt tcc att gcc tgg agg acc	548
Ser Ser Gln Glu Arg Ser Ser Pro Ala Ser Ser Ile Ala Trp Arg Thr	
135 140 145	
cct gag cct gtc cct cag cag gcc tgg ccg aat ttc ctt ccg ctc gtg	596
Pro Glu Pro Val Pro Gln Gln Ala Trp Pro Asn Phe Leu Pro Leu Val	
150 155 160 165	
gtg ctg gtc ctg ctc ctg acc ttg gcg gtg ata gcg atc ctc ctg ttt	644
Val Leu Val Leu Leu Leu Thr Leu Ala Val Ile Ala Ile Leu Leu Phe	
170 175 180	
att ctg ctc tgg cat ctc tgc tgg ccc aag gag aaa gcc gac ccc tat	692
Ile Leu Leu Trp His Leu Cys Trp Pro Lys Glu Lys Ala Asp Pro Tyr	
185 190 195	
ccc tat cct ggc ttg gtc tgc gga gtc ccc aac acc cac acc cct tcc	740
Pro Tyr Pro Gly Leu Val Cys Gly Val Pro Asn Thr His Thr Pro Ser	
200 205 210	
tcc tcg cat ctg tcc tcc cca ggc gcc ctg gag aca ggg gac aca tgg	788
Ser Ser His Leu Ser Ser Pro Gly Ala Leu Glu Thr Gly Asp Thr Trp	
215 220 225	
aag gag gcc tca cta ctt cca ctc ctg agc agg gaa ctg tcc agt ctg	836

Lys Glu Ala Ser Leu Leu Pro Leu Leu Ser Arg Glu Leu Ser Ser Leu
 230 235 240 245
 gcg tca caa ccc ctg tct cgc ctc ctg gat gag ctg gag gtg ctg gaa 884
 Ala Ser Gln Pro Leu Ser Arg Leu Leu Asp Glu Leu Glu Val Leu Glu
 250 255 260
 gag ctg att gta ctg ctg gac cct gag cct ggg cca ggt ggg ggt atg 932
 Glu Leu Ile Val Leu Leu Asp Pro Glu Pro Gly Pro Gly Gly Gly Met
 265 270 275
 gcc cat ggc act act cga cac ctg gcc gca aga tat ggg ctg cct gct 980
 Ala His Gly Thr Thr Arg His Leu Ala Ala Arg Tyr Gly Leu Pro Ala
 280 285 290
 gcc tgg tcc acc ttt gcc tat tcg ctg agg ccg agt cgc tcg ccg ctg 1028
 Ala Trp Ser Thr Phe Ala Tyr Ser Leu Arg Pro Ser Arg Ser Pro Leu
 295 300 305
 cgg gct ctg att gag atg gtg gtg gca agg gag ccc tct gcc tcc ctg 1076
 Arg Ala Leu Ile Glu Met Val Val Ala Arg Glu Pro Ser Ala Ser Leu
 310 315 320 325
 ggc cag ctt ggc aca cac ctc gcc cag cta ggg cgg gca gat gca ttg 1124
 Gly Gln Leu Gly Thr His Leu Ala Gln Leu Gly Arg Ala Asp Ala Leu
 330 335 340
 cgg gtg ctg tcc aag ctt ggc tca tct ggg gtt tgc tgg gct 1166
 Arg Val Leu Ser Lys Leu Gly Ser Ser Gly Val Cys Trp Ala
 345 350 355
 taacacccaa taaagaactt tgctgacta 1195

<210> 108

<211> 355

<212> PRT

<213> Homo sapiens

<400> 108

Met Gly Pro Gly Arg Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu

1 5 10 15

Ala Pro Pro Pro Glu Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp

20 25 30

Asn Pro Asp Asn Lys Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro

35 40 45

Pro Pro Cys Pro Asp Tyr Glu Phe Arg Glu Asn Cys Gly Leu Asn Asp

50 55 60

His Gly Asp Phe Val Thr Pro Pro Phe Arg Lys Cys Ser Ser Gly Gln

65 70 75 80

Cys Asn Pro Asp Gly Ala Glu Leu Cys Ser Pro Cys Gly Gly Gly Ala

85 90 95

Val Thr Pro Thr Pro Ala Ala Gly Gly Gly Arg Thr Pro Trp Arg Cys

100 105 110

Arg Glu Arg Pro Val Pro Ala Lys Gly His Cys Pro Leu Thr Pro Gly

115 120 125

Asn Pro Gly Ala Pro Ser Ser Gln Glu Arg Ser Ser Pro Ala Ser Ser

130 135 140

Ile Ala Trp Arg Thr Pro Glu Pro Val Pro Gln Gln Ala Trp Pro Asn

145 150 155 160

Phe Leu Pro Leu Val Val Leu Val Leu Leu Leu Thr Leu Ala Val Ile

165 170 175

Ala Ile Leu Leu Phe Ile Leu Leu Trp His Leu Cys Trp Pro Lys Glu

180 185 190

Lys Ala Asp Pro Tyr Pro Tyr Pro Gly Leu Val Cys Gly Val Pro Asn
 195 200 205
 Thr His Thr Pro Ser Ser Ser His Leu Ser Ser Pro Gly Ala Leu Glu
 210 215 220
 Thr Gly Asp Thr Trp Lys Glu Ala Ser Leu Leu Pro Leu Leu Ser Arg
 225 230 235 240
 Glu Leu Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg Leu Leu Asp Glu
 245 250 255
 Leu Glu Val Leu Glu Glu Leu Ile Val Leu Leu Asp Pro Glu Pro Gly
 260 265 270
 Pro Gly Gly Gly Met Ala His Gly Thr Thr Arg His Leu Ala Ala Arg
 275 280 285
 Tyr Gly Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr Ser Leu Arg Pro
 290 295 300
 Ser Arg Ser Pro Leu Arg Ala Leu Ile Glu Met Val Val Ala Arg Glu
 305 310 315 320
 Pro Ser Ala Ser Leu Gly Gln Leu Gly Thr His Leu Ala Gln Leu Gly
 325 330 335
 Arg Ala Asp Ala Leu Arg Val Leu Ser Lys Leu Gly Ser Ser Gly Val
 340 345 350
 Cys Trp Ala
 355

<210> 109

<211> 685

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (156).. (656)

<400> 109

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tccccacat caccgcgtcc tttcttctgc cggatttccc cggaaagtgt agcagaggcg 120
ctgtgtttgg aagtcccgt atcacggccc cccag atg ggg cct gga cga tgc      173
                                Met Gly Pro Gly Arg Cys
                                1              5

ctc ctg acg gcc ttg ttg ctt ctg gcc ctg gcg cca ccg ccg gaa gcc      221
Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu Ala Pro Pro Pro Glu Ala
                10              15              20

tcc cag tac tgc ggc cgc ctt gaa tac tgg aac cca gac aac aag tgc      269
Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp Asn Pro Asp Asn Lys Cys
                25              30              35

tgc agc agc tgc ctg caa cgc ttc ggg ccg ccc ccc tgc ccg gaa ctg      317
Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro Pro Pro Cys Pro Glu Leu
                40              45              50

tcc agt ctg gcg tca caa ccc ctg tct cgc ctc ctg gat gag ctg gag      365
Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg Leu Leu Asp Glu Leu Glu
                55              60              65              70

gtg ctg gaa gag ctg att gta ctg ctg gac cct gag cct ggg cca ggt      413
Val Leu Glu Glu Leu Ile Val Leu Leu Asp Pro Glu Pro Gly Pro Gly
                75              80              85

ggg ggt atg gcc cat ggc act act cga cac ctg gcc gca aga tat ggg      461
Gly Gly Met Ala His Gly Thr Thr Arg His Leu Ala Ala Arg Tyr Gly
                90              95              100

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ctg cct gct gcc tgg tcc acc ttt gcc tat tcg ctg agg ccg agt cgc 509
 Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr Ser Leu Arg Pro Ser Arg
 105 110 115
 tcg ccg ctg cgg gct ctg att gag atg gtg gtg gca agg gag ccc tct 557
 Ser Pro Leu Arg Ala Leu Ile Glu Met Val Val Ala Arg Glu Pro Ser
 120 125 130
 gcc tcc ctg ggc cag ctt ggc aca cac ctc gcc cag cta ggg cgg gca 605
 Ala Ser Leu Gly Gln Leu Gly Thr His Leu Ala Gln Leu Gly Arg Ala
 135 140 145 150
 gat gca ttg cgg gtg ctg tcc aag ctt ggc tca tct ggg gtt tgc tgg 653
 Asp Ala Leu Arg Val Leu Ser Lys Leu Gly Ser Ser Gly Val Cys Trp
 155 160 165
 gct taacacccaa taaagaactt tgctgacta 685
 Ala

<210> 110

<211> 167

<212> PRT

<213> Homo sapiens

<400> 110

Met Gly Pro Gly Arg Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu
 1 5 10 15
 Ala Pro Pro Pro Glu Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp
 20 25 30
 Asn Pro Asp Asn Lys Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro
 35 40 45
 Pro Pro Cys Pro Glu Leu Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg

50 55 60
 Leu Leu Asp Glu Leu Glu Val Leu Glu Glu Leu Ile Val Leu Leu Asp
 65 70 75 80
 Pro Glu Pro Gly Pro Gly Gly Gly Met Ala His Gly Thr Thr Arg His
 85 90 95
 Leu Ala Ala Arg Tyr Gly Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr
 100 105 110
 Ser Leu Arg Pro Ser Arg Ser Pro Leu Arg Ala Leu Ile Glu Met Val
 115 120 125
 Val Ala Arg Glu Pro Ser Ala Ser Leu Gly Gln Leu Gly Thr His Leu
 130 135 140
 Ala Gln Leu Gly Arg Ala Asp Ala Leu Arg Val Leu Ser Lys Leu Gly
 145 150 155 160
 Ser Ser Gly Val Cys Trp Ala
 165

<210> 111

<211> 2887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175).. (1287)

<400> 111

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 gccctgggtc attttaaact ctcagagtga acgtcttgat aggaccgaca agacgcatga 120
 catgtactta gaaagcttat cttagagcca cactgagatt ggaaccgca aaat atg 177

Met

1

cca gga aac gcc acc cca gtg acc acc act gcc ccg tgg gcc tcc ctg 225
 Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser Leu

5 10 15

ggc ctc tcc gcc aag acc tgc aac aac gtg tcc ttc gaa gag agc agg 273
 Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser Arg

20 25 30

ata gtc ctg gtc gtg gtg tac agc gcg gtg tgc acg ctg ggg gtg ccg 321
 Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val Pro

35 40 45

gcc aac tgc ctg act gcg tgg ctg gcg ctg ctg cag gta ctg cag gcc 369
 Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln Gly

50 55 60 65

aac gtg ctg gcc gtc tac ctg ctc tgc ctg gca ctc tgc gag ctg ctg 417
 Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu

70 75 80

tac aca ggc acg ctg cca ctc tgg gtc atc tat atc cgc aac cag cac 465
 Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln His

85 90 95

cgc tgg acc cta ggc ctg ctg gcc tgc aag gtg acc gcc tac atc ttc 513
 Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe

100 105 110

ttc tgc aac atc tac gtc agc atc ctc ttc ctg tgc tgc atc tcc tgc 561
 Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys

115 120 125

gac cgc ttc gtg gcc gtg gtg tac gcg ctg gag agt cgg ggc cgc cgc 609

Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg	
130	135 140 145
cgc cgg agg acc gcc atc ctc atc tcc gcc tgc atc ttc atc ctc gtc	657
Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu Val	
150	155 160
ggg atc gtt cac tac ccg gtg ttc cag acg gaa gac aag gag acc tgc	705
Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr Cys	
165	170 175
ttt gac atg ctg cag atg gac agc agg att gcc ggg tac tat tac gcc	753
Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala	
180	185 190
agg ttc acc gtt ggc ttt gcc atc cct ctc tcc atc atc gcc ttc acc	801
Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr	
195	200 205
aac cac cgg att ttc agg agc atc aag cag agc atg ggc tta agc gct	849
Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser Ala	
210	215 220 225
gcc cag aag gcc aag gtg aag cac tcg gcc atc gcg gtg gtt gtc atc	897
Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile	
230	235 240
ttc cta gtc tgc ttc gcc ccg tac cac ctg gtt ctc ctc gtc aaa gcc	945
Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala	
245	250 255
gct gcc ttt tcc tac tac aga gga gac agg aac gcc atg tgc ggc ttg	993
Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu	
260	265 270
gag gaa agg ctg tac aca gcc tct gtg gtg ttt ctg tgc ctg tcc acg	1041

Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr
 275 280 285
 gtg aac ggc gtg gct gac ccc att atc tac gtg ctg gcc acg gac cat 1089
 Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His
 290 295 300 305
 tcc cgc caa gaa gtg tcc aga atc cat aag ggg tgg.aaa gag tgg tcc 1137
 Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser
 310 315 320
 atg aag aca gac gtc acc agg ctc acc cac agc agg gac acc gag gag 1185
 Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu
 325 330 335
 ctg cag tcg ccc gtg gcc ctt gca gac cac tac acc ttc tcc agg ccc 1233
 Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro
 340 345 350
 gtg cac cca cca ggg tca cca tgc cct gca aag agg ctg att gag gag 1281
 Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu
 355 360 365
 tcc tgc tgagccact gtgtggcagg gggatggcag gttgggggtc ctggggccag 1337
 Ser Cys
 370
 caatgtggtt cctgtgcact gagcccacca gccacagtgc ccatgtcccc tctggaagac 1397
 aaactaccaa tttctcgttc ctgaagccac tccctccgtg accactggcc ccaggctttc 1457
 ccacatggaa ggtggctgca tgccaagggg aggagcgaca cctccaggct tccgggagcc 1517
 cagagagcat gtggcaggca gtggggcctc ttcatcagca gcctgcctgg ctggctccct 1577
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cagcactgtg gcagcgccca ggagggcata gggcagccta ccacctcaa gggggcaggc 1817
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gtccacgccc agaacaacag ttggcaggac aggtgtgaca cagccacagc agaggcaagg 1997
ggtgccagga gtccccagcg gcacccctcg ggagatgctg gtgaggggtc cgtacagggt 2057
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aggatcagtt gaggtcagga gtttgagacc agcctcggca acatggcaaa atcttgtctc 2837
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<210> 112

<211> 371

<212> PRT

<213> Homo sapiens

<400> 112

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser

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20	25	30	
Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val			
35	40	45	
Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln			
50	55	60	
Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu			
65	70	75	80
Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln			
85	90	95	
His Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile			
100	105	110	
Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser			
115	120	125	
Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg			
130	135	140	
Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu			
145	150	155	160
Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr			
165	170	175	
Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr			
180	185	190	
Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe			
195	200	205	
Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser			
210	215	220	

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val
225 230 235 240
Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
245 250 255
Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
260 265 270
Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
275 280 285
Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
290 295 300
His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp
305 310 315 320
Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
325 330 335
Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
340 345 350
Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
355 360 365
Glu Ser Cys
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<210> 113

<211> 2066

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98).. (556)

<400> 113

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cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca gcg 115

Met Asn Val Gly Thr Ala

1

5

cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc atc 163

His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile

10

15

20

tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg ctg 211

Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu Leu

25

30

35

agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac ctc 259

Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn Leu

40

45

50

att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg aca 307

Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly Thr

55

60

65

70

ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac tgg 355

Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp

75

80

85

gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc ttg 403

Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe Leu

90

95

100

acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act aag 451

Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr Lys

105

110

115

tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc gtg 499
 Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser Val
 120 125 130
 ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga atc 547
 Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly Ile
 135 140 145 150
 aat aag tac tgagagtgca gccccttccc ctgccaggg tggcagggga 596
 Asn Lys Tyr
 ggggtagggt aaaaggcatg tgctgcaaca ctgaagacag aaagaagaag cctctggaca 656
 ctgccagaga tgggggttga gcctctggcc taatttcccc cctcgcttcc ccagtagcc 716
 aacttggagt agctttagt ggggttggg taggccccct gggctctgac cttttctgaa 776
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 gttttctccc tcctgaccct gcatctccca ccccggtgat catagggaac tttcacctta 1976
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 acgcaaataa aagggcaaca tgtttctgtt 2066

<210> 114

<211> 153

<212> PRT

<213> Homo sapiens

<400> 114

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Met	Asn	Ser	Arg	Gly	Ile	Trp	Leu	Ser	Tyr	Val	Leu	Ala	Ile	Gly	Leu
				20				25						30	
Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
			35					40						45	
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
			50					55						60	
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
			65					70						75	
Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Val	Gln	Phe	Thr
				85				90						95	
Ala	Ser	Arg	Lys	Phe	Leu	Thr	Ile	Thr	Pro	Ile	Val	Leu	Tyr	Phe	Leu
					100					105					110
Thr	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Gln	Ile	His	Phe	Val	Leu	Asn	Thr

115 120 125
 Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly
 130 135 140
 Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150

<210> 115

<211> 2709

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148).. (2502)

<400> 115

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 gcctttccgg aggaggaagc tctgaaaaac agggggccca gtgccattcc gcagggaatt 120
 gtcgcttgog ttcagctgtt ctacaca atg gac tca gta cct gcc act gtg cct 174

Met Asp Ser Val Pro Ala Thr Val Pro

1

5

tct atc gcc gct acc ccg ggg gac ccg gaa ctt gtg gga ccc ttg tct 222
 Ser Ile Ala Ala Thr Pro Gly Asp Pro Glu Leu Val Gly Pro Leu Ser
 10 15 20 25
 gtg ctc tac gca gcc ttc ata gcc aag ctg ctg gag cta gtt gct aca 270
 Val Leu Tyr Ala Ala Phe Ile Ala Lys Leu Leu Glu Leu Val Ala Thr
 30 35 40
 ttg cct gat gat gtt cag cct ggg cct gat ttt tat gga ctg cca tgg 318
 Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Leu Pro Trp

45	50	55	
aaa cct gta ttt atc act gcc ttc ttg gga att gct tcg ttt gcc att			366
Lys Pro Val Phe Ile Thr Ala Phe Leu Gly Ile Ala Ser Phe Ala Ile			
60	65	70	
ttc tta tgg aga act gtc ctt gtt gtg aag gat aga gta tat caa gtc			414
Phe Leu Trp Arg Thr Val Leu Val Val Lys Asp Arg Val Tyr Gln Val			
75	80	85	
acg gaa cag caa att tct gag aag ttg aag act atc atg aaa gaa aat			462
Thr Glu Gln Gln Ile Ser Glu Lys Leu Lys Thr Ile Met Lys Glu Asn			
90	95	100	105
aca gaa ctt gta caa aaa ttg tca aat tat gaa cag aag atc aag gaa			510
Thr Glu Leu Val Gln Lys Leu Ser Asn Tyr Glu Gln Lys Ile Lys Glu			
110	115	120	
tca aag aaa cat gtt cag gaa acc agg aaa caa aat atg att ctc tct			558
Ser Lys Lys His Val Gln Glu Thr Arg Lys Gln Asn Met Ile Leu Ser			
125	130	135	
gat gaa gca att aaa tat aag gat aaa atc aag aca ctt gaa aaa aat			606
Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile Lys Thr Leu Glu Lys Asn			
140	145	150	
cag gaa att ctg gat gac aca gct aaa aat ctt cgt gtt atg cta gaa			654
Gln Glu Ile Leu Asp Asp Thr Ala Lys Asn Leu Arg Val Met Leu Glu			
155	160	165	
tct gag aga gaa cag aat gtc aag aat cag gac ttg ata tca gaa aac			702
Ser Glu Arg Glu Gln Asn Val Lys Asn Gln Asp Leu Ile Ser Glu Asn			
170	175	180	185
aag aaa tct ata gag aag tta aag gat gtt att tca atg aat gcc tca			750
Lys Lys Ser Ile Glu Lys Leu Lys Asp Val Ile Ser Met Asn Ala Ser			

190	195	200	
gaa ttt tca gag gtt cag att gca ctt aat gaa gct aag ctt agt gaa			798
Glu Phe Ser Glu Val Gln Ile Ala Leu Asn Glu Ala Lys Leu Ser Glu			
205	210	215	
gag aag gtg aag tct gaa tgc cat cgg gtt caa gaa gaa aat gct agg			846
Glu Lys Val Lys Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala Arg			
220	225	230	
ctt aag aag aaa aaa gag cag ttg cag cag gaa atc gaa gac tgg agt			894
Leu Lys Lys Lys Lys Glu Gln Leu Gln Gln Glu Ile Glu Asp Trp Ser			
235	240	245	
aaa tta cat gct gag ctc agt gag caa atc aaa tca ttt gag aag tct			942
Lys Leu His Ala Glu Leu Ser Glu Gln Ile Lys Ser Phe Glu Lys Ser			
250	255	260	265
cag aaa gat ttg gaa gta gct ctt act cac aag gat gat aat att aat			990
Gln Lys Asp Leu Glu Val Ala Leu Thr His Lys Asp Asp Asn Ile Asn			
270	275	280	
gct ttg act aac tgc att aca cag ttg aat ctg tta gag tgt gaa tct			1038
Ala Leu Thr Asn Cys Ile Thr Gln Leu Asn Leu Leu Glu Cys Glu Ser			
285	290	295	
gaa tct gag ggt caa aat aaa ggt gga aat gat tca gat gaa tta gca			1086
Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn Asp Ser Asp Glu Leu Ala			
300	305	310	
aat gga gaa gtg gga ggt gac cgg aat gag aag atg aaa aat caa att			1134
Asn Gly Glu Val Gly Gly Asp Arg Asn Glu Lys Met Lys Asn Gln Ile			
315	320	325	
aag cag atg atg gat gtc tct cgg aca cag act gca ata tcg gta gtt			1182
Lys Gln Met Met Asp Val Ser Arg Thr Gln Thr Ala Ile Ser Val Val			

330	335	340	345	
gaa gag gat cta aag ctt tta cag ctt aag cta aga gcc tcc gtg tcc				1230
Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys Leu Arg Ala Ser Val Ser				
	350	355	360	
act aaa tgt aac ctg gaa gac cag gta aag aaa ttg gaa gat gac cgc				1278
Thr Lys Cys Asn Leu Glu Asp Gln Val Lys Lys Leu Glu Asp Asp Arg				
	365	370	375	
aac tca cta caa gct gcc aaa gct gga ctg gaa gat gaa tgc aaa acc				1326
Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu Glu Asp Glu Cys Lys Thr				
	380	385	390	
ttg agg cag aaa gtg gag att ctg aat gag ctc tat cag cag aag gag				1374
Leu Arg Gln Lys Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys Glu				
	395	400	405	
atg gct ttg caa aag aaa ctg agt caa gaa gag tat gaa cgg caa gaa				1422
Met Ala Leu Gln Lys Lys Leu Ser Gln Glu Glu Tyr Glu Arg Gln Glu				
410	415	420	425	
aga gag cac agg ctg tca gct gca gat gaa aag gca gtt tcg gct gca				1470
Arg Glu His Arg Leu Ser Ala Ala Asp Glu Lys Ala Val Ser Ala Ala				
	430	435	440	
gag gaa gta aaa act tac aag cgg aga att gaa gaa atg gag gat gaa				1518
Glu Glu Val Lys Thr Tyr Lys Arg Arg Ile Glu Glu Met Glu Asp Glu				
	445	450	455	
tta cag aag aca gag cgg tca ttt aaa aac cag atc gct acc cat gag				1566
Leu Gln Lys Thr Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His Glu				
	460	465	470	
aag aaa gct cat gaa aac tgg ctc aaa gct cgt gct gca gaa aga gct				1614
Lys Lys Ala His Glu Asn Trp Leu Lys Ala Arg Ala Ala Glu Arg Ala				

475	480	485	
ata gct gaa gag aaa agg gaa gct gcc aat ttg aga cac aaa tta tta			1662
Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu Leu			
490	495	500	505
gaa tta aca caa aag atg gca atg ctg caa gaa gaa cct gtg att gta			1710
Glu Leu Thr Gln Lys Met Ala Met Leu Gln Glu Glu Pro Val Ile Val			
	510	515	520
aaa cca atg cca gga aaa cca aat aca caa aac cct cca cgg aga ggt			1758
Lys Pro Met Pro Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg Gly			
	525	530	535
cct ctg agc cag aat ggg tct ttt ggc cca tcc cct gtg agt ggt gga			1806
Pro Leu Ser Gln Asn Gly Ser Phe Gly Pro Ser Pro Val Ser Gly Gly			
	540	545	550
gaa tgc tcc cct cca ttg aca gtg gag cca ccc gtg aga cct ctc tct			1854
Glu Cys Ser Pro Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu Ser			
	555	560	565
gct act ctc aat cga aga gat atg cct aga agt gaa ttt gga tca gtg			1902
Ala Thr Leu Asn Arg Arg Asp Met Pro Arg Ser Glu Phe Gly Ser Val			
570	575	580	585
gac ggg cct cta cct cat cct cga tgg tca gct gag gca tct ggg aaa			1950
Asp Gly Pro Leu Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly Lys			
	590	595	600
ccc tct cct tct gat cca gga tct ggt aca gct acc atg atg aac agc			1998
Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr Ala Thr Met Met Asn Ser			
	605	610	615
agc tca aga ggc tct tcc cct acc agg gta ctc gat gaa ggc aag gtt			2046
Ser Ser Arg Gly Ser Ser Pro Thr Arg Val Leu Asp Glu Gly Lys Val			

620	625	630	
aat atg gct cca aaa ggg ccc cct cct ttc cca gga gtc cct ctc atg			2094
Asn Met Ala Pro Lys Gly Pro Pro Pro Phe Pro Gly Val Pro Leu Met			
635	640	645	
agc acc ccc atg gga ggc cct gta cca cca ccc att cga tat gga cca			2142
Ser Thr Pro Met Gly Gly Pro Val Pro Pro Pro Ile Arg Tyr Gly Pro			
650	655	660	665
cca cct cag ctc tgc gga cct ttt ggg cct cgg cca ctt cct cca ccc			2190
Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro Arg Pro Leu Pro Pro Pro			
670	675	680	
ttt ggc cct ggt atg cgt cca cca cta ggc tta aga gaa ttt gca cca			2238
Phe Gly Pro Gly Met Arg Pro Pro Leu Gly Leu Arg Glu Phe Ala Pro			
685	690	695	
ggc gtt cca cca gga aga cgg gac ctg cct ctc cac cct cgg gga ttt			2286
Gly Val Pro Pro Gly Arg Arg Asp Leu Pro Leu His Pro Arg Gly Phe			
700	705	710	
tta cct gga cac gca cca ttt aga cct tta ggt tca ctt ggc cca aga			2334
Leu Pro Gly His Ala Pro Phe Arg Pro Leu Gly Ser Leu Gly Pro Arg			
715	720	725	
gag tac ttt att cct ggt acc cga tta cca ccc cca acc cat ggt ccc			2382
Glu Tyr Phe Ile Pro Gly Thr Arg Leu Pro Pro Pro Thr His Gly Pro			
730	735	740	745
cag gaa tac cca cca cca cct gct gta aga gac tta ctg ccg tca ggc			2430
Gln Glu Tyr Pro Pro Pro Pro Ala Val Arg Asp Leu Leu Pro Ser Gly			
750	755	760	
tct aga gat gag cct cca cct gcc tct cag agc act agc cag gac tgt			2478
Ser Arg Asp Glu Pro Pro Pro Ala Ser Gln Ser Thr Ser Gln Asp Cys			

765 770 775
 tca cag gct tta aaa cag agc cca taaaactatg acctctgagg ttccattgga 2532
 Ser Gln Ala Leu Lys Gln Ser Pro

780 785
 aagaaagtgt actgtgcatt atccattaca gtaaaggatt tcattggcctt caaaatccaa 2592
 aagttttattt taaaaggttt gttgtagaa ctaagctgcc ttggcagtgt gcatttttga 2652
 gccaaacaat tcaaaaatgt cattttctcc ctaaataaaa atcacctttt aagctag 2709

<210> 116

<211> 785

<212> PRT

<213> Homo sapiens

<400> 116

Met Asp Ser Val Pro Ala Thr Val Pro Ser Ile Ala Ala Thr Pro Gly
 1 5 10 15
 Asp Pro Glu Leu Val Gly Pro Leu Ser Val Leu Tyr Ala Ala Phe Ile
 20 25 30
 Ala Lys Leu Leu Glu Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro
 35 40 45
 Gly Pro Asp Phe Tyr Gly Leu Pro Trp Lys Pro Val Phe Ile Thr Ala
 50 55 60
 Phe Leu Gly Ile Ala Ser Phe Ala Ile Phe Leu Trp Arg Thr Val Leu
 65 70 75 80
 Val Val Lys Asp Arg Val Tyr Gln Val Thr Glu Gln Gln Ile Ser Glu
 85 90 95
 Lys Leu Lys Thr Ile Met Lys Glu Asn Thr Glu Leu Val Gln Lys Leu
 100 105 110

Ser Asn Tyr Glu Gln Lys Ile Lys Glu Ser Lys Lys His Val Gln Glu
 115 120 125
 Thr Arg Lys Gln Asn Met Ile Leu Ser Asp Glu Ala Ile Lys Tyr Lys
 130 135 140
 Asp Lys Ile Lys Thr Leu Glu Lys Asn Gln Glu Ile Leu Asp Asp Thr
 145 150 155 160
 Ala Lys Asn Leu Arg Val Met Leu Glu Ser Glu Arg Glu Gln Asn Val
 165 170 175
 Lys Asn Gln Asp Leu Ile Ser Glu Asn Lys Lys Ser Ile Glu Lys Leu
 180 185 190
 Lys Asp Val Ile Ser Met Asn Ala Ser Glu Phe Ser Glu Val Gln Ile
 195 200 205
 Ala Leu Asn Glu Ala Lys Leu Ser Glu Glu Lys Val Lys Ser Glu Cys
 210 215 220
 His Arg Val Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys Lys Glu Gln
 225 230 235 240
 Leu Gln Gln Glu Ile Glu Asp Trp Ser Lys Leu His Ala Glu Leu Ser
 245 250 255
 Glu Gln Ile Lys Ser Phe Glu Lys Ser Gln Lys Asp Leu Glu Val Ala
 260 265 270
 Leu Thr His Lys Asp Asp Asn Ile Asn Ala Leu Thr Asn Cys Ile Thr
 275 280 285
 Gln Leu Asn Leu Leu Glu Cys Glu Ser Glu Ser Glu Gly Gln Asn Lys
 290 295 300
 Gly Gly Asn Asp Ser Asp Glu Leu Ala Asn Gly Glu Val Gly Gly Asp
 305 310 315 320
 Arg Asn Glu Lys Met Lys Asn Gln Ile Lys Gln Met Met Asp Val Ser

325 330 335
Arg Thr Gln Thr Ala Ile Ser Val Val Glu Glu Asp Leu Lys Leu Leu
340 345 350
Gln Leu Lys Leu Arg Ala Ser Val Ser Thr Lys Cys Asn Leu Glu Asp
355 360 365
Gln Val Lys Lys Leu Glu Asp Asp Arg Asn Ser Leu Gln Ala Ala Lys
370 375 380
Ala Gly Leu Glu Asp Glu Cys Lys Thr Leu Arg Gln Lys Val Glu Ile
385 390 395 400
Leu Asn Glu Leu Tyr Gln Gln Lys Glu Met Ala Leu Gln Lys Lys Leu
405 410 415
Ser Gln Glu Glu Tyr Glu Arg Gln Glu Arg Glu His Arg Leu Ser Ala
420 425 430
Ala Asp Glu Lys Ala Val Ser Ala Ala Glu Glu Val Lys Thr Tyr Lys
435 440 445
Arg Arg Ile Glu Glu Met Glu Asp Glu Leu Gln Lys Thr Glu Arg Ser
450 455 460
Phe Lys Asn Gln Ile Ala Thr His Glu Lys Lys Ala His Glu Asn Trp

465 470 475 480
Leu Lys Ala Arg Ala Ala Glu Arg Ala Ile Ala Glu Glu Lys Arg Glu
485 490 495
Ala Ala Asn Leu Arg His Lys Leu Leu Glu Leu Thr Gln Lys Met Ala
500 505 510
Met Leu Gln Glu Glu Pro Val Ile Val Lys Pro Met Pro Gly Lys Pro
515 520 525
Asn Thr Gln Asn Pro Pro Arg Arg Gly Pro Leu Ser Gln Asn Gly Ser

530	535	540	
Phe Gly Pro Ser Pro Val Ser Gly Gly Glu Cys Ser Pro Pro Leu Thr			
545	550	555	560
Val Glu Pro Pro Val Arg Pro Leu Ser Ala Thr Leu Asn Arg Arg Asp			
565	570	575	
Met Pro Arg Ser Glu Phe Gly Ser Val Asp Gly Pro Leu Pro His Pro			
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Arg Trp Ser Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser Asp Pro Gly			
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Ser Gly Thr Ala Thr Met Met Asn Ser Ser Ser Arg Gly Ser Ser Pro			
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625	630	635	640
Pro Pro Phe Pro Gly Val Pro Leu Met Ser Thr Pro Met Gly Gly Pro			
645	650	655	
Val Pro Pro Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu Cys Gly Pro			
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Phe Gly Pro Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly Met Arg Pro			
675	680	685	
Pro Leu Gly Leu Arg Glu Phe Ala Pro Gly Val Pro Pro Gly Arg Arg			
690	695	700	
Asp Leu Pro Leu His Pro Arg Gly Phe Leu Pro Gly His Ala Pro Phe			
705	710	715	720
Arg Pro Leu Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile Pro Gly Thr			
725	730	735	
Arg Leu Pro Pro Pro Thr His Gly Pro Gln Glu Tyr Pro Pro Pro Pro			
740	745	750	

Ala Val Arg Asp Leu Leu Pro Ser Gly Ser Arg Asp Glu Pro Pro Pro

755

760

765

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770

775

780

Pro

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<400> 117

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Lys Thr Ser Glu Thr Ala Ala Lys Gly Val Asn Thr Gly Gly Arg Glu

10

15

20

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Pro Asn Thr Met Val Glu Lys Glu Arg Pro Leu Ala Asp Lys Lys Ala

25

30

35

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Gln Arg Pro Phe Glu Arg Ser Asp Phe Ser Asp Ser Ile Lys Ile Gln

40

45

50

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 Lys Asn Asp Asn Pro Glu Glu His Leu Lys Thr Ser Gly Leu Ala Gly
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 Glu Pro Glu Gly Glu Leu Ser Lys Glu Asp His Gly Asn Thr Glu Lys
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 Tyr Met Gly Thr Glu Ser Gln Gly Ser Ala Ala Ala Glu Pro Glu Asp
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 Asp Ser Phe His Trp Thr Pro His Thr Ser Val Glu Pro Gly His Ser
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 Gln Ser Leu Gln Arg Phe Gln Lys Tyr Phe Asn Val His Glu Leu Glu
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 Pro Leu Glu Glu Gly Leu Gly Gly Ala Met Glu Glu Met Gln Pro Leu
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 Val Pro Glu Glu Pro Thr His Leu Asp Gln Arg Val Ile Gly Asp Thr
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 330 335 340

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 Lys Ser Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp
 375 380 385 390
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 Phe Tyr Gly Leu Pro Trp Lys Pro Val Phe Ile Thr Ala Phe Leu Gly
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 440 445 450
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 Gln Asn Met Ile Leu Ser Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile
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Asp Leu Ile Ser Glu Asn Lys Lys Ser Ile Glu Lys Leu Lys Asp Val
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Ile Ser Met Asn Ala Ser Glu Phe Ser Glu Val Gln Ile Ala Leu Asn
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Glu Ala Lys Leu Ser Glu Glu Lys Val Lys Ser Glu Cys His Arg Val
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Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys Lys Glu Gln Leu Gln Gln
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615 620 625 630

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Leu Leu Glu Cys Glu Ser Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn	
635 640 645	
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Lys Met Lys Asn Gln Ile Lys Gln Met Met Asp Val Ser Arg Thr Gln	
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Thr Ala Ile Ser Val Val Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys	
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Lys Leu Glu Asp Asp Arg Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu	
715 720 725	
gaa gat gaa tgc aaa acc ttg agg cag aaa gtg gag att ctg aat gag	2264
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730 735 740	
ctc tat cag cag aag gag atg gct ttg caa aag aag ctg agt caa gaa	2312
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Glu Tyr Glu Arg Gln Glu Arg Glu His Arg Leu Ser Ala Ala Asp Glu	
760 765 770	

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775 780 785 790	
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Gln Ile Ala Thr His Glu Lys Lys Ala His Glu Asn Trp Leu Lys Ala	
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cgt gct gca gaa aga gct ata gct gaa gag aaa agg gaa gct gcc aat	2552
Arg Ala Ala Glu Arg Ala Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn	
825 830 835	
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Ser Pro Val Ser Gly Gly Glu Cys Ser Pro Pro Leu Thr Val Glu Pro	
890 895 900	
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Pro Val Arg Pro Leu Ser Ala Thr Leu Asn Arg Arg Asp Met Pro Arg	
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 gct gag gca tct ggg aaa ccc tct cct tct gat cca gga tct ggt aca 2888
 Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr
 935 940 945 950
 gct acc atg atg aac agc agc tca aga ggc tct tcc cct acc agg gta 2936
 Ala Thr Met Met Asn Ser Ser Ser Arg Gly Ser Ser Pro Thr Arg Val
 955 960 965
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 970 975 980
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 Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro
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 Leu His Pro Arg Gly Phe Leu Pro Gly His Ala Pro Phe Arg Pro Leu
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 Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile Pro Gly Thr Arg Leu Pro
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 Pro Pro Thr His Gly Pro Gln Glu Tyr Pro Pro Pro Pro Ala Val Arg
 1080 1085 1090
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20

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Lys Asp Ser Asp Tyr Leu Lys Asn Asp Asn Pro Glu Glu His Leu Lys		
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Thr Ser Gly Leu Ala Gly Glu Pro Glu Gly Glu Leu Ser Lys Glu Asp		
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His Gly Asn Thr Glu Lys Tyr Met Gly Thr Glu Ser Gln Gly Ser Ala		
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Ala Ala Glu Pro Glu Asp Asp Ser Phe His Trp Thr Pro His Thr Ser		
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Val Glu Pro Gly His Ser Asp Lys Arg Glu Asp Leu Leu Ile Ile Ser		
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Ser Phe Phe Lys Glu Gln Gln Ser Leu Gln Arg Phe Gln Lys Tyr Phe		
145	150	155
Asn Val His Glu Leu Glu Ala Leu Leu Gln Glu Met Ser Ser Lys Leu		
165	170	175
Lys Ser Ala Gln Gln Glu Ser Leu Pro Tyr Asn Met Glu Lys Val Leu		
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Asp Lys Val Phe Arg Ala Ser Glu Ser Gln Ile Leu Ser Ile Ala Glu		
195	200	205
Lys Met Leu Asp Thr Arg Val Ala Glu Asn Arg Asp Leu Gly Met Asn		
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Leu Ile Tyr Phe Val Arg Tyr Lys His Ser Thr Ala Glu Glu Thr Ala		
245	250	255

Thr Leu Val Met Ala Pro Pro Leu Glu Glu Gly Leu Gly Gly Ala Met
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Glu Glu Met Gln Pro Leu His Glu Asp Asn Phe Ser Arg Glu Lys Thr
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Arg Val Ile Gly Asp Thr His Ala Ser Glu Val Ser Gln Lys Pro Asn
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325 330 335
Met Asp Ala Ile Asp Ala Asn Lys Gln Pro Glu Thr Ala Ala Glu Glu
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 Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys
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 625 630 635 640
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 675 680 685

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 Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys Glu Met Ala Leu Gln
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 755 760 765
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 770 775 780
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 Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His Glu Lys Lys Ala His
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 820 825 830
 Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu Leu Glu Leu Thr Gln
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 850 855 860
 Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg Gly Pro Leu Ser Gln
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 885 890 895
 Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu Ser Ala Thr Leu Asn

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915	920	925
Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser		
930	935	940
Asp Pro Gly Ser Gly Thr Ala Thr Met Met Asn Ser Ser Ser Arg Gly		
945	950	955
Ser Ser Pro Thr Arg Val Leu Asp Glu Gly Lys Val Asn Met Ala Pro		
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Lys Gly Pro Pro Pro Phe Pro Gly Val Pro Leu Met Ser Thr Pro Met		
980	985	990
Gly Gly Pro Val Pro Pro Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu		
995	1000	1005
Cys Gly Pro Phe Gly Pro Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly		
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Met Arg Pro Pro Leu Gly Leu Arg Glu Phe Ala Pro Gly Val Pro Pro		
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Gly Arg Arg Asp Leu Pro Leu His Pro Arg Gly Phe Leu Pro Gly His		
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Ala Pro Phe Arg Pro Leu Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile		
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Pro Gly Thr Arg Leu Pro Pro Pro Thr His Gly Pro Gln Glu Tyr Pro		
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Pro Pro Pro Ala Val Arg Asp Leu Leu Pro Ser Gly Ser Arg Asp Glu		
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Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys Ala Ile
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Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu Ala Gln
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Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu Ala Pro
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gtt gat gtc ttg acc cag ata ggt cga tct gtg cga ggg aca ctg gat      248
Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr Leu Asp
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Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser Ser Ser

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Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe Phe Ala			
85	90	95	
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Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu Ala Gly			
100	105	110	
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Asp Tyr Leu Ala Gln Gly Pro Glu Ala Gln Pro Trp Pro Gly Pro Asp			
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Ser Ala Pro Arg Leu Gly Leu Gly Leu Ala Gly Ala Asp Pro Val Gly			
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Gly Ala Arg Val Glu Pro Pro Gln Val Gln Ile Leu Val Val Val Ala			
180	185	190	
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Asn Ile Gln Thr Arg Thr Leu Lys Ala Glu Val Glu Lys Gly Ser Met			
195	200	205	210
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aagagctgag ctgcttcggg gccatgcagc cctcctgcca gccccctgcc cttttcttgc 800
cctgtctctg aaccttcaga acattgatcc ttgccgcagc cccactagcc aagagaaaca 860
gagaaagacc attccccctg cctgtcctcg cggccctgtc ttctgagggt ctctgtctgg 920
ggttggctct cttaacctt tctctgctcc cagcctgcct caccaggga ggttggaggg 980
gcctccctct ggcttctgca tctgcgccag caaacatcac tgccgttggt ctctcatgac 1040
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ttctgaagtt gctccttggc caaatctcca gctcccttct tgttttcctc atcctcctac 1160
cctgtactcc caccaaacca tggctcctta aggcacgtc ctgtcctcct cattgcccag 1220
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gtggctgctt tgtgtcaaga aaagagcagt cactctcaga atcttgattc cccatcagcc 1460
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ttatatgccc tgtgggggtt tcagagaccc tgaaagagga gggaggaccc gcctccttgt 1580
ctgcacaact gcatgcactt ctctcccat cgctccaca cctgaaaccg agaaggagtt 1640
gctgaccagt gccaccccg gcagcccgagg aggaacacag gcagctcctt tcccttcacg 1700
tggtctgcag agagcagggt gagctgccag ctgccccctc ccaccagggt accctgtctt 1760
ggtggttagg ggccactttt cctttgaggc tctagtggag gtggatgtcc ttctctgcca 1820
ggcttggcac atgatgtgaa gaataaatgc ccaattctta ctgttcagggt ttgatgtgga 1880
atcacagctg cagtgatata tattctttat cagtgccttg ttggttttta ataaagtgca 1940
cgctatttta ttatcttggt ctgaataaaa tgtatttact cc 1982

<210> 120

<211> 210

<212> PRT

<213> Homo sapiens

<400> 120

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys
 1 5 10 15
 Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu
 20 25 30
 Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu
 35 40 45
 Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr
 50 55 60
 Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser
 65 70 75 80
 Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe
 85 90 95
 Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu
 100 105 110
 Ala Gly Asp Tyr Leu Ala Gln Gly Pro Glu Ala Gln Pro Trp Pro Gly
 115 120 125
 Pro Asp Leu Pro Ala Val Gly Ser Arg Gly Pro Gly Arg Leu Leu Ala
 130 135 140
 Ala Val Ser Ala Pro Arg Leu Gly Leu Gly Leu Ala Gly Ala Asp Pro
 145 150 155 160
 Val Gly Pro Glu Ala Cys His Leu Pro Gly Arg Leu Arg Gly Pro Asp
 165 170 175
 Glu Val Gly Ala Arg Val Glu Pro Pro Gln Val Gln Ile Leu Val Val
 180 185 190
 Val Ala Asn Ile Gln Thr Arg Thr Leu Lys Ala Glu Val Glu Lys Gly
 195 200 205
 Ser Met

210

<210> 121

<211> 2077

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)..(801)

<400> 121

ggcgcggggtt tgggtggcgcg tttcagcgaa gtcgcacgtg aaggatagca gtggcctgag 60
 aaagacccag tc atg gca gcc tcc agc atc agt tca cca tgg gga aag cat 111

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His

1

5

10

gtg ttc aaa gcc att ctg atg gtc cta gtg gcc ctt atc ctc ctc cac 159
 Val Phe Lys Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His

15

20

25

tca gca ttg gcc cag tcc cgt cga gac ttt gca cca cca ggc caa cag 207
 Ser Ala Leu Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln

30

35

40

45

aag aga gaa gcc cca gtt gat gtc ttg acc cag ata ggt cga tct gtg 255
 Lys Arg Glu Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val

50

55

60

cga ggg aca ctg gat gcc tgg att ggg cca gag acc atg cac ctg gtg 303
 Arg Gly Thr Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val

65

70

75

tca gag tct tcg tcc caa gtg ttg tgg gcc atc tca tca gcc att tct 351

Ser Glu Ser Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser
 80 85 90
 gtg gcc ttc ttt gct ctg tct ggg atc gcc gca cag ctg ctg aat gcc 399
 Val Ala Phe Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala
 95 100 105
 ttg gga cta gct ggt gat tac ctc gcc cag ggc ctg aag ctc agc cct 447
 Leu Gly Leu Ala Gly Asp Tyr Leu Ala Gln Gly Leu Lys Leu Ser Pro
 110 115 120 125
 ggc cag gtc cag acc ttc ctg ctg tgg gga gca ggg gcc ctg gtc gtc 495
 Gly Gln Val Gln Thr Phe Leu Leu Trp Gly Ala Gly Ala Leu Val Val
 130 135 140
 tac tgg ctg ctg tct ctg ctc ctc ggc ttg gtc ttg gcc ttg ctg ggg 543
 Tyr Trp Leu Leu Ser Leu Leu Leu Gly Leu Val Leu Ala Leu Leu Gly
 145 150 155
 cgg atc ctg tgg ggc ctg aag ctt gtc atc ttc ctg gcc ggc ttc gtg 591
 Arg Ile Leu Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val
 160 165 170
 gcc ctg atg agg tcg gtg cct gac cct tcc acc cgg gcc ctg cta ctc 639
 Ala Leu Met Arg Ser Val Pro Asp Pro Ser Thr Arg Ala Leu Leu Leu
 175 180 185
 ctg gcc ttg ctg atc ctc tac gcc ctg ctg agc cgg ctc act ggc tcc 687
 Leu Ala Leu Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser
 190 195 200 205
 cga gcc tct ggg gcc caa ctc gag gcc aag gtg cga ggg ctg gaa cgc 735
 Arg Ala Ser Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg
 210 215 220
 cag gtg gag gag ctg cgc tgg cgc cag agg cga gcg gcc aag ggg gcc 783

Gln Val Glu Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala

225

230

235

cgc agt gtg gag gag gag tgagccgat gcccacaca ccgccagtgt 831

Arg Ser Val Glu Glu Glu

240

cataccaaag agctgagctg cttcggggcc atgcagccct cctgccagcc ccctgccctt 891
 ttcttgccct gtctctgaac cttcagaaca ttgatccttg ccgcagcccc actagccaag 951
 agaaacagag aaagaccatt cccctgcct gtccttgagg ccctgtcttc tgaggttctc 1011
 tgtctgggggt tggtctctt aaccctttct ctgtccag cctgcctcac cagggaaggt 1071
 tggagggggc tccctctggc ttctgcatct gcgccagcaa acatcactgc cgttggtctc 1131
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 gccaggcttg gcacatgat tgaagaataa atgccaatt cttactgttc aggtttgatg 1971
 tggaatcaca gctgcagtga tatatatatt ttatcagtgc ttggttggt ttaaataaag 2031
 tgcacgtat ttattatct tgttctgaat aaaatgtatt tactcc 2077

<210> 122

<211> 243

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys
1 5 10 15
Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu
20 25 30
Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu
35 40 45
Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr
50 55 60
Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser
65 70 75 80
Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe
85 90 95
Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu
100 105 110
Ala Gly Asp Tyr Leu Ala Gln Gly Leu Lys Leu Ser Pro Gly Gln Val
115 120 125
Gln Thr Phe Leu Leu Trp Gly Ala Gly Ala Leu Val Val Tyr Trp Leu
130 135 140
Leu Ser Leu Leu Leu Gly Leu Val Leu Ala Leu Leu Gly Arg Ile Leu
145 150 155 160
Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val Ala Leu Met
165 170 175

Arg Ser Val Phe Asp Pro Ser Thr Arg Ala Leu Leu Leu Leu Ala Leu
 180 185 190
 Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser Arg Ala Ser
 195 200 205
 Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg Gln Val Glu
 210 215 220
 Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala Arg Ser Val
 225 230 235 240
 Glu Glu Glu

<210> 123

<211> 1937

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (347).. (1534)

<400> 123

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 caccctgccc tggtgaaagg gctcccgcac cgcccgggtgc tccccatctg cctggcggtg 120
 tgcgcagagc tggaaagcat ggctgttata aatgaattct gattttgggg agcagatgcc 180
 aacttagagc ctcgtagcaa tctctctgtc tttaaaagat gaggtgactt ggtgattttc 240
 ctggaaaatt ataggtgccc agctaagacc tgaatgccat caccctcccc agggctctgc 300
 agttttctcg tggatgaacc ttgatggatt tgttggtgct tgagaa atg gcg atg 355
 Met Ala Met

1

atc gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag 403

Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys
 5 10 15
 agt tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta 451
 Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu
 20 25 30 35
 ttt tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg 499
 Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp
 40 45 50
 cct gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag 547
 Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu
 55 60 65
 cct gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa 595
 Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu
 70 75 80
 ttc cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag 643
 Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu
 85 90 95
 aga gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc 691
 Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe
 100 105 110 115
 atc ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc 739
 Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala
 120 125 130
 tgg gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt 787
 Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser
 135 140 145
 cat gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat 835

His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His
 150 155 160
 tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc 883
 Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser
 165 170 175
 tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac 931
 Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn
 180 185 190 195
 agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa 979
 Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu
 200 205 210
 gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag gca 1027
 Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala
 215 220 225
 cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc 1075
 Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala
 230 235 240
 cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac 1123
 Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn
 245 250 255
 tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt 1171
 Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe
 260 265 270 275
 aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg 1219
 Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu
 280 285 290
 tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc 1267

Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala
 295 300 305
 tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct 1315
 Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser
 310 315 320
 ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc 1363
 Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile
 325 330 335
 acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat 1411
 Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp
 340 345 350 355
 gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc 1459
 Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu
 360 365 370
 aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg 1507
 Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu
 375 380 385
 aac ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat 1554
 Asn Leu Leu Gly Lys Arg Lys Thr Arg
 390 395
 aaatatcaaa gcccaagaaa tggaactttg ggcagagatc atgttagaat caagtggatg 1614
 atgagaccaa ttacaggcgc tctctctgca cagcacagaa attctcaatc actgaaatga 1674
 gtaactgcaa aataaatagt tgattgtact gttctcatgc tataaaagtg gacaggtact 1734
 ctacaacaaa tctgttttct catttttatac aaatatatgt atcatcaaag gttgcatctg 1794
 tacagtatgt aaatgctatt aatgtcgtca ctacatgca cgacagtcct tgttccccca 1854
 ggaagggcct ggtggcccca gcacacactt gggattatgt gtatacataa ataaatattg 1914
 ggctgtttcc ctcttctgt gaa 1937

<210> 124

<211> 396

<212> PRT

<213> Homo sapiens

<400> 124

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
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 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu
 100 105 110
 Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
 115 120 125
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg
 130 135 140
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
 145 150 155 160
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys

	165		170		175										
Val	Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val
	180		185		190										
Met	Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser
	195		200		205										
Glu	Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser
	210		215		220										
Arg	Glu	Ala	Arg	Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu	Pro
225			230		235									240	
Thr	Ser	Ala	Pro	Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg	Arg	Ser
	245		250		255										
Asp	Ala	Asn	Cys	Ser	Gly	Glu	Asp	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp
	260		265		270										
Ile	Pro	Phe	Lys	Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln
	275		280		285										
Lys	Leu	Leu	Trp	Trp	Leu	Gln	Pro	Arg	Leu	Val	Leu	Ser	Gly	His	Thr
	290		295		300										
His	Ser	Ala	Cys	Glu	Val	His	His	Gly	Gly	Arg	Val	Pro	Glu	Leu	Ser
305			310		315									320	
Val	Pro	Ser	Phe	Ser	Trp	Arg	Asn	Arg	Asn	Asn	Pro	Ser	Phe	Ile	Met
	325		330		335										
Gly	Ser	Ile	Thr	Pro	Thr	Asp	Tyr	Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro
	340		345		350										
Arg	Glu	Asp	Val	Val	Leu	Ile	Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu
	355		360		365										
Val	Val	Leu	Thr	Leu	Thr	His	Phe	Gly	Leu	Leu	Ala	Ser	Pro	Phe	Leu
	370		375		380										

Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

385

390

395

<210> 125

<211> 1748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (347)..(1345)

<400> 125

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 caccctgccc tgggtgaaagg gctcccgcac cgcccgggtgc tccccatctg cctggcgttg 120
 tgcgcagagc tggaaagcat ggctgttata aatgaattct gattttgggg agcagatgcc 180
 aacttagagc ctcgtaacaa tctctctgtc tttaaaagat gaggtgactt ggtgattttc 240
 ctggaaaatt ataggtgccc agctaagacc tgaatgccat caccctcccc agggctctgc 300
 agttttctcg tgggtgaacc ttgatggatt tgttggtgct tgagaa atg gcg atg 355

Met Ala Met

1

atc gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag 403

Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys

5

10

15

agt tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta 451

Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu

20

25

30

35

ttt tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg 499

Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp

40	45	50	
cct gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag			547
Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu			
55	60	65	
cct gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa			595
Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu			
70	75	80	
ttc cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag			643
Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu			
85	90	95	
aga gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc			691
Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe			
100	105	110	115
atc ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc			739
Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala			
120	125	130	
tgg gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt			787
Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser			
135	140	145	
cat gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat			835
His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His			
150	155	160	
tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc			883
Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser			
165	170	175	
tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac			931
Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn			

180	185	190	195	
agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa	979			
Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu				
200	205	210		
gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag ctg	1027			
Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Leu				
215	220	225		
ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc	1075			
Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser				
230	235	240		
gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca	1123			
Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro				
245	250	255		
tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc	1171			
Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser				
260	265	270	275	
atc acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag	1219			
Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu				
280	285	290		
gat gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc	1267			
Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val				
295	300	305		
ctc aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt	1315			
Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly				
310	315	320		
ttg aac ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat	1365			
Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg				

325

330

aaatatcaaa gcccaagaaa tggaactttg ggcagagatc atgttagaat caagtggatg 1425
 atgagaccaa ttacaggccg tctctctgca cagcacagaa attctcaatc actgaaatga 1485
 gtaactgcaa aataaatagt tgattgtact gttctcatgc tataaaagtg gacaggtact 1545
 ctacaacaaa tctgttttct catTTTTtate aaatatatgt atcatcaaag gttgcatctg 1605
 tacagtatgt aaatgctatt aatgtcgtca ctcacatgca cgacagtcct tgttccccca 1665
 ggaagggcct ggtggcccca gcacacactt gggattatgt gtatacataa ataaatattg 1725
 ggctgtttcc ctcttcctgt gaa 1748

<210> 126

<211> 333

<212> PRT

<213> Homo sapiens

<400> 126

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
 1 5 10 15
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu

100	105	110	
Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr			
115	120	125	
Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg			
130	135	140	
His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile			
145	150	155	160
Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys			
165	170	175	
Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val			
180	185	190	
Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser			
195	200	205	
Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser			
210	215	220	
Arg Glu Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His			
225	230	235	240
Thr His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu			
245	250	255	
Ser Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile			
260	265	270	
Met Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu			
275	280	285	
Pro Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe			
290	295	300	
Leu Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe			

305 310 315 320
 Leu Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

325 330

<210> 127

<211> 2529

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (673)

<400> 127

tgttgcttga gaa atg gcg atg atc gaa ttg ggg ttt gga aga cag aat 49

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn

1 5 10

ttt cat cca tta aag agg aag agt tca ttg ctg ttg aaa ctc ata gct 97

Phe His Pro Leu Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala

15 20 25

gtt gtc ttt gct gtg ctt cta ttt tgt gaa ttt tta atc tat tac tta 145

Val Val Phe Ala Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu

30 35 40

gcg atc ttt cag tgt aat tgg cct gaa gtg aaa acc aca gcc tct gat 193

Ala Ile Phe Gln Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp

45 50 55 60

ggt gaa cag acc aca cgt gag cct gtg ctc aaa gcc atg ttt ttg gct 241

Gly Glu Gln Thr Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala

65 70 75

gac acc cat ttg ctt ggg gaa ttc cta ggc cac tgg ctg gac aaa tta 289
 Asp Thr His Leu Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu
 80 85 90
 cga agg gaa tgg cag atg gag aga gcg ttc cag aca gct ctg tgg ttg 337
 Arg Arg Glu Trp Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu
 95 100 105
 ctg cag ccg gaa gtc gtc ttc atc ctg ggg gat atc ttt gat gaa ggg 385
 Leu Gln Pro Glu Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly
 110 115 120
 aag tgg agc acc cct gag gcc tgg gcg gat gat gtg gag cgg ttt cag 433
 Lys Trp Ser Thr Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln
 125 130 135 140
 aaa atg ttc aga cac cca agt cat gta cag ctg aag gta gtt gct gga 481
 Lys Met Phe Arg His Pro Ser His Val Gln Leu Lys Val Val Ala Gly
 145 150 155
 aac cat gac att ggc ttc cat tat gag atg aac aca tac aaa gta gaa 529
 Asn His Asp Ile Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu
 160 165 170
 cgc ttt gag aaa gtg ttc agc tct gaa aga ctg ttt tct tgg aaa ggc 577
 Arg Phe Glu Lys Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly
 175 180 185
 att aac ttt gtg atg gtc aac agc gtg gcg ctg aac ggg atg gct gtg 625
 Ile Asn Phe Val Met Val Asn Ser Val Ala Leu Asn Gly Met Ala Val
 190 195 200
 gca tct gct ctg aaa cag aag cag agc tca ttg aag ttt ctc aca gac 673
 Ala Ser Ala Leu Lys Gln Lys Gln Ser Ser Leu Lys Phe Leu Thr Asp
 205 210 215 220

tgaactgctc ccgagaggta ggagagcatc tgaatgccac aggtgccttc tgtcccggtg 733
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tataaatatc aaagcccaag aagtggaact ttgggcagag atcatgtag aatcaagtgg 2353
 atgatgagac caattacagg ccgctctctct gcacagcaca gaaattctca atcactgaaa 2413
 tgagtaactg caaaataaat agttgattgt actgttctca tgctataaaa gtggacaggt 2473
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<210> 128

<211> 220

<212> PRT

<213> Homo sapiens

<400> 128

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 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu
 100 105 110
 Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
 115 120 125
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg

130 135 140
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
 145 150 155 160
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys
 165 170 175
 Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val
 180 185 190
 Met Val Asn Ser Val Ala Leu Asn Gly Met Ala Val Ala Ser Ala Leu
 195 200 205
 Lys Gln Lys Gln Ser Ser Leu Lys Phe Leu Thr Asp
 210 215 220

<210> 129

<211> 1910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (454).. (1182)

<400> 129

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 cagatgccaa cttagagcct cgtaccaatc tctctgtctt taaaagatga ggtgacttgg 180
 tgattttcct ggaaaattat agcgatcttt cagtgttaatt ggcctgaagt gaaaaccaca 240
 gcctctgatg gtgaacagac cacacgtgag cctgtgctca aagccatggt tttggctgac 300
 acccatttgc ttagggaatt cctaggccac tggctggaca aattacgaag agatggagtt 360
 ttgctgtgtt gcccatgctg gttttgaact cctggcctca agtgatcctc cctccttggc 420

ctcccaaagc attgaaatta cagggaatgg cag atg gag aga gcg ttc cag aca 474
Met Glu Arg Ala Phe Gln Thr
1 5

gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc ctg ggg gat atc 522
Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile Leu Gly Asp Ile
10 15 20

ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg gcg gat gat gtg 570
Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp Ala Asp Asp Val
25 30 35

gag cgg ttt cag aaa atg ttc aga cac cca agt cat gta cag ctg aag 618
Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His Val Gln Leu Lys
40 45 50 55

gta gtt gct gga aac cat gac att ggc ttc cat tat gag atg aac aca 666
Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr Glu Met Asn Thr
60 65 70

tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct gaa aga ctg ttt 714
Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser Glu Arg Leu Phe
75 80 85

tct tgg aaa ggc att aac ttt gtg atg gtc aac agc gtg gcg ctg aac 762
Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser Val Ala Leu Asn
90 95 100

ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca gag ctc att gaa 810
Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala Glu Leu Ile Glu
105 110 115

gtt tct cac aga ctg aac tgc tcc cga gag gca cgt ggc tcc agc cgg 858
Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg Gly Ser Ser Arg
120 125 130 135

tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct gtc ctc ctg cag 906
 Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro Val Leu Leu Gln
 140 145 150
 cat tat cct ctg tat cgg aga agt gat gct aac tgt tct ggg gaa gac 954
 His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys Ser Gly Glu Asp
 155 160 165
 gct gct cct gca gag gaa agg gac atc cca ttt aag gag aac tat gac 1002
 Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys Glu Asn Tyr Asp
 170 175 180
 gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg tgg ctc cag ccg 1050
 Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp Trp Leu Gln Pro
 185 190 195
 cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc gag gtg cac cac 1098
 Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys Glu Val His His
 200 205 210 215
 ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc agt tgg agg aac 1146
 Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe Ser Trp Arg Asn
 220 225 230
 aga aac aac ccc agt ttc atc atg gga aca gat gct tagttgagca 1192
 Arg Asn Asn Pro Ser Phe Ile Met Gly Thr Asp Ala
 235 240
 tcaaggggca ggaagacacc tttccctcct tggttcctgc tgaccgatga ccctggaact 1252
 ccacggtgcc tctctgaatc tctgttatgg atcccccaact atatttgatg ggaaccagct 1312
 gagccagggg ccagttttga cagggttagca tcacgccac agactacacc ctctccaagt 1372
 gctacctccc acgtgaggat gtggttttga tcatctactg tggagtggcg ggcttccttg 1432
 tggctcctcac actcactcac tttgggcttc tagcctcacc ttttctttct ggtttgaact 1492
 tgctcggaag gcgtaagaca agatgaagag caggcgccat tataaatatc aaagcccaag 1552

aaatggaact ttgggcagag atcatgttag aatcaagtgg atgatgagac caattacagg 1612
 ccgtctctct gcacagcaca gaaattctca atcactgaaa tgagtaactg caaaataaat 1672
 agttgattgt gctgttctca tgctataaaa gtggacaggt actctacaac aaatctgttt 1732
 tctcattttt atcaaataata tgtatcatca aaggttgcac ctgtacagta tgtaaagtct 1792
 attaatgtcg tcactcacat gcacgacagc ccttgttccc ccaggaaggg cctgggtggcc 1852
 ccagcacaca cttgggatta tgtgtataca taaataaata ttgggctgtt tccctctt 1910

<210> 130

<211> 243

<212> PRT

<213> Homo sapiens

<400> 130

Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val
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Val	Phe	Ile	Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro
			20						25					30	
Glu	Ala	Trp	Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His
			35						40					45	
Pro	Ser	His	Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly
			50						55					60	
Phe	His	Tyr	Glu	Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val
			65						70					75	
Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met
				85					90					95	
Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu
				100					105					110	
Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg

115 120 125
 Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr
 130 135 140
 Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp
 145 150 155 160
 Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile
 165 170 175
 Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys
 180 185 190
 Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His
 195 200 205
 Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val
 210 215 220
 Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly
 225 230 235 240
 Thr Asp Ala

<210> 131

<211> 539

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (471)

<400> 131

gcttcccgag ctggcggggt ccgtggtgcg ggatcgagat tgcgggct atg gcg ccg 57

Met Ala Pro

1

aag gtt ttt cgt cag tac tgg gat atc ccc gat ggc acc gat tgc cac 105
Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr Asp Cys His
5 10 15
cgc aaa gcc tac agc acc acc agt att gcc agc gtc gct ggc ctg acc 153
Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala Gly Leu Thr
20 25 30 35
gcc gct gcc tac aga gtc aca ctc aat cct ccg ggc acc ttc ctt gaa 201
Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr Phe Leu Glu
40 45 50
gga gtg gct aag gtt gga caa tac acg ttc act gca gct gct gtc ggg 249
Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala Ala Val Gly
55 60 65
gcc gtg ttt ggc ctc acc acc tgc atc agc gcc cat gtc cgc gag aag 297
Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val Arg Glu Lys
70 75 80
ccc gac gac ccc ctg aac tac ttc ctc ggt ggc tgc gcc gga ggc ctg 345
Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala Gly Gly Leu
85 90 95
act ctg gga gca cgc acg cac aac tac ggg att ggc gcc gcc gcc tgc 393
Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala Ala Ala Cys
100 105 110 115
gtg tac ttt ggc ata gcg gcc tcc ctg gtc aag atg ggc cgg ctg gag 441
Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly Arg Leu Glu
120 125 130
ggc tgg gag gtg ttt gca aaa ccc aag gtg tgagccctgt gcctgccggg 491
Gly Trp Glu Val Phe Ala Lys Pro Lys Val

135

140

acctccagcc tgcagaatgc gtccagaaat aaattctgtg tctgtgtg

539

<210> 132

<211> 141

<212> PRT

<213> Homo sapiens

<400> 132

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr

1

5

10

15

Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala

20

25

30

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr

35

40

45

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala

50

55

60

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val

65

70

75

80

Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala

85

90

95

Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala

100

105

110

Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly

115

120

125

Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val

130

135

140

<210> 133

<211> 2091

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168).. (596)

<400> 133

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 cgcctgcatac acctccatcc agcccggggc cccaagggg gagcctc atg acg tgg 176

Met Thr Trp

1

ccc cta acg ggc cat cag cgg ggg gcc tgg cca tcc ccc agt cct cct 224

Pro Leu Thr Gly His Gln Arg Gly Ala Trp Pro Ser Pro Ser Pro Pro

5

10

15

cct cct cct ccc ggc ctc cca ccc gag ccc gag gtg ccc cca gcc ctg 272

Pro Pro Pro Pro Gly Leu Pro Pro Glu Pro Glu Val Pro Pro Ala Leu

20

25

30

35

gag tgc tgg gac ccc acg cct cag agc ccc agc tgg ccc ctc cag cct 320

Glu Cys Trp Asp Pro Thr Pro Gln Ser Pro Ser Trp Pro Leu Gln Pro

40

45

50

gca ccc ccg ccg ccc ctg ctg ttc ctg ggc ccc ctg gcc ccc gct cac 368

Ala Pro Pro Pro Pro Leu Leu Phe Leu Gly Pro Leu Ala Pro Ala His

55

60

65

cac agc ggg agc cac agc gag tat ccc atg agc agt tcc ggg ctg ccc 416

His Ser Gly Ser His Ser Glu Tyr Pro Met Ser Ser Ser Gly Leu Pro

70	75	80	
tgc agc tgg tgg tgg acc cag gcg acc ccc gct cct acc tgg aca act	464		
Cys Ser Trp Trp Trp Thr Gln Ala Thr Pro Ala Pro Thr Trp Thr Thr			
85	90	95	
tca tca aga ttg gcg agg gct cca cgg gca tcg tgt gca tcg cca ccg	512		
Ser Ser Arg Leu Ala Arg Ala Pro Arg Ala Ser Cys Ala Ser Pro Pro			
100	105	110	115
tgc gca gct cgg gca agc tgg tgg ccg tca aga aga tgg acc tgc gca	560		
Cys Ala Ala Arg Ala Ser Trp Trp Pro Ser Arg Arg Trp Thr Cys Ala			
120	125	130	
agc agc aga ggc gcg agc tgc tct tca acg agg tgg taatcatgag	606		
Ser Ser Arg Gly Ala Ser Cys Ser Ser Thr Arg Trp			
135	140		
ggactaccag caccgagaatg tgggtggagat gtacaacagc tacctggtgg gggacgagct	666		
ctgggtggtc atggagttcc tggaaggagg cgccctcacc gacatcgtca cccacaccag	726		
gatgaacgag gagcagatcg cggccgtgtg ccttgcaagt ctgcaggccc tgtcgggtgct	786		
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aaggaagtgc ctggtcggca cgccctactg gatggcccca gagctcatct cccgccttcc	966		
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gccaccccga ctgaagaacc tgcacaaggt gtcgccatcc ctgaagggtc tcttgaccg	1146		
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cctggccaag gcagggccgc ctgccagcat cgtgcccctc atgcgccaga accgcaccag	1266		
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aggccagtag ggggccaggc ctcccactcc tcccagcccg ggagatgctc cgcgtggcac	1386		
caccctcctt gctgggggta gatgagaccc tactactgaa ctccagtttt gatctcgtga	1446		

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 gggacaggcc ctcccccatg ttcttctgtc tccaggaagg gcagcggccc tcccatcact 1566
 ggaagtctgc agtgggggtc gctgggggtg gagagaacac taagaggatga acatgtatga 1626
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 aatgactact gcacctggac agcctcctct tttctagaag tctatttata ttgtcatttt 1926
 ataacactct agccccctgcc cttattgggg gacagatggt ccctgtcctg cggggtggcc 1986
 ctggcagaac cactgcctga agaaccaggt tcctgcccgg tcagcgcagc cccagcccgc 2046
 ccaccctgc ctgagttag tttacaatt aaaacattgt cttgt 2091

<210> 134

<211> 143

<212> PRT

<213> Homo sapiens

<400> 134

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				20					25					30	
Pro	Ala	Leu	Glu	Cys	Trp	Asp	Pro	Thr	Pro	Gln	Ser	Pro	Ser	Trp	Pro
				35					40					45	
Leu	Gln	Pro	Ala	Pro	Pro	Pro	Pro	Leu	Leu	Phe	Leu	Gly	Pro	Leu	Ala
				50					55					60	
Pro	Ala	His	His	Ser	Gly	Ser	His	Ser	Glu	Tyr	Pro	Met	Ser	Ser	Ser
65							70					75			80

Gly Leu Pro Cys Ser Trp Trp Trp Thr Gln Ala Thr Pro Ala Pro Thr
 85 90 95
 Trp Thr Thr Ser Ser Arg Leu Ala Arg Ala Pro Arg Ala Ser Cys Ala
 100 105 110
 Ser Pro Pro Cys Ala Ala Arg Ala Ser Trp Trp Pro Ser Arg Arg Trp
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 Thr Cys Ala Ser Ser Arg Gly Ala Ser Cys Ser Ser Thr Arg Trp
 130 135 140

<210> 135

<211> 2091

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (548).. (1267)

<400> 135

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 cgcctgcatc acctccatcc agcccggggc cccaagggg gagcctcatg acgtggcccc 180
 taacggggcca tcagcggggg gcctggccat ccccagtc tctcctcct cctcccggcc 240
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 ccagctggcc cctccagcct gcacccccgc cgccctgtt gttcctgggc cccttgcccc 360
 ccgctcacca cagcgggagc cacagcgagt atcccatgag cagttccggg ctgccctgca 420
 gctggtggtg gaccagggcg accccgctc ctacctggac aacttcatca agattggcga 480
 gggctccacg ggcatcgtgt gcatcgccac cgtgcgcagc tcgggcaagc tgggtggccgt 540
 caagaag atg gac ctg cgc aag cag cag agg cgc gag ctg ctc ttc aac 589

Met	Asp	Leu	Arg	Lys	Gln	Gln	Arg	Arg	Glu	Leu	Leu	Phe	Asn		
1				5					10						
gag gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg														637	
Glu	Val	Val	Ile	Met	Arg	Asp	Tyr	Gln	His	Glu	Asn	Val	Val	Glu	Met
15				20					25					30	
tac aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc														685	
Tyr	Asn	Ser	Tyr	Leu	Val	Gly	Asp	Glu	Leu	Trp	Val	Val	Met	Glu	Phe
				35					40				45		
ctg gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac														733	
Leu	Glu	Gly	Gly	Ala	Leu	Thr	Asp	Ile	Val	Thr	His	Thr	Arg	Met	Asn
				50				55					60		
gag gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg														781	
Glu	Glu	Gln	Ile	Ala	Ala	Val	Cys	Leu	Ala	Val	Leu	Gln	Ala	Leu	Ser
				65				70					75		
gtg ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg														829	
Val	Leu	His	Ala	Gln	Gly	Val	Ile	His	Arg	Asp	Ile	Lys	Ser	Asp	Ser
				80				85					90		
atc ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc														877	
Ile	Leu	Leu	Thr	His	Asp	Gly	Arg	Val	Lys	Leu	Ser	Asp	Phe	Gly	Phe
				95				100					105		110
tgc gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc														925	
Cys	Ala	Gln	Val	Ser	Lys	Glu	Val	Pro	Arg	Arg	Lys	Ser	Leu	Val	Gly
				115				120					125		
acg ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg														973	
Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Leu	Ile	Ser	Arg	Leu	Pro	Tyr	Gly
				130				135					140		
cca gag gta gac atc tgg tcg ctg ggg ata atg gtg att gag atg gtg														1021	

Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val
 145 150 155
 gac gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag 1069
 Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys
 160 165 170
 atg att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg 1117
 Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val
 175 180 185 190
 tcg cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct 1165
 Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro
 195 200 205
 gcc cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc 1213
 Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala
 210 215 220
 aag gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc 1261
 Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg
 225 230 235
 acc aga tgaggcccag cgcccttccc ctcaaccaa gagccccccg ggtcaccccc 1317
 Thr Arg
 240
 gcccactga ggccagtagg gggccaggcc tccactcct ccagcccgg gagatgctcc 1377
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 tgtcatttta taacactcta gccctgccc ttattggggg acagatgggc cctgtcctgc 1977
 ggggtggccc tggcagaacc actgcctgaa gaaccaggtt cctgcccggc cagcgcagcc 2037
 ccagcccgcc caccctgcc tcgagttagt ttacaatta aaacattgtc ttgt 2091

<210> 136

<211> 240

<212> PRT

<213> Homo sapiens

<400> 136

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1 5 10 15

Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr Asn

20 25 30

Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu

35 40 45

Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu

50 55 60

Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val Leu

65 70 75 80

His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu

85 90 95

Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys Ala

100 105 110

Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr Pro
 115 120 125
 Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu
 130 135 140
 Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp Gly
 145 150 155 160
 Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met Ile
 165 170 175
 Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser Pro
 180 185 190
 Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala Gln
 195 200 205
 Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys Ala
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 Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr Arg
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<210> 137

<211> 2278

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (137).. (1450)

<400> 137

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ccgagtcgcc ggcacc atg ttt ggg aag agg aag aag cgg gtg gag atc tcc 172
 Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser
 1 5 10
 gcg ccg tcc aac ttc gag cac cgc gtg cac acg ggc ttc gac cag cac 220
 Ala Pro Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Gln His
 15 20 25
 gag cag aag ttc acg ggg ctg ccc cgc cag tgg cag agc ctg atc gag 268
 Glu Gln Lys Phe Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu
 30 35 40
 gag tcg gct cgc cgg ccc aag ccc ctc gtc gac ccc gcc tgc atc acc 316
 Glu Ser Ala Arg Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr
 45 50 55 60
 tcc atc cag ccc ggg gcc ccc aag ggg gag cct cat gac gtg gcc cct 364
 Ser Ile Gln Pro Gly Ala Pro Lys Gly Glu Pro His Asp Val Ala Pro
 65 70 75
 aac ggg cca tca gcg ggg ggc ctg gcc atc ccc cag tcc tcc tcc tcc 412
 Asn Gly Pro Ser Ala Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser
 80 85 90
 tcc tcc cgg cct ccc acc cga gcc cga ggt gcc ccc agc cct gga gtg 460
 Ser Ser Arg Pro Pro Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val
 95 100 105
 ctg gga ccc cac gcc tca gag ccc cag ctg gcc cct cca gcc tgc acc 508
 Leu Gly Pro His Ala Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr
 110 115 120
 ccc gcc gcc cct gct gtt cct ggg ccc cct ggc ccc cgc tca cca cag 556
 Pro Ala Ala Pro Ala Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln
 125 130 135 140

cgg gag cca cag cga gta tcc cat gag cag ttc cgg gct gcc ctg cag 604
 Arg Glu Pro Gln Arg Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln
 145 150 155
 ctg gtg gtg gac cca ggc gac ccc cgc tcc tac ctg gac aac ttc atc 652
 Leu Val Val Asp Pro Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile
 160 165 170
 aag att ggc gag ggc tcc acg ggc atc gtg tgc atc gcc acc gtg cgc 700
 Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg
 175 180 185
 agc tcg ggc aag ctg gtg gcc gtc aag aag atg gac ctg cgc aag cag 748
 Ser Ser Gly Lys Leu Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln
 190 195 200
 cag agg cgc gag ctg ctc ttc aac gag gtg gta atc atg agg gac tac 796
 Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr
 205 210 215 220
 cag cac gag aat gtg gtg gag atg tac aac agc tac ctg gtg ggg gac 844
 Gln His Glu Asn Val Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp
 225 230 235
 gag ctc tgg gtg gtc atg gag ttc ctg gaa gga ggc gcc ctc acc gac 892
 Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp
 240 245 250
 atc gtc acc cac acc agg atg aac gag gag cag atc gcg gcc gtg tgc 940
 Ile Val Thr His Thr Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys
 255 260 265
 ctt gca gtg ctg cag gcc ctg tcg gtg ctc cac gcc cag ggc gtc atc 988
 Leu Ala Val Leu Gln Ala Leu Ser Val Leu His Ala Gln Gly Val Ile
 270 275 280

cac cgg gac atc aag agc gac tcg atc ctg ctg acc cat gat ggc agg 1036
 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
 285 290 295 300
 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg 1084
 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
 305 310 315
 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag 1132
 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
 320 325 330
 ctc atc tcc cgc ctt ccc tac ggg cca gag gta gac atc tgg tcg ctg 1180
 Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu
 335 340 345
 ggg ata atg gtg att gag atg gtg gac gga gag ccc ccc tac ttc aac 1228
 Gly Ile Met Val Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn
 350 355 360
 gag cca ccc ctc aaa gcc atg aag atg att cgg gac aac ctg cca ccc 1276
 Glu Pro Pro Leu Lys Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro
 365 370 375 380
 cga ctg aag aac ctg cac aag gtg tcg cca tcc ctg aag ggc ttc ctg 1324
 Arg Leu Lys Asn Leu His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu
 385 390 395
 gac cgc ctg ctg gtg cga gac cct gcc cag cgg gcc acg gca gcc gag 1372
 Asp Arg Leu Leu Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu
 400 405 410
 ctg ctg aag cac cca ttc ctg gcc aag gca ggg ccg cct gcc agc atc 1420
 Leu Leu Lys His Pro Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile
 415 420 425

gtg ccc ctc atg cgc cag aac cgc acc aga tgaggcccag cgcccttccc 1470

Val Pro Leu Met Arg Gln Asn Arg Thr Arg

430

435

ctcaacaaaa gagcccccg ggtcaccccc gccccactga ggccagtagg gggccaggcc 1530
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 atgagaccct actactgaac tccagttttg atctcgtgac ttttagaaaa acacagggac 1650
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 acaggtcagg gccccccacc ctctccagcc cctgcagcaa atgactactg cacctggaca 2070
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<210> 138

<211> 438

<212> PRT

<213> Homo sapiens

<400> 138

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5

10

15

Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe

20

25

30

Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg
 35 40 45
 Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro
 50 55 60
 Gly Ala Pro Lys Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser
 65 70 75 80
 Ala Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro
 85 90 95
 Pro Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His
 100 105 110
 Ala Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro
 115 120 125
 Ala Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln
 130 135 140
 Arg Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp
 145 150 155 160
 Pro Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu
 165 170 175
 Gly Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys
 180 185 190
 Leu Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu
 195 200 205
 Leu Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn
 210 215 220
 Val Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val
 225 230 235 240
 Val Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His

245 250 255
 Thr Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu
 260 265 270
 Gln Ala Leu Ser Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile
 275 280 285
 Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser
 290 295 300
 Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys
 305 310 315 320
 Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg
 325 330 335
 Leu Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val
 340 345 350
 Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu
 355 360 365
 Lys Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn
 370 375 380
 Leu His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu
 385 390 395 400
 Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His
 405 410 415
 Pro Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met
 420 425 430
 Arg Gln Asn Arg Thr Arg
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<210> 139

434/861

<211> 3025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (428).. (2200)

<400> 139

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gccctagag gagtggtcac ctgcctgagg gcacttctgt cccaccagca tcagaccagg 180
tgtgtgcagg ctctctatgg gatgccgcca tcagaatgtc tcttcctcag cccctttgtt 240
ttttaaagtg gctttggtcg accatttgct ctgtgcttgg tactgtgtca agggcccgat 300
tgaagaccac agatcctaaa gataggggag tgtcgcgaca aggctgcctg gggtgccctc 360
ttaaccagg ggatcagtaa cctgtgtctg agtcaatata caaaggccgc accgagtccc 420
cggcacc atg ttt ggg aag agg aag aag cgg gtg gag atc tcc gcg ccg 469
      Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro
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tcc aac ttc gag cac cgc gtg cac acg ggc ttc gac cag cac gag cag 517
Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln
      15              20              25              30
aag ttc acg ggg ctg ccc cgc cag tgg cag agc ctg atc gag gag tcg 565
Lys Phe Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser
            35              40              45
gct cgc cgg ccc aag ccc ctc gtc gac ccc gcc tgc atc acc tcc atc 613
Ala Arg Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile
            50              55              60
cag ccc ggg gcc ccc aag acc atc gtg cgg ggc agc aaa ggt gcc aaa 661

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Gln Pro Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys
 65 70 75
 gat ggg gcc ctc acg ctg ctg ctg gac gag ttt gag aac atg tcg gtg 709
 Asp Gly Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val
 80 85 90
 aca cgc tcc aac tcc ctg cgg aga gac agc ccg ccg ccg ccc gcc cgt 757
 Thr Arg Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg
 95 100 105 110
 gcc cgc cag gaa aat ggg atg cca gag gag ccg gcc acc acg gcc aga 805
 Ala Arg Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg
 115 120 125
 ggg ggc cca ggg aag gca ggc agc cga ggc cgg ttc gcc ggt cac agc 853

 Gly Gly Pro Gly Lys Ala Gly Ser Arg Gly Arg Phe Ala Gly His Ser
 130 135 140
 gag gcg ggt ggc ggc agt ggt gac agg cga cgg gcg ggg cca gag aag 901
 Glu Ala Gly Gly Gly Ser Gly Asp Arg Arg Arg Ala Gly Pro Glu Lys
 145 150 155
 agg ccc aag tct tcc agg gag ggc tca ggg ggt ccc cag gag tcc tcc 949
 Arg Pro Lys Ser Ser Arg Glu Gly Ser Gly Gly Pro Gln Glu Ser Ser
 160 165 170
 cgg gac aaa cgc ccc ctc tcc ggg cct gat gtc ggc acc ccc cag cct 997
 Arg Asp Lys Arg Pro Leu Ser Gly Pro Asp Val Gly Thr Pro Gln Pro
 175 180 185 190
 gct ggt ctg gcc agt ggg gcg aaa ctg gca gct ggc cgg ccc ttt aac 1045
 Ala Gly Leu Ala Ser Gly Ala Lys Leu Ala Ala Gly Arg Pro Phe Asn
 195 200 205

acc tac ccg agg gct gac acg gac cac cca tcc cgg ggt gcc cag ggg 1093
 Thr Tyr Pro Arg Ala Asp Thr Asp His Pro Ser Arg Gly Ala Gln Gly
 210 215 220
 gag cct cat gac gtg gcc cct aac ggg cca tca gcg ggg ggc ctg gcc 1141
 Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu Ala
 225 230 235
 atc ccc cag tcc tcc tcc tcc tcc tcc cgg cct ccc acc cga gcc cga 1189
 Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala Arg
 240 245 250
 ggt gcc ccc agc cct gga gtg ctg gga ccc cac gcc tca gag ccc cag 1237
 Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro Gln
 255 260 265 270
 ctg gcc cct cca gcc tgc acc ccc gcc gcc cct gct gtt cct ggg ccc 1285
 Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly Pro
 275 280 285
 cct ggc ccc cgc tca cca cag cgg gag cca cag cga gta tcc cat gag 1333
 Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His Glu
 290 295 300
 cag ttc cgg gct gcc ctg cag ctg gtg gtg gac cca ggc gac ccc cgc 1381
 Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro Arg
 305 310 315
 tcc tac ctg gac aac ttc atc aag att ggc gag ggc tcc acg ggc atc 1429
 Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile
 320 325 330
 gtg tgc atc gcc acc gtg cgc agc tcg ggc aag ctg gtg gcc gtc aag 1477
 Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val Lys
 335 340 345 350

aag atg gac ctg cgc aag cag cag agg cgc gag ctg ctc ttc aac gag	1525
Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
355 360 365	
gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg tac	1573
Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr	
370 375 380	
aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc ctg	1621
Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu	
385 390 395	
gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac gag	1669
Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu	
400 405 410	
gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg gtg	1717
Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val	
415 420 425 430	
ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg atc	1765
Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile	
435 440 445	
ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc tgc	1813
Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys	
450 455 460	
gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc acg	1861
Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr	
465 470 475	
ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg cca	1909
Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro	
480 485 490	

gag gta gac atc tgg tgc ctg ggg ata atg gtg att gag atg gtg gac 1957
 Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp
 495 500 505 510
 gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag atg 2005
 Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met
 515 520 525
 att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg tgc 2053
 Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser
 530 535 540
 cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct gcc 2101
 Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala
 545 550 555
 cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc aag 2149
 Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys
 560 565 570
 gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc acc 2197
 Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr
 575 580 585 590
 aga tgaggcccag cgcccttccc ctcaaccaa gagcccccg ggtaaccccc 2250
 Arg
 gcccactga ggccagtagg gggccaggcc tccactcct ccagcccgg gagatgctcc 2310
 gcgtggcacc accctccttg ctgggggtag atgagaccct actactgaac tccagttttg 2370
 atctcgtgac ttttagaaaa acacaggac tcgtggggagc aagcgaggct ccaggagccc 2430
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 cccatcactg gaagtctgca gtgggggtcg ctgggggtgg agagaacact aagaggtgaa 2550
 catgtatgag tgtgtgcacg cgtgtgagtg tgcatgtgtg tgtgtgcaaa ggtccagcca 2610
 cccgctctc cagcctgcaa ggggtgtctg ggccttgcc tgacaccag cccctctcc 2670

ccctgagcca ttgtgggggt cgatcatgaa tgtccgaaga gtggcctttt cccgtagccc 2730
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<210> 140

<211> 591

<212> PRT

<213> Homo sapiens

<400> 140

Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn

1 5 10 15

Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe

20 25 30

Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg

35 40 45

Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro

50 55 60

Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly

65 70 75 80

Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg

85 90 95

Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg

100 105 110

Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly

115 120 125
Pro Gly Lys Ala Gly Ser Arg Gly Arg Phe Ala Gly His Ser Glu Ala
130 135 140
Gly Gly Gly Ser Gly Asp Arg Arg Arg Ala Gly Pro Glu Lys Arg Pro
145 150 155 160
Lys Ser Ser Arg Glu Gly Ser Gly Gly Pro Gln Glu Ser Ser Arg Asp
165 170 175
Lys Arg Pro Leu Ser Gly Pro Asp Val Gly Thr Pro Gln Pro Ala Gly
180 185 190
Leu Ala Ser Gly Ala Lys Leu Ala Ala Gly Arg Pro Phe Asn Thr Tyr
195 200 205
Pro Arg Ala Asp Thr Asp His Pro Ser Arg Gly Ala Gln Gly Glu Pro
210 215 220
His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu Ala Ile Pro
225 230 235 240
Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala Arg Gly Ala
245 250 255
Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro Gln Leu Ala
260 265 270
Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly Pro Pro Gly
275 280 285
Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His Glu Gln Phe
290 295 300
Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro Arg Ser Tyr
305 310 315 320
Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys
325 330 335

Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val Lys Lys Met
 340 345 350
 Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val
 355 360 365
 Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr Asn Ser
 370 375 380
 Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly
 385 390 395 400
 Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu Gln
 405 410 415
 Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val Leu His
 420 425 430
 Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu
 435 440 445
 Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln
 450 455 460
 Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr
 465 470 475 480
 Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu Val
 485 490 495
 Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp Gly Glu
 500 505 510
 Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met Ile Arg
 515 520 525
 Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser Pro Ser
 530 535 540
 Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala Gln Arg

545	550	555	560
Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys Ala Gly			
	565	570	575
Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr Arg			
	580	585	590

<210> 141

<211> 2556

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227).. (1729)

<400> 141

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cgcgagggcg cggagttcca ggccgagcag ttaggcgcgc agcgactgcg gcgccgagcc 120
gatgagtaac ccgaagcccc tagaggagtg gtcacctgcc tgagggcact tctgtccac 180
cagcatcaga ccaggtgtgt gcaggccgca ccgagtcccc ggcacc atg ttt ggg 235
                                     Met Phe Gly

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1

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aag agg aag aag cgg gtg gag atc tcc gcg cgc tcc aac ttc gag cac 283
Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn Phe Glu His
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cgc gtg cac acg ggc ttc gac cag cac gag cag aag ttc acg ggg ctg 331
Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe Thr Gly Leu
      20              25              30              35
ccc cgc cag tgg cag agc ctg atc gag gag tcg gct cgc cgg ccc aag 379

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Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg Arg Pro Lys
 40 45 50
 ccc ctc gtc gac ccc gcc tgc atc acc tcc atc cag ccc ggg gcc ccc 427
 Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro Gly Ala Pro
 55 60 65
 aag acc atc gtg cgg ggc agc aaa ggt gcc aaa gat ggg gcc ctc acg 475
 Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly Ala Leu Thr
 70 75 80
 ctg ctg ctg gac gag ttt gag aac atg tcg gtg aca cgc tcc aac tcc 523
 Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg Ser Asn Ser
 85 90 95
 ctg cgg aga gac agc ccg ccg ccg ccc gcc cgt gcc cgc cag gaa aat 571
 Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg Gln Glu Asn
 100 105 110 115
 ggg atg cca gag gag ccg gcc acc acg gcc aga ggg ggc cca ggg aag 619
 Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly Pro Gly Lys
 120 125 130
 ggg gag cct cat gac gtg gcc cct aac ggg cca tca gcg ggg ggc ctg 667
 Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu
 135 140 145
 gcc atc ccc cag tcc tcc tcc tcc tcc tcc cgg cct ccc acc cga gcc 715
 Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala
 150 155 160
 cga ggt gcc ccc agc cct gga gtg ctg gga ccc cac gcc tca gag ccc 763
 Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro
 165 170 175
 cag ctg gcc cct cca gcc tgc acc ccc gcc gcc cct gct gtt cct ggg 811

Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly
 180 185 190 195
 ccc cct ggc ccc cgc tca cca cag cgg gag cca cag cga gta tcc cat 859
 Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His
 200 205 210
 gag cag ttc cgg gct gcc ctg cag ctg gtg gtg gac cca ggc gac ccc 907
 Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro
 215 220 225
 cgc tcc tac ctg gac aac ttc atc aag att ggc gag ggc tcc acg ggc 955
 Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly
 230 235 240
 atc gtg tgc atc gcc acc gtg cgc agc tcg ggc aag ctg gtg gcc gtc 1003
 Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val
 245 250 255
 aag aag atg gac ctg cgc aag cag cag agg cgc gag ctg ctc ttc aac 1051
 Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn
 260 265 270 275
 gag gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg 1099
 Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met
 280 285 290
 tac aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc 1147
 Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe
 295 300 305
 ctg gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac 1195
 Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn
 310 315 320
 gag gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg 1243

Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser
 325 330 335
 gtg ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg 1291
 Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser
 340 345 350 355
 atc ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc 1339
 Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe
 360 365 370
 tgc gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc 1387
 Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly
 375 380 385
 acg ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg 1435
 Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly
 390 395 400
 cca gag gta gac atc tgg tcg ctg ggg ata atg gtg att gag atg gtg 1483
 Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val
 405 410 415
 gac gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag 1531
 Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys
 420 425 430 435
 atg att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg 1579
 Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val
 440 445 450
 tcg cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct 1627
 Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro
 455 460 465
 gcc cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc 1675

Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala

470

475

480

aag gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc 1723

Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg

485

490

495

acc aga tgaggcccag cgcccttccc ctcaaccaa gagccccccg ggtcaccccc 1779

Thr Arg

500

gccccactga ggccagtagg gggccaggcc tcccactcct cccagcccgg gagatgctcc 1839

gcgtggcacc accctccttg ctgggggtag atgagaccct actactgaac tccagttttg 1899

atctcgtgac ttttagaaaa acacagggaac tcgtgggagc aagcgaggct cccaggaccc 1959

ccaccctctg ggacaggccc tccccatgt tcttctgtct ccaggaaggg cagcggccct 2019

cccatcactg gaagtctgca gtgggggtcg ctgggggtgg agagaacact aagaggtgaa 2079

catgtatgag tgtgtgcacg cgtgtgagtg tgcattgttg tgtgtgtgca aaggtccagc 2139

caccccgctc tccagcccgc aagggtgtgc tggcgcttg cctgacaccc agccccctct 2199

ccccctgagc cattgtgggg gtcgatcatg aatgtccgaa gagggtgctt ttcccgtagc 2259

cctgcgcccc ctttctgttg ctggatgggg agacaggta gggcccccca ccctctccag 2319

ccccctgcagc aaatgactac tgcacctgga cagcctcctc ttttctagaa gtctatttat 2379

attgtcattt tataacactc tagccctgc cttattggg ggacagatgg tccctgtcct 2439

gcgggggtggc cctggcagaa ccaactgcctg aagaaccagg ttctgcccg gtcagcgcag 2499

ccccagcccg cccaccctg cctcgagtta gttttacaat taaaacattg tcttggt 2556

<210> 142

<211> 501

<212> PRT

<213> Homo sapiens

<400> 142

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 Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe
 20 25 30
 Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg
 35 40 45
 Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro
 50 55 60
 Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly
 65 70 75 80
 Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg
 85 90 95
 Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg
 100 105 110
 Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly
 115 120 125
 Pro Gly Lys Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala
 130 135 140
 Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro
 145 150 155 160
 Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala
 165 170 175
 Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala
 180 185 190
 Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg
 195 200 205
 Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro

210 215 220
Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly
225 230 235 240
Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu
245 250 255
Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu
260 265 270
Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val
275 280 285
Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val
290 295 300
Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr
305 310 315 320
Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln
325 330 335
Ala Leu Ser Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys
340 345 350
Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp
355 360 365
Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser
370 375 380
Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu
385 390 395 400
Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile
405 410 415
Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys
420 425 430

Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu

435

440

445

His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val

450

455

460

Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro

465

470

475

480

Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg

485

490

495

Gln Asn Arg Thr Arg

500

<210> 143

<211> 2030

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (169).. (1086)

<400> 143

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cctggagggg caatttgcatt atttctcaa agaaccatcc agaacctgag cagcctgtct 120
tcagacagag agaggccac ggctgtttct tgaaatctgg cgctggga atg gcc atg 177

Met Ala Met

1

tgg aac agg cca tgc cag agg ctg cct cag cag cct ctg gta gct gag 225
Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu

5

10

15

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ccc act gca gag ggg gag cca cac ctg ccc acg ggc cgg gag ctg act 273
Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr
    20                25                30                35
gag gcc aac cgc ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc 321
Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser
                40                45                50
cag tta ttt cct gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg 369
Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met
                55                60                65
gca ggc ctg gtg cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc 417
Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr
                70                75                80
atg act gct ttt gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt 465
Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe
                85                90                95
gtt caa att tta ctg aag gac ccc atc ttg aag gac gac ccg acg gtg 513
Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val
100                105                110                115
atc act cag gac ctt ctg agc ttc tca ctc aag gat ggg cac tat gac 561
Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp
                120                125                130
gcc cgg gcc aga gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg 609
Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val
                135                140                145
ccc ttg gag gag ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg 657
Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu
                150                155                160

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aag gaa atc aaa gaa gag gaa tct gaa atg gcc gag gca tcc cga aag 705
Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys
165 170 175
aag aaa gaa aac cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg 753
Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu
180 185 190 195
gcg act gtc gga ggc gga acg gtg atc ggt gtg act gga ggt cta gct 801
Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala
200 205 210
gca ccc ctt gtt gcc gct gga gca gcg acg att att ggc agc gcc ggg 849
Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly
215 220 225
gca gcg gct ctg ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg 897
Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu
230 235 240
ttt ggt gca gct gga gct ggc ctg aca gga tac aag atg aag aag cga 945
Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg
245 250 255
gtg gga gcc att gaa gag ttc acg ttt ctg ccg cct cat cag gcg aga 993
Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Pro His Gln Ala Arg
260 265 270 275
ccc ccc acc agg ttg ggc aaa ccc agg gtc cca tat ctg gag aca cct 1041
Pro Pro Thr Arg Leu Gly Lys Pro Arg Val Pro Tyr Leu Glu Thr Pro
280 285 290
cca aat tgg cca tgt cca cag acc cca gcc aag ccc agg tgc cag 1086
Pro Asn Trp Pro Cys Pro Gln Thr Pro Ala Lys Pro Arg Cys Gln
295 300 305

tagggctgga ccagtctgaa ggggcctccc ttctgctgc tgccagccct gaaaggcccc 1146
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<210> 144

<211> 306

<212> PRT

<213> Homo sapiens

<400> 144

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

1

5

10

15

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg

20

25

30

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile

35	40	45
Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr		
50	55	60
Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val		
65	70	75
80		
Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala		
85	90	95
Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp		
100	105	110
Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly		
115	120	125
His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu		
130	135	140
Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu		
145	150	155
160		
Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala		
165	170	175
Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu		
180	185	190
Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly		
195	200	205
Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly		
210	215	220
Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met		
225	230	235
240		
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met		
245	250	255

Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Pro His

260

265

270

Gln Ala Arg Pro Pro Thr Arg Leu Gly Lys Pro Arg Val Pro Tyr Leu

275

280

285

Glu Thr Pro Pro Asn Trp Pro Cys Pro Gln Thr Pro Ala Lys Pro Arg

290

295

300

Cys Gln

305

<210> 145

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (272).. (2011)

<400> 145

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 ctgctgactt ttgagtggat tttacagctg ggtaaactga ggctcagaga gggcaatttg 180
 catatttctc caaagaacca tccagaacct gagcagcctg tcttcagaca gagagaggcc 240
 cacggctgtt tcttgaaatc tggcgctggg a atg gcc atg tgg aac agg cca 292

Met Ala Met Trp Asn Arg Pro

1

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tgc cag agg ctg cct cag cag cct ctg gta gct gag ccc act gca gag 340

Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu

10

15

20

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ggg gag cca cac ctg ccc acg ggc cgg gag ctg act gag gcc aac cgc 388
Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg
    25                30                35

ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc cag tta ttt cct 436
Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser Gln Leu Phe Pro
    40                45                50                55

gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg gca ggc ctg gtg 484
Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met Ala Gly Leu Val
                60                65                70

cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc atg act gct ttt 532
Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr Met Thr Ala Phe
                75                80                85

gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt gtt caa att tta 580
Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe Val Gln Ile Leu
                90                95                100

ctg aag gac ccc atc ttg aag gac gac ccg acg gtg atc act cag gac 628
Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val Ile Thr Gln Asp
    105                110                115

ctt ctg agc ttc tca ctc aag gat ggg cac tat gac gcc cgg gcc aga 676
Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp Ala Arg Ala Arg
    120                125                130                135

gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg ccc ttg gag gag 724
Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val Pro Leu Glu Glu
                140                145                150

ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg aag gaa atc aaa 772
Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu Lys Glu Ile Lys
                155                160                165

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gaa gag gaa tct gaa atg gcc gag gca tcc cga aag aag aaa gaa aac 820
 Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys Lys Lys Glu Asn
 170 175 180
 cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg gcg act gtc gga 868
 Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu Ala Thr Val Gly
 185 190 195
 ggc gga acg gtg atc ggt gtg act gga ggt cta gct gca ccc ctt gtt 916
 Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala Ala Pro Leu Val
 200 205 210 215
 gcc gct gga gca gcg acg att att ggc agc gcc ggg gca gcg gct ctg 964
 Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly Ala Ala Ala Leu
 220 225 230
 ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg ttt ggt gca gct 1012
 Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu Phe Gly Ala Ala
 235 240 245
 gga gct ggc ctg aca gga tac aag atg aag aag cga gtg gga gcc att 1060
 Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg Val Gly Ala Ile
 250 255 260
 gaa gag ttc acg ttt ctg cct ctg acg gag ggc agg cag ctg cac atc 1108
 Glu Glu Phe Thr Phe Leu Pro Leu Thr Glu Gly Arg Gln Leu His Ile
 265 270 275
 acc atc gcc gtc acg ggg tgg ctc gct tct ggc aaa tac cgc acc ttc 1156
 Thr Ile Ala Val Thr Gly Trp Leu Ala Ser Gly Lys Tyr Arg Thr Phe
 280 285 290 295
 agt gcc ccg tgg gct gcc ctg gcc cac agc cgt gag cag tac tgc ctg 1204
 Ser Ala Pro Trp Ala Ala Leu Ala His Ser Arg Glu Gln Tyr Cys Leu
 300 305 310

gcc tgg gaa gcc aag tac ctg atg gag ctc ggc aat gcc ctg gag acc 1252
 Ala Trp Glu Ala Lys Tyr Leu Met Glu Leu Gly Asn Ala Leu Glu Thr
 315 320 325
 atc ctc agt ggt ctc gcc aac atg gtg gcc cag gag gcc cta aag tac 1300
 Ile Leu Ser Gly Leu Ala Asn Met Val Ala Gln Glu Ala Leu Lys Tyr
 330 335 340
 aca gtg ttg tct ggc att gtg gct gcc ctg acc tgg cca gcc tca ctc 1348
 Thr Val Leu Ser Gly Ile Val Ala Ala Leu Thr Trp Pro Ala Ser Leu
 345 350 355
 ctc agt gtc gcc aat gtc atc gac aac ccc tgg ggg gtg tgt ctc cat. 1396
 Leu Ser Val Ala Asn Val Ile Asp Asn Pro Trp Gly Val Cys Leu His
 360 365 370 375
 cga tca gca gag gtt ggc aag cac ctg gcc cac atc ctg ctc tcc cgg 1444
 Arg Ser Ala Glu Val Gly Lys His Leu Ala His Ile Leu Leu Ser Arg
 380 385 390
 cag cag ggg cga cga cct gtc acc ttg att ggc ttc agc ctg gga gcc 1492
 Gln Gln Gly Arg Arg Pro Val Thr Leu Ile Gly Phe Ser Leu Gly Ala
 395 400 405
 aga gtc atc tac ttc tgt ctg cag gag atg gct caa gag aaa gat tgc 1540
 Arg Val Ile Tyr Phe Cys Leu Gln Glu Met Ala Gln Glu Lys Asp Cys
 410 415 420
 caa gga atc atc gag gac gtc atc ctg ctg ggt gcg cct gtg gag gga 1588
 Gln Gly Ile Ile Glu Asp Val Ile Leu Leu Gly Ala Pro Val Glu Gly
 425 430 435
 gaa gcc aag cat tgg gag cct ttc cgg aag gtg gtg tcc ggg agg atc 1636
 Glu Ala Lys His Trp Glu Pro Phe Arg Lys Val Val Ser Gly Arg Ile
 440 445 450 455

atc aac ggc tac tgc agg gga gac tgg ctg ctg agt ttc gtg tac cgc 1684
 Ile Asn Gly Tyr Cys Arg Gly Asp Trp Leu Leu Ser Phe Val Tyr Arg
 460 465 470
 aca tcc tcg gtg cag ctc cac gtc gcc ggc cta cag ccc gtg ctg ctg 1732
 Thr Ser Ser Val Gln Leu His Val Ala Gly Leu Gln Pro Val Leu Leu
 475 480 485
 cag gac agg agg gtg gag aac gtg gac ctg acc tct gtg gtc agc ggc 1780
 Gln Asp Arg Arg Val Glu Asn Val Asp Leu Thr Ser Val Val Ser Gly
 490 495 500
 cac ctg gac tat gcc aag cag atg gat gcc atc ctg aag gcc gtg ggc 1828
 His Leu Asp Tyr Ala Lys Gln Met Asp Ala Ile Leu Lys Ala Val Gly
 505 510 515
 atc cgc acc aag cca ggc tgg gac gag aag ggg ctc ttg ctg gcc cca 1876
 Ile Arg Thr Lys Pro Gly Trp Asp Glu Lys Gly Leu Leu Leu Ala Pro
 520 525 530 535
 ggc tgc ctg ccc tcc gag gag cct cgc cag gca gca gct gcc gcc tca 1924
 Gly Cys Leu Pro Ser Glu Glu Pro Arg Gln Ala Ala Ala Ala Ala Ser
 540 545 550
 tca gct ttg gag tct ggc tgt cca tca gga ggt ccc gag ggc tct ctg 1972
 Ser Ala Leu Glu Ser Gly Cys Pro Ser Gly Gly Pro Glu Gly Ser Leu
 555 560 565
 ggg cct gag gct ccc aca cca gct ttc ccc tgg cct caa taaaaccagg 2021
 Gly Pro Glu Ala Pro Thr Pro Ala Phe Pro Trp Pro Gln
 570 575 580
 tgc atg cctg ttcttccatc cacactccag ggctgccac cagctgacag gcaccatcaa 2081
 ctggcagcaa cagagcaggc gcaggtacaa agaaggcagc tcactcctgc tcttaggaga 2141
 tccaatcaga tctgccctgt acagccatgt aggctgtgcg ctgcataact ccaggacat 2201

gagtcacaca gacacaatgt gagtgtgctc ccccgatcatg caacatctgg acacaactaa 2261
 cagagcatgg tgaatacatg ctgaattgca ttcagtatgg ctgtgaacta ggcctgggga 2321
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<210> 146

<211> 580

<212> PRT

<213> Homo sapiens

<400> 146

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 20 25 30
 Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 35 40 45
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 50 55 60
 Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val
 65 70 75 80
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala
 85 90 95
 Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp
 100 105 110
 Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly
 115 120 125
 His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu

130	135	140	
Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu			
145	150	155	160
Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala			
	165	170	175
Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu			
	180	185	190
Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly			
	195	200	205
Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly			
	210	215	220
Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met			
225	230	235	240
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met			
	245	250	255
Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Leu Thr			
	260	265	270
Glu Gly Arg Gln Leu His Ile Thr Ile Ala Val Thr Gly Trp Leu Ala			
	275	280	285
Ser Gly Lys Tyr Arg Thr Phe Ser Ala Pro Trp Ala Ala Leu Ala His			
	290	295	300
Ser Arg Glu Gln Tyr Cys Leu Ala Trp Glu Ala Lys Tyr Leu Met Glu			
305	310	315	320
Leu Gly Asn Ala Leu Glu Thr Ile Leu Ser Gly Leu Ala Asn Met Val			
	325	330	335
Ala Gln Glu Ala Leu Lys Tyr Thr Val Leu Ser Gly Ile Val Ala Ala			
	340	345	350

Leu Thr Trp Pro Ala Ser Leu Leu Ser Val Ala Asn Val Ile Asp Asn
 355 360 365
 Pro Trp Gly Val Cys Leu His Arg Ser Ala Glu Val Gly Lys His Leu
 370 375 380
 Ala His Ile Leu Leu Ser Arg Gln Gln Gly Arg Arg Pro Val Thr Leu
 385 390 395 400
 Ile Gly Phe Ser Leu Gly Ala Arg Val Ile Tyr Phe Cys Leu Gln Glu
 405 410 415
 Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
 420 425 430
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
 435 440 445
 Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp
 450 455 460
 Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala
 465 470 475 480
 Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp
 485 490 495
 Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp
 500 505 510
 Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu
 515 520 525
 Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg
 530 535 540
 Gln Ala Ala Ala Ala Ala Ser Ser Ala Leu Glu Ser Gly Cys Pro Ser
 545 550 555 560
 Gly Gly Pro Glu Gly Ser Leu Gly Pro Glu Ala Pro Thr Pro Ala Phe

565

570

575

Pro Trp Pro Gln

580

<210> 147

<211> 2281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (272).. (1891)

<400> 147

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 ctgctgactt ttgagtggat ttacagctg ggtaactga ggctcagaga gggcaatttg 180
 catatttctc caaagaacca tccagaacct gagcagctg tcttcagaca gagagaggcc 240
 cacggctggt tcttgaaatc tggcgctggg a atg gcc atg tgg aac agg cca 292

Met Ala Met Trp Asn Arg Pro

1

5

tgc cag agg ctg cct cag cag cct ctg gta gct gag ccc act gca gag 340
 Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu

10

15

20

ggg gag cca cac ctg ccc acg ggc cgg gag ctg act gag gcc aac cgc 388
 Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg

25

30

35

ttc gcc tat gct gcc ctg tgt ggc atc tcc ctg tcc cag tta ttt cct 436
 Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser Gln Leu Phe Pro

40	45	50	55	
gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg gca ggc ctg gtg				484
Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met Ala Gly Leu Val				
	60	65	70	
cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc atg act gct ttt				532
Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr Met Thr Ala Phe				
	75	80	85	
gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt gtt caa att tta				580
Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe Val Gln Ile Leu				
	90	95	100	
ctg aag gac ccc atc ttg aag gac gac ccg acg gtg atc act cag gac				628
Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val Ile Thr Gln Asp				
	105	110	115	
ctt ctg agc ttc tca ctc aag gat ggg cac tat gac gcc cgg gcc aga				676
Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp Ala Arg Ala Arg				
	120	125	130	135
gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg ccc ttg gag gag				724
Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val Pro Leu Glu Glu				
	140	145	150	
ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg aag gaa atc aaa				772
Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu Lys Glu Ile Lys				
	155	160	165	
gaa gag gaa tct gaa atg gcc gag gca tcc cga aag aag aaa gaa aac				820
Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys Lys Lys Glu Asn				
	170	175	180	
cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg gcg act gtc gga				868
Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu Ala Thr Val Gly				

185	190	195	
ggc gga acg gtg atc ggt gtg act gga ggt cta gct gca ccc ctt gtt	916		
Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala Ala Pro Leu Val			
200	205	210	215
gcc gct gga gca gcg acg att att ggc agc gcc ggg gca gcg gct ctg	964		
Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly Ala Ala Ala Leu			
	220	225	230
ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg ttt ggt gca gct	1012		
Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu Phe Gly Ala Ala			
	235	240	245
gga gct ggc ctg aca ggc acc ttc agt gcc ccg tgg gct gcc ctg gcc	1060		
Gly Ala Gly Leu Thr Gly Thr Phe Ser Ala Pro Trp Ala Ala Leu Ala			
	250	255	260
cac agc cgt gag cag tac tgc ctg gcc tgg gaa gcc aag tac ctg atg	1108		
His Ser Arg Glu Gln Tyr Cys Leu Ala Trp Glu Ala Lys Tyr Leu Met			
	265	270	275
gag ctc ggc aat gcc ctg gag acc atc ctc agt ggt ctc gcc aac atg	1156		
Glu Leu Gly Asn Ala Leu Glu Thr Ile Leu Ser Gly Leu Ala Asn Met			
280	285	290	295
gtg gcc cag gag gcc cta aag tac aca gtg ttg tct ggc att gtg gct	1204		
Val Ala Gln Glu Ala Leu Lys Tyr Thr Val Leu Ser Gly Ile Val Ala			
	300	305	310
gcc ctg acc tgg cca gcc tca ctc ctc agt gtc gcc aat gtc atc gac	1252		
Ala Leu Thr Trp Pro Ala Ser Leu Leu Ser Val Ala Asn Val Ile Asp			
	315	320	325
aac ccc tgg ggg gtg tgt ctc cat cga tca gca gag gtt ggc aag cac	1300		
Asn Pro Trp Gly Val Cys Leu His Arg Ser Ala Glu Val Gly Lys His			

330	335	340	
ctg gcc cac atc ctg ctc tcc cgg cag cag ggg cga cga cct gtc acc			1348
Leu Ala His Ile Leu Leu Ser Arg Gln Gln Gly Arg Arg Pro Val Thr			
345	350	355	
ttg att ggc ttc agc ctg gga gcc aga gtc atc tac ttc tgt ctg cag			1396
Leu Ile Gly Phe Ser Leu Gly Ala Arg Val Ile Tyr Phe Cys Leu Gln			
360	365	370	375
gag atg gct caa gag aaa gat tgc caa gga atc atc gag gac gtc atc			1444
Glu Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile			
	380	385	390
ctg ctg ggt gcg cct gtg gag gga gaa gcc aag cat tgg gag cct ttc			1492
Leu Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe			
	395	400	405
cgg aag gtg gtg tcc ggg agg atc atc aac ggc tac tgc agg gga gac			1540
Arg Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp			
	410	415	420
tgg ctg ctg agt ttc gtg tac cgc aca tcc tcg gtg cag ctc cac gtc			1588
Trp Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val			
	425	430	435
gcc ggc cta cag ccc gtg ctg ctg cag gac agg agg gtg gag aac gtg			1636
Ala Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val			
440	445	450	455
gac ctg acc tct gtg gtc agc ggc cac ctg gac tat gcc aag cag atg			1684
Asp Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met			
	460	465	470
gat gcc atc ctg aag gcc gtg ggc atc cgc acc aag cca ggc tgg gac			1732
Asp Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp			

475 480 485
 gag aag ggg ctc ttg ctg gcc cca ggc tgc ctg ccc tcc gag gag cct 1780
 Glu Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro
 490 495 500
 cgc cag gca gca gct gcc gcc tca tca gct ttg gag tct ggc tgt cca 1828
 Arg Gln Ala Ala Ala Ala Ser Ser Ala Leu Glu Ser Gly Cys Pro
 505 510 515
 tca gga ggt ccc gag ggc tct ctg ggg cct gag gct ccc aca cca gct 1876
 Ser Gly Gly Pro Glu Gly Ser Leu Gly Pro Glu Ala Pro Thr Pro Ala
 520 525 530 535
 ttc ccc tgg cct caa taaaaccagg tgcattgcctg ttcttccatc cacactccag 1931
 Phe Pro Trp Pro Gln
 540
 ggctgcccac cagctgacag gcaccatcaa ctggcagcaa cagagcaggc gcaggtacaa 1991
 agaaggcagc tcaactcctgc tcttaggaga tccaatcaga tctgccctgt acagccatgt 2051
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 ttcagtatgg ctgtgaacta ggccctgggga caagaatgaa ttttacatgg aaagaatttc 2231
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<210> 148

<211> 540

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

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15

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 Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 35 40 45
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 50 55 60
 Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val
 65 70 75 80
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala
 85 90 95
 Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp
 100 105 110
 Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly
 115 120 125
 His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu
 130 135 140
 Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu
 145 150 155 160
 Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala
 165 170 175
 Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu
 180 185 190
 Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly
 195 200 205
 Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly
 210 215 220
 Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met

225 230 235 240
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Thr Phe Ser
 245 250 255
Ala Pro Trp Ala Ala Leu Ala His Ser Arg Glu Gln Tyr Cys Leu Ala
 260 265 270
Trp Glu Ala Lys Tyr Leu Met Glu Leu Gly Asn Ala Leu Glu Thr Ile
 275 280 285
Leu Ser Gly Leu Ala Asn Met Val Ala Gln Glu Ala Leu Lys Tyr Thr
 290 295 300
Val Leu Ser Gly Ile Val Ala Ala Leu Thr Trp Pro Ala Ser Leu Leu
305 310 315 320
Ser Val Ala Asn Val Ile Asp Asn Pro Trp Gly Val Cys Leu His Arg
 325 330 335
Ser Ala Glu Val Gly Lys His Leu Ala His Ile Leu Leu Ser Arg Gln
 340 345 350
Gln Gly Arg Arg Pro Val Thr Leu Ile Gly Phe Ser Leu Gly Ala Arg
 355 360 365
Val Ile Tyr Phe Cys Leu Gln Glu Met Ala Gln Glu Lys Asp Cys Gln
 370 375 380
Gly Ile Ile Glu Asp Val Ile Leu Leu Gly Ala Pro Val Glu Gly Glu
385 390 395 400
Ala Lys His Trp Glu Pro Phe Arg Lys Val Val Ser Gly Arg Ile Ile
 405 410 415
Asn Gly Tyr Cys Arg Gly Asp Trp Leu Leu Ser Phe Val Tyr Arg Thr
 420 425 430
Ser Ser Val Gln Leu His Val Ala Gly Leu Gln Pro Val Leu Leu Gln
 435 440 445

Asp Arg Arg Val Glu Asn Val Asp Leu Thr Ser Val Val Ser Gly His
 450 455 460
 Leu Asp Tyr Ala Lys Gln Met Asp Ala Ile Leu Lys Ala Val Gly Ile
 465 470 475 480
 Arg Thr Lys Pro Gly Trp Asp Glu Lys Gly Leu Leu Leu Ala Pro Gly
 485 490 495
 Cys Leu Pro Ser Glu Glu Pro Arg Gln Ala Ala Ala Ala Ala Ser Ser
 500 505 510
 Ala Leu Glu Ser Gly Cys Pro Ser Gly Gly Pro Glu Gly Ser Leu Gly
 515 520 525
 Pro Glu Ala Pro Thr Pro Ala Phe Pro Trp Pro Gln
 530 535 540

<210> 149

<211> 2237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (169).. (1059)

<400> 149

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 tcagacagag agaggccac ggctgtttct tgaaatctgg cgctggga atg gcc atg 177
 Met Ala Met

1

tgg aac agg cca tgc cag agg ctg cct cag cag cct ctg gta gct gag 225

Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu
 5 10 15
 ccc act gca gag ggg gag cca cac ctg ccc acg ggc cgg gag ctg act 273
 Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr
 20 25 30 35
 gag gcc aac cgc ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc 321
 Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser
 40 45 50
 cag tta ttt cct gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg 369
 Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met
 55 60 65
 gca ggc ctg gtg cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc 417
 Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr
 70 75 80
 atg act gct ttt gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt 465
 Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe
 85 90 95
 gtt caa att tta ctg aag gac ccc atc ttg aag gac gac ccg acg gtg 513
 Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val
 100 105 110 115
 atc act cag gac ctt ctg agc ttc tca ctc aag gat ggg cac tat gac 561
 Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp
 120 125 130
 gcc cgg gcc aga gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg 609
 Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val
 135 140 145
 ccc ttg gag gag ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg 657

Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu
 150 155 160
 aag gaa atc aaa gaa gag gaa tct gaa atg gcc gag gca tcc cga aag 705
 Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys
 165 170 175
 aag aaa gaa aac cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg 753
 Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu
 180 185 190 195
 gcg act gtc gga ggc gga acg gtg atc ggt gtg act gga ggt cta gct 801
 Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala
 200 205 210
 gca ccc ctt gtt gcc gct gga gca gcg acg att att ggc agc gcc ggg 849
 Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly
 215 220 225
 gca gcg gct ctg ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg 897
 Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu
 230 235 240
 ttt ggt gca gct gga gct ggc ctg aca gga tac aag atg aag aag cga 945
 Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg
 245 250 255
 gtg gga gcc att gaa gag ttc acg ttt ctg gca aat acc gca cct tca 993
 Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Ala Asn Thr Ala Pro Ser
 260 265 270 275
 gtg ccc cgt ggg ctg ccc tgg ccc aca gcc gtg agc agt act gcc tgg 1041
 Val Pro Arg Gly Leu Pro Trp Pro Thr Ala Val Ser Ser Thr Ala Trp
 280 285 290
 cct ggg aag cca agt acc tgatggagct cggcaatgcc ctggagacca 1089

Pro Gly Lys Pro Ser Thr

295

tcctcagtgg tctcgccaac atggtggccc aggaggccct aaagtacaca gtgttgtctg 1149
 gcatttgtggc tgccctgacc tggccagcct cactcctcag tgtcgccaat gtcacgaca 1209
 acccctgggg ggtgtgtctc catcgatcag cagaggttgg caagcacctg gccacatcc 1269
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 cttccatcca cactccaggg ctgccacca gctgacaggc accatcaact ggcagcaaca 1929
 gagcaggcgc aggtacaaag aaggcagctc actcctgctc ttaggagatc caatcagatc 1989
 tgccctgtac agccatgtag gctgtgcgct gcataactcc agggacatga gtcacacaga 2049
 cacaatgtga gtgtgtctcc ccgtcatgca acatctggac acaactaaca gagcatgggtg 2109
 aatacatgct gaattgcatt cagtatggct gtgaactagg cctggggaca agaatgaatt 2169
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 ataagaag 2237

<210> 150

<211> 297

<212> PRT

<213> Homo sapiens

<400> 150

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

1 5 10 15

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg

20 25 30

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile

35 40 45

Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr

50 55 60

Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val

65 70 75 80

Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala

85 90 95

Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp

100 105 110

Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly

115 120 125

His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu

130 135 140

Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu

145 150 155 160

Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala

165 170 175

Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu

180 185 190

Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly

195 200 205

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Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly
 210 215 220
 Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met
 225 230 235 240
 Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met
 245 250 255
 Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Ala Asn Thr
 260 265 270
 Ala Pro Ser Val Pro Arg Gly Leu Pro Trp Pro Thr Ala Val Ser Ser
 275 280 285
 Thr Ala Trp Pro Gly Lys Pro Ser Thr
 290 295

<210> 151

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (57).. (239)

<400> 151

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Met

1

gcc gag gca ggg ggc gag ggc gag ggc gag gtg tgc ctg gtc atg ctg 107

Ala Glu Ala Gly Gly Glu Gly Glu Gly Glu Val Cys Leu Val Met Leu

5

10

15

tgg tgg atc acc gtc cca ggg cat tgg aga ttt ctg cat tta cgg aga 155
 Trp Trp Ile Thr Val Pro Gly His Trp Arg Phe Leu His Leu Arg Arg
 20 25 30
 gcg ata gag aag atc ttc ttc ctc att ttg cgc aat atg gtg aaa ttg 203
 Ala Ile Glu Lys Ile Phe Phe Leu Ile Leu Arg Asn Met Val Lys Leu
 35 40 45
 aag att gtc aga ttg atg att cct cac ttc atg cag taattacatt 249
 Lys Ile Val Arg Leu Met Ile Pro His Phe Met Gln
 50 55 60
 caagacaaga gcagaagctg aagcagctgc agttcatgga gctcgtttca aagggaaga 309
 tctaaaactg gcatggaata aaccagtaac taatatttca gctgttgaaa cagaagaagt 369
 tgagcctgat gaagaagaat ttcaggaaga gtctttggtg gatgactcat tacttcaaga 429
 tgatgatgaa gaagaagagg acaatgaatc tcgttcttgg agaagatgat ttgactgata 489
 attgatctgc atatgctaga actctacctg tggttcatta gtattatcta atgtactttt 549
 acatatttgt aaaaacaatt tttggtaaaa tgtgatgaag atggatttca caaatagaca 609
 aaaaagaaga aaact 624

<210> 152

<211> 61

<212> PRT

<213> Homo sapiens

<400> 152

Met Ala Glu Ala Gly Gly Glu Gly Glu Gly Glu Val Cys Leu Val Met
 1 5 10 15
 Leu Trp Trp Ile Thr Val Pro Gly His Trp Arg Phe Leu His Leu Arg
 20 25 30

Arg Ala Ile Glu Lys Ile Phe Phe Leu Ile Leu Arg Asn Met Val Lys

35

40

45

Leu Lys Ile Val Arg Leu Met Ile Pro His Phe Met Gln

50

55

60

<210> 153

<211> 1570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (156).. (917)

<400> 153

ctgcttttgaa ggctgcacag aaaaccttac ttgtttccac ctctgcagtt gataataatg 60
 aagcacagaa aaaaaaacag gaggcattga aacttcagca ggatgtaagg aaaaggaaac 120
 aagaaatttt agaaaagcac attgaaacac agaag atg tta att tca aaa ctg 173

Met Leu Ile Ser Lys Leu

1

5

gag aaa aac aaa aca atg aag tct gaa gat aaa gca gaa ata atg aaa 221
 Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys

10

15

20

act tta gag gtt ttg aca aaa aat att acc aag ttg aaa gat gag gtc 269
 Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val

25

30

35

aaa gct gct tct cct gga cgc tgt ctt cca aaa agt ata aaa acc aag 317
 Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys

40

45

50

act cag atg cag aag gaa tta ctt gac aca gaa ctg gat tta tat aag 365
 Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys
 55 60 65 70
 aag atg cag gct gga gaa gaa gtc act gaa ctt agg aga aag tat aca 413
 Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr
 75 80 85
 gaa tta cag ctg gaa gct gcc aaa cga ggg att ctt tca tct ggt cgg 461
 Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg
 90 95 100
 ggc aga gga att cat tca aga ggt cga ggt gca gtt cat ggc cga ggc 509
 Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg Gly
 105 110 115
 agg ggg cga ggg cga ggg cga ggt gtg cct ggt cat gct gtg gtg gat 557
 Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val Asp
 120 125 130
 cac cgt ccc agg gca ttg gag att tct gca ttt acg gag agc gat aga 605
 His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp Arg
 135 140 145 150
 gaa gat ctt ctt cct cat ttt gcg caa tat ggt gaa att gaa gat tgt 653
 Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp Cys
 155 160 165
 cag att gat gat tcc tca ctt cat gca gta att aca ttc aag aca aga 701
 Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr Arg
 170 175 180
 gca gaa gct gaa gca gct gca gtt cat gga gct cgt ttc aaa ggg caa 749
 Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln
 185 190 195

gat cta aaa ctg gca tgg aat aaa cca gta act aat att tca gct gtt 797
 Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala Val
 200 205 210
 gaa aca gaa gaa gtt gag cct gat gaa gaa gaa ttt cag gaa gag tct 845
 Glu Thr Glu Glu Val Glu Pro Asp Glu Glu Glu Phe Gln Glu Glu Ser
 215 220 225 230
 ttg gtg gat gac tca tta ctt caa gat gat gat gaa gaa gaa gag gac 893
 Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu Asp
 235 240 245
 aat gaa tct cgt tct tgg aga aga tgatttgact gatcattgat ctgcatatgc 947
 Asn Glu Ser Arg Ser Trp Arg Arg
 250
 tagaactcta cctgtgtttc attagtatta tctaattgtac ttttacatat ttgtaaaaac 1007
 aatttttgggt aaaatgtgat gaagatggat ttcacaaata gacaaaaaag aagaaaacta 1067
 ccttctgac ttgtattttg aaagattgat gtttgcattt tacttcagta aacaattgct 1127
 aaagacatca cactagaaac atatgcaatg tttttattac atacttctac tggacatcac 1187
 agaattcttt gggttctttg taatttaatg aataggtctg aaaacttatg accaatactt 1247
 gttataactt agaggacttt gttttattcc aaataaggaa tgaatttgca tttaaaatct 1307
 taatgaatgt tttcaaaact gaatagataa catagtactc taactaaagt ctccaagtta 1367
 tgtattataa tattacatag tagtatgctt aggctttact atgtattagc cttttgttgg 1427
 actgtgtatg tattttacca tatgggtttt aatgataatg gtgtatgact gctttacatg 1487
 agtccttatg catccagatg ttataataaa gtggaatggt ctcttttaaaa aaaaaaaagg 1547
 aaagaaaaga gaaaagcaat gac 1570

<210> 154

<211> 254

<212> PRT

<213> Homo sapiens

<400> 154

Met Leu Ile Ser Lys Leu Glu Lys Asn Lys Thr Met Lys Ser Glu Asp
 1 5 10 15
 Lys Ala Glu Ile Met Lys Thr Leu Glu Val Leu Thr Lys Asn Ile Thr
 20 25 30
 Lys Leu Lys Asp Glu Val Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro
 35 40 45
 Lys Ser Ile Lys Thr Lys Thr Gln Met Gln Lys Glu Leu Leu Asp Thr
 50 55 60
 Glu Leu Asp Leu Tyr Lys Lys Met Gln Ala Gly Glu Glu Val Thr Glu
 65 70 75 80
 Leu Arg Arg Lys Tyr Thr Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly
 85 90 95
 Ile Leu Ser Ser Gly Arg Gly Arg Gly Ile His Ser Arg Gly Arg Gly
 100 105 110
 Ala Val His Gly Arg Gly Arg Gly Arg Gly Arg Gly Val Pro
 115 120 125
 Gly His Ala Val Val Asp His Arg Pro Arg Ala Leu Glu Ile Ser Ala
 130 135 140
 Phe Thr Glu Ser Asp Arg Glu Asp Leu Leu Pro His Phe Ala Gln Tyr
 145 150 155 160
 Gly Glu Ile Glu Asp Cys Gln Ile Asp Asp Ser Ser Leu His Ala Val
 165 170 175
 Ile Thr Phe Lys Thr Arg Ala Glu Ala Glu Ala Ala Val His Gly
 180 185 190
 Ala Arg Phe Lys Gly Gln Asp Leu Lys Leu Ala Trp Asn Lys Pro Val

195 200 205
 Thr Asn Ile Ser Ala Val Glu Thr Glu Glu Val Glu Pro Asp Glu Glu
 210 215 220
 Glu Phe Gln Glu Glu Ser Leu Val Asp Asp Ser Leu Leu Gln Asp Asp
 225 230 235 240
 Asp Glu Glu Glu Glu Asp Asn Glu Ser Arg Ser Trp Arg Arg
 245 250

<210> 155

<211> 2661

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6)..(2045)

<400> 155

tttgt atg aga gga gac atg tgt cct ttt gat cat gga agt gat cca gta 50

Met Arg Gly Asp Met Cys Pro Phe Asp His Gly Ser Asp Pro Val

1 5 10 15

gtt gta gaa gat gtg aat ctt cct ggt atg ctg cct ttc cca gca cag 98

Val Val Glu Asp Val Asn Leu Pro Gly Met Leu Pro Phe Pro Ala Gln

20 25 30

cct cct gtt gtt gaa gga cca cct cct cct gga ctc ccc cca cct cca 146

Pro Pro Val Val Glu Gly Pro Pro Pro Pro Gly Leu Pro Pro Pro Pro

35 40 45

cca att ctt aca ccc cca cct gtg aat ctc agg ccc cca gta cca cag 194

Pro Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro

50	55	60	
cca ggt cca ttg cca ccc agt ctc cca cct gtt aca gga cca cca cct			242
Pro Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro			
65	70	75	
cca ctt cct cct ttg cag cca tct ggc atg gat gct cct cca aac tct			290
Pro Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser			
80	85	90	95
gca acc agt tct gtt cct act gta gta aca act ggc att cat cac cag			338
Ala Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln			
100	105	110	
cct cct cct gct cca ccc tct ctt ttt act gca gat aca tat gac aca			386
Pro Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr			
115	120	125	
gat ggc tac aat cct gaa gcc cca agc ata aca aac act tcc aga cct			434
Asp Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro			
130	135	140	
atg tat aga cac aga gtg cat gca caa agg ccc aac ttg ata gga cta			482
Met Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu			
145	150	155	
aca tca ggg gat atg gat ttg cca ccc aga gaa aag cct ccc aat aaa			530
Thr Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys			
160	165	170	175
agc agt atg agg ata gta gtg gac tca gaa tca agg aaa aga acc att			578
Ser Ser Met Arg Ile Val Val Asp Ser Glu Ser Arg Lys Arg Thr Ile			
180	185	190	
ggt tct gga gag cct gga gtt cct aca aag aag act tgg ttt gat aaa			626
Gly Ser Gly Glu Pro Gly Val Pro Thr Lys Lys Thr Trp Phe Asp Lys			

195	200	205	
cca aat ttt aat aga aca aac agc cca ggc ttt cag aag aag gtt caa	674		
Pro Asn Phe Asn Arg Thr Asn Ser Pro Gly Phe Gln Lys Lys Val Gln			
210	215	220	
ttt gga aat gaa aat acc aag ctt gaa ctt aga aaa gtt cct cca gaa	722		
Phe Gly Asn Glu Asn Thr Lys Leu Glu Leu Arg Lys Val Pro Pro Glu			
225	230	235	
tta aat aat atc agc aaa ctt aat gaa cat ttt agt cga ttt gga acc	770		
Leu Asn Asn Ile Ser Lys Leu Asn Glu His Phe Ser Arg Phe Gly Thr			
240	245	250	255
ttg gtt aac tta cag gtt gct tat aat ggt gat cct gaa ggt gcc cta	818		
Leu Val Asn Leu Gln Val Ala Tyr Asn Gly Asp Pro Glu Gly Ala Leu			
260	265	270	
atc caa ttt gca aca tac gaa gaa gca aag aaa gca ata tca agt acg	866		
Ile Gln Phe Ala Thr Tyr Glu Glu Ala Lys Lys Ala Ile Ser Ser Thr			
275	280	285	
gaa gca gta tta aac aat cgc ttt att aag gtt tat tgg cac aga gaa	914		
Glu Ala Val Leu Asn Asn Arg Phe Ile Lys Val Tyr Trp His Arg Glu			
290	295	300	
gga agc acc caa cag tta caa act act tct cca aag gta atg cag cct	962		
Gly Ser Thr Gln Gln Leu Gln Thr Thr Ser Pro Lys Val Met Gln Pro			
305	310	315	
tta gtc cag cag ccc att ttg cct gtt gtg aag cag tca gtc aaa gag	1010		
Leu Val Gln Gln Pro Ile Leu Pro Val Val Lys Gln Ser Val Lys Glu			
320	325	330	335
cgg ctg ggt cca gta cct tca agt act att gaa cct gca gaa gcc cag	1058		
Arg Leu Gly Pro Val Pro Ser Ser Thr Ile Glu Pro Ala Glu Ala Gln			

340	345	350	
agt gcc tct tca gac ctt cct cag gtg ttg tct aca tct act ggc cta			1106
Ser Ala Ser Ser Asp Leu Pro Gln Val Leu Ser Thr Ser Thr Gly Leu			
355	360	365	
aca aaa aca gtg tat aat cca gct gct ttg aag gct gca cag aaa acc			1154
Thr Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr			
370	375	380	
tta ctt gtt tcc acc tct gca gtt gat aat aat gaa gca cag aaa aaa			1202
Leu Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys			
385	390	395	
aaa cag gag gca ttg aaa ctt cag cag gat gta agg aaa agg aaa caa			1250
Lys Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln			
400	405	410	415
gaa att tta gaa aag cac att gaa aca cag aag atg tta att tca aaa			1298
Glu Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys			
420	425	430	
ctg gag aaa aac aaa aca atg aag tct gaa gat aaa gca gaa ata atg			1346
Leu Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met			
435	440	445	
aaa act tta gag gtt ttg aca aaa aat att acc aag ttg aaa gat gag			1394
Lys Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu			
450	455	460	
gtc aaa gct gct tct cct gga cgc tgt ctt cca aaa agt ata aaa acc			1442
Val Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr			
465	470	475	
aag act cag atg cag aag gaa tta ctt gac aca gaa ctg gat tta tat			1490

Lys Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr
 480 485 490 495
 aag aag atg cag gct gga gaa gaa gtc act gaa ctt agg aga aag tat 1538
 Lys Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr
 500 505 510
 aca gaa tta cag ctg gaa gct gcc aaa cga ggg att ctt tca tct ggt 1586
 Thr Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly
 515 520 525
 cgg ggc aga gga att cat tca aga ggt cga ggt gca gtt cat ggc cga 1634
 Arg Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg
 530 535 540
 ggc agg ggg cga ggg cga ggg cga ggt gtg cct ggt cat gct gtg gtg 1682
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val
 545 550 555
 gat cac cgt ccc agg gca ttg gag att tct gca ttt acg gag agc gat 1730
 Asp His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp
 560 565 570 575
 aga gaa gat ctt ctt cct cat ttt gcg caa tat ggt gaa att gaa gat 1778
 Arg Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp
 580 585 590
 tgt cag att gat gat tcc tca ctt cat gca gta att aca ttc aag aca 1826
 Cys Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr
 595 600 605
 aga gca gaa gct gaa gca gct gca gtt cat gga gct cgt ttc aaa ggg 1874
 Arg Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly
 610 615 620
 caa gat cta aaa ctg gca tgg aat aaa cca gta act aat att tca gct 1922

Gln Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala
 625 630 635
 gtt gaa aca gaa gaa gtt ggg cct gat gaa gaa gaa ttt cag gaa gag 1970
 Val Glu Thr Glu Glu Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu
 640 645 650 655
 tct ttg gtg gat gac tca tta ctt caa gat gat gat gaa gaa gaa gag 2018
 Ser Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu
 660 665 670
 gac aat gaa tct cgt tct tgg aga aga tgatttgact gatcattgat 2065
 Asp Asn Glu Ser Arg Ser Trp Arg Arg
 675 680
 ctgcatatgc tagaactcta cctgtgtttc attagtatta tctaattgtac ttttacatat 2125
 ttgtaaaaac aatTTTTTggt aaaatgtgat gaagatggat ttcacaaata gacaaaaaag 2185
 aagaaaacta ccttctgatac ttgtatTTTg aaagattgat gtttgcattt tacttcagta 2245
 aacaattgct aaagacatca cactagaaac atatgcaatg tttttattac atacttctac 2305
 tggacatcac agaattcttt gggttctttg taatttaatg aataggtctg aaaacttatg 2365
 accaataactt gttataactt agaggacttt gttttattcc aaataaggaa tgaatttgca 2425
 tttaaaatct taatgaatgt tttcaaaact gaatagataa catagtactc taactaaagt 2485
 ctccaagtta tgtattataa tattacatag tagtatgctt aggctttact atgtattagc 2545
 cttttgttgg actgtgtatg tattttacca taagggtttt aatgataatg gtgtatgact 2605
 gctttacatg agtccttatg catccagatg ttataataaa gtggaatggc ctcttt 2661

<210> 156

<211> 680

<212> PRT

<213> Homo sapiens

<400> 156

Met Arg Gly Asp Met Cys Pro Phe Asp His Gly Ser Asp Pro Val Val
 1 5 10 15
 Val Glu Asp Val Asn Leu Pro Gly Met Leu Pro Phe Pro Ala Gln Pro
 20 25 30
 Pro Val Val Glu Gly Pro Pro Pro Pro Gly Leu Pro Pro Pro Pro Pro
 35 40 45
 Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro Pro
 50 55 60
 Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro Pro
 65 70 75 80
 Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser Ala
 85 90 95
 Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln Pro
 100 105 110
 Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr Asp
 115 120 125
 Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro Met
 130 135 140
 Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu Thr
 145 150 155 160
 Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys Ser
 165 170 175
 Ser Met Arg Ile Val Val Asp Ser Glu Ser Arg Lys Arg Thr Ile Gly
 180 185 190
 Ser Gly Glu Pro Gly Val Pro Thr Lys Lys Thr Trp Phe Asp Lys Pro
 195 200 205
 Asn Phe Asn Arg Thr Asn Ser Pro Gly Phe Gln Lys Lys Val Gln Phe

210	215	220	
Gly Asn Glu Asn Thr Lys Leu Glu Leu Arg Lys Val Pro Pro Glu Leu			
225	230	235	240
Asn Asn Ile Ser Lys Leu Asn Glu His Phe Ser Arg Phe Gly Thr Leu			
	245	250	255
Val Asn Leu Gln Val Ala Tyr Asn Gly Asp Pro Glu Gly Ala Leu Ile			
	260	265	270
Gln Phe Ala Thr Tyr Glu Glu Ala Lys Lys Ala Ile Ser Ser Thr Glu			
	275	280	285
Ala Val Leu Asn Asn Arg Phe Ile Lys Val Tyr Trp His Arg Glu Gly			
	290	295	300
Ser Thr Gln Gln Leu Gln Thr Thr Ser Pro Lys Val Met Gln Pro Leu			
305	310	315	320
Val Gln Gln Pro Ile Leu Pro Val Val Lys Gln Ser Val Lys Glu Arg			
	325	330	335
Leu Gly Pro Val Pro Ser Ser Thr Ile Glu Pro Ala Glu Ala Gln Ser			
	340	345	350
Ala Ser Ser Asp Leu Pro Gln Val Leu Ser Thr Ser Thr Gly Leu Thr			
	355	360	365
Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr Leu			
	370	375	380
Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys Lys			
385	390	395	400
Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln Glu			
	405	410	415
Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys Leu			
	420	425	430

Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys
435 440 445
Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val
450 455 460
Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys
465 470 475 480
Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys
485 490 495
Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr
500 505 510
Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg
515 520 525
Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg Gly
530 535 540
Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val Asp
545 550 555 560
His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp Arg
565 570 575
Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp Cys
580 585 590
Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr Arg
595 600 605
Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln
610 615 620
Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala Val
625 630 635 640
Glu Thr Glu Glu Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu Ser

	645	650	655
Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu Asp			
	660	665	670
Asn Glu Ser Arg Ser Trp Arg Arg			
	675	680	

<210> 157

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128).. (883)

<400> 157

cacgcgagtt cccgtctttc ctggctgtcc tccttgggtt cgggtgaaag cgcttggggg 60
 ttcagtgggc catgatcccc gagctgctgg agaactgaag gcggacggtc tcctgcgaaa 120
 ccaggca atg gcg gag ctg gag ttt gtt cag atc atc atc atc gtg gtg 169

Met Ala Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val

1

5

10

gtg atg atg gtg atg gtg gtg gtg atc acg tgc ctg ctg agc cac tac 217

Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His Tyr

15

20

25

30

aag ctg tct gca cgg tcc ttc atc agc cgg cac agc cag ggg cgg agg 265

Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg

35

40

45

aga gaa gat gcc ctg tcc tca gaa gga tgc ctg tgg ccc tcg gag agc 313

Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser

50	55	60	
aca gtg tca ggc aac gga atc cca gag ccg cag gtc tac gcc ccg cct			361
Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro			
65	70	75	
cgg ccc acc gac cgc ctg gcc gtg ccg ccc ttc gcc cag cgg gag cgc			409
Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg			
80	85	90	
ttc cac cgc ttc cag ccc acc tat ccg tac ctg cag cac gag atc gac			457
Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp			
95	100	105	110
ctg ccg ccc acc atc tcg ctg tca gac ggg gag gag ccc cca ccc tac			505
Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr			
115	120	125	
cag ggc ccc tgc acc ctc cag ctt cgg gac ccc gag cag cag ctg gaa			553
Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu			
130	135	140	
ctg aac cgg gag tcg gtg cgc gca ccc cca aac aga acc atc ttc gac			601
Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp			
145	150	155	
agt gac ctg atg gat agt gcc agg ctg ggc ggc ccc tgc ccc ccc agc			649
Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser			
160	165	170	
agt aac tcg ggc atc agc gcc acg tgc tac ggc agc ggc ggg cgc atg			697
Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met			
175	180	185	190
gag ggg ccg ccg ccc acc tac agc gag gtc atc ggc cac tac ccg ggg			745
Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly			

195	200	205	
tcc tcc ttc cag cac cag cag agc agt ggg ccg ccc tcc ttg ctg gag			793
Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu			
210	215	220	
ggg acc cgg ctc cac cac aca cac atc gcg ccc cta gag agc gca gcc			841
Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala			
225	230	235	
atc tgg agc aaa gag aag gat aaa cag aaa gga cac cct ctc			883
Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu			
240	245	250	
taggggtcccc agggggggccg ggctggggct gcgtaggtga aaaggcagaa cactccgcgc			943
ttcttagaag aggagtgaga ggaaggcggg gggcgcagca acgcatcgtg tggccctccc			1003
ctccacctc cctgtgtata aatatttaca tgtgatgtct ggtctgaatg cacaagctaa			1063
gagagcttgc aaaaaaaaaa ag			1085

<210> 158

<211> 252

<212> PRT

<213> Homo sapiens

<400> 158

Met	Ala	Glu	Leu	Glu	Phe	Val	Gln	Ile	Ile	Ile	Ile	Val	Val	Val	Met
1					5					10				15	
Met	Val	Met	Val	Val	Val	Ile	Thr	Cys	Leu	Leu	Ser	His	Tyr	Lys	Leu
					20					25				30	
Ser	Ala	Arg	Ser	Phe	Ile	Ser	Arg	His	Ser	Gln	Gly	Arg	Arg	Arg	Glu
					35					40				45	
Asp	Ala	Leu	Ser	Ser	Glu	Gly	Cys	Leu	Trp	Pro	Ser	Glu	Ser	Thr	Val

50 55 60
Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro
65 70 75 80
Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe His
85 90 95
Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu Pro
100 105 110
Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly
115 120 125
Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn
130 135 140
Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp
145 150 155 160
Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn
165 170 175
Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly
180 185 190
Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser
195 200 205
Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr
210 215 220
Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp
225 230 235 240
Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
245 250

<210> 159

<211> 1383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (321).. (1181)

<400> 159

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 ttccggacgc caccgcggg cactgccgac gccccgggg ctgccgaggg gaggcgggg 120
 gggcgcagcg gagcgcggtc ccgcgcactg agccccgcgg cgccccggga acttggcggc 180
 gacccgagcc cggcgagccg gggcgcgcct cccccgccgc gcgcctcctg catgcggggc 240
 cccagctccg ggcgccggcc ggagcccccc ccggccgccc ccgagcccc cgcgccccgc 300
 gccgcgccgc cgcgccgtcc atg cac cgc ttg atg ggg gtc aac agc acc gcc 353

Met His Arg Leu Met Gly Val Asn Ser Thr Ala

1

5

10

gcc gcc gcc gcc ggg cag ccc aat gtc tcc tgc acg tgc aac tgc aaa 401
 Ala Ala Ala Ala Gly Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys

15

20

25

cgc tct ttg ttc cag agc atg gag atc acg gag ctg gag ttt gtt cag 449
 Arg Ser Leu Phe Gln Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln

30

35

40

atc atc atc atc gtg gtg gtg atg atg gtg atg gtg gtg atc acg 497
 Ile Ile Ile Ile Val Val Val Met Met Val Met Val Val Val Ile Thr

45

50

55

tgc ctg ctg agc cac tac aag ctg tct gca cgg tcc ttc atc agc cgg 545
 Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg

60

65

70

75

cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa gga tgc	593
His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys	
80 85 90	
ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca gag ccg	641
Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro	
95 100 105	
cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg ccg ccc	689
Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro	
110 115 120	
ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat ccg tac	737
Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr	
125 130 135	
ctg cag cac gag atc gac ctg ccg ccc acc atc tcg ctg tca gac ggg	785
Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly	
140 145 150 155	
gag gag ccc cca ccc tac cag ggc ccc tgc acc ctc cag ctt cgg gac	833
Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp	
160 165 170	
ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca ccc cca	881
Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro	
175 180 185	
aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg ctg ggc	929
Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly	
190 195 200	
ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg tgc tac	977
Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr	
205 210 215	

ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc gag gtc 1025
 Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val
 220 225 230 235
 atc ggc cac tac ccg ggg tcc tcc ttc cag cac cag cag agc agt ggg 1073
 Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly
 240 245 250
 ccg ccc tcc ttg ctg gag ggg acc cgg ctc cac cac aca cac atc gcg 1121
 Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His Ile Ala
 255 260 265
 ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa cag aaa 1169
 Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys
 270 275 280
 gga cac cct ctc taggggtcccc agggggggccg ggctggggct gcgtaggtga 1221
 Gly His Pro Leu
 285
 aaaggcagaa cactccgcgc ttcttagaag aggagtgaga ggaaggcggg gggcgcagca 1281
 acgcacgtg tggccctccc ctccacctc cctgtgtata aatatttaca tgtgatgtct 1341
 ggtctgaatg cacaagctaa gagagcttgc aaaaaaaaaa ag 1383

<210> 160

<211> 287

<212> PRT

<213> Homo sapiens

<400> 160

Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly
 1 5 10 15
 Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln

	20	25	30
Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val			
	35	40	45
Val Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His			
	50	55	60
Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg			
	65	70	75
Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu			
	85	90	95
Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro			
	100	105	110
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu			
	115	120	125
Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile			
	130	135	140
Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro			
	145	150	155
Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu			
	165	170	175
Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe			
	180	185	190
Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro			
	195	200	205
Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg			
	210	215	220
Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro			
	225	230	235
			240

Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu
 245 250 255
 Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala
 260 265 270
 Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
 275 280 285

<210> 161

<211> 761

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (138).. (623)

<400> 161

attaaaccag tccccattgc gctggcctcc acttgcttac ttggggcgcg aggaggttgg 60
 agagcttttt tctgggaccc aagcaaaggc atccacgctg ctgctaagct gaaattgaag 120
 ctcacacatc ctggaaa atg cta gca ccc ata cca gaa ccc aag cct gga 170
 Met Leu Ala Pro Ile Pro Glu Pro Lys Pro Gly
 1 5 10
 gac ctg att gag att ttc cgc cct atg tac aga cac tgg gcc atc tat 218
 Asp Leu Ile Glu Ile Phe Arg Pro Met Tyr Arg His Trp Ala Ile Tyr
 15 20 25
 gtt ggt gat gga tac gtg atc cac ctg gct cct cca agt gaa atc gca 266
 Val Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu Ile Ala
 30 35 40
 gga gct ggg gca gcc agc atc atg tct gct ttg act gac aag gcc ata 314

Gly Ala Gly Ala Ala Ser Ile Met Ser Ala Leu Thr Asp Lys Ala Ile
 45 50 55
 gtg aag aaa gaa ctg ctg tgc cat gtg gcc ggg aag gac aag tac cag 362
 Val Lys Lys Glu Leu Leu Cys His Val Ala Gly Lys Asp Lys Tyr Gln
 60 65 70 75
 gtc aat aac aaa cat gac gag gag tac acc cca ctg cct ctg agc aag 410
 Val Asn Asn Lys His Asp Glu Glu Tyr Thr Pro Leu Pro Leu Ser Lys
 80 85 90
 atc atc cag cgg gct gag aga ctg gtg ggg cag gag gtg ctc tac agg 458
 Ile Ile Gln Arg Ala Glu Arg Leu Val Gly Gln Glu Val Leu Tyr Arg
 95 100 105
 ctg acc agc gag aac tgt gag cac ttt gtg aat gaa cta cgc tat gga 506
 Leu Thr Ser Glu Asn Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly
 110 115 120
 gtt cct cgg agt gat cag gtc aga gat gcg gtc aag gcg gta ggc atc 554
 Val Pro Arg Ser Asp Gln Val Arg Asp Ala Val Lys Ala Val Gly Ile
 125 130 135
 gct gga gtg ggc ttg gcg gcc ttg ggc ctc gtt gga gtc atg ctc tcc 602
 Ala Gly Val Gly Leu Ala Ala Leu Gly Leu Val Gly Val Met Leu Ser
 140 145 150 155
 aga aac aag aaa cag aag caa tgagctgaat gactgccag tttttgggct 653
 Arg Asn Lys Lys Gln Lys Gln
 160
 cttcttttgc tagagggttt ggagtttgat ttatagattc tattgcttta taattagggtt 713
 tattttcaca acatacaata aaccacaaga aaggaatttt tgtgagga 761

<210> 162

<211> 162

<212> PRT

<213> Mus musculus

<400> 162

Met Leu Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Met Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30
Val Ile His Leu Ala Pro Pro Ser Glu Ile Ala Gly Ala Gly Ala Ala
35 40 45
Ser Ile Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60
Leu Cys His Val Ala Gly Lys Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80
Asp Glu Glu Tyr Thr Pro Leu Pro Leu Ser Lys Ile Ile Gln Arg Ala
85 90 95
Glu Arg Leu Val Gly Gln Glu Val Leu Tyr Arg Leu Thr Ser Glu Asn
100 105 110
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Pro Arg Ser Asp
115 120 125
Gln Val Arg Asp Ala Val Lys Ala Val Gly Ile Ala Gly Val Gly Leu
130 135 140
Ala Ala Leu Gly Leu Val Gly Val Met Leu Ser Arg Asn Lys Lys Gln
145 150 155 160
Lys Gln

<210> 163

<211> 676

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55).. (540)

<400> 163

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acatctacgc agcgaaatcg agcctggcct tgagggtcca caccgcgagg gaag atg 57
                                         Met
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cgt gcg ccc att cca gag cct aag cct gga gac ctg att gag att ttt 105
Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile Phe
          5              10              15

cgc cct ttc tac aga cac tgg gcc atc tat gtt ggc gat gga tat gtg 153
Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr Val
          20              25              30

gtt cat ctg gcc cct cca agt gag gtc gca gga gct ggt gca gcc agt 201
Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala Ser
          35              40              45

gtc atg tcc gcc ctg act gac aag gcc atc gtg aag aag gaa ttg ctg 249
Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu Leu
          50              55              60              65

tat gat gtg gcc ggg agt gac aag tac cag gtc aac aac aaa cat gat 297
Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His Asp
          70              75              80

gac aag tac tcg ccg ctg ccc tgc agc aaa atc atc cag cgg gcg gag 345
Asp Lys Tyr Ser Pro Leu Pro Cys Ser Lys Ile Ile Gln Arg Ala Glu

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85	90	95	
gag ctg gtg ggg cag gag gtg ctc tac aag ctg acc agt gag aac tgc			393
Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn Cys			
100	105	110	
gag cac ttt gtg aat gag ctg cgc tat gga gtc gcc cgc agt gac cag			441
Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp Gln			
115	120	125	
gtc aga gat gtc atc atc gct gca agc gtt gca gga atg ggc ttg gca			489
Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu Ala			
130	135	140	145
gcc atg agc ctt att gga gtc atg ttc tca aga aac aag cga caa aag			537
Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln Lys			
150	155	160	
caa taactgaaaa agactgtcct gtcagc gatg actttataca tcaagggggt			590
Gln			
cttgttttgc tagagagttt ggggtttggt ttgtggattt cattgtgatt tataataagg			650
cttattttca cagaataaaa taaagc			676

<210> 164

<211> 162

<212> PRT

<213> Homo sapiens

<400> 164

Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile

1

5

10

15

Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr

20

25

30

Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
 35 40 45
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
 50 55 60
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
 65 70 75 80
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Ser Lys Ile Ile Gln Arg Ala
 85 90 95
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
 100 105 110
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
 115 120 125
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
 130 135 140
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
 145 150 155 160
 Lys Gln

<210> 165

<211> 2126

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (37)..(1743)

<400> 165

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																1						5
agg	ggg	ctc	agc	ggc	gag	agc	cca	acg	cag	tgc	cga	tgg	gga	tac	ttg	102						
Arg	Gly	Leu	Ser	Gly	Glu	Ser	Pro	Thr	Gln	Cys	Arg	Trp	Gly	Tyr	Leu							
				10					15					20								
tcg	ctg	ctg	gtg	ctg	acg	ctg	agc	ggc	tgc	tca	ggc	cgt	atc	cac	cgg	150						
Ser	Leu	Leu	Val	Leu	Thr	Leu	Ser	Gly	Cys	Ser	Gly	Arg	Ile	His	Arg							
				25					30					35								
ctg	act	ctc	aca	ggg	gag	aag	cga	gct	gac	atc	caa	ctg	aac	agc	ttc	198						
Leu	Thr	Leu	Thr	Gly	Glu	Lys	Arg	Ala	Asp	Ile	Gln	Leu	Asn	Ser	Phe							
				40					45					50								
gga	ttc	tac	acc	aat	ggt	tcc	ctg	gaa	gta	gag	ctg	agc	tta	ctg	cga	246						
Gly	Phe	Tyr	Thr	Asn	Gly	Ser	Leu	Glu	Val	Glu	Leu	Ser	Leu	Leu	Arg							
				55					60					65				70				
ctc	agc	ctc	cag	gag	aca	gaa	aag	aag	ttg	cca	aag	gtg	ggg	ttc	agc	294						
Leu	Ser	Leu	Gln	Glu	Thr	Glu	Lys	Lys	Leu	Pro	Lys	Val	Gly	Phe	Ser							
				75					80					85								
ttg	agc	aga	gtt	cgg	tct	ggc	agt	gtc	cgc	tcc	tac	tcg	aga	cgg	aac	342						
Leu	Ser	Arg	Val	Arg	Ser	Gly	Ser	Val	Arg	Ser	Tyr	Ser	Arg	Arg	Asn							
				90					95					100								
tcc	cat	gaa	tgc	cct	ctg	gat	aga	aac	agc	agc	aac	ttc	ctg	gtc	ctg	390						
Ser	His	Glu	Cys	Pro	Leu	Asp	Arg	Asn	Ser	Ser	Asn	Phe	Leu	Val	Leu							
				105					110					115								
ttc	ctc	atc	aat	atc	aag	gac	ctg	cag	gtc	caa	gtc	cga	aaa	tat	ggg	438						
Phe	Leu	Ile	Asn	Ile	Lys	Asp	Leu	Gln	Val	Gln	Val	Arg	Lys	Tyr	Gly							
				120					125					130								
gag	cag	aag	ttg	ttc	atc	tcc	cct	ggc	ctt	ctc	cct	gaa	gct	ccc	acc	486						

Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu Leu Pro Glu Ala Pro Thr
 135 140 145 150
 cag tca ggt ccc ccg aaa cca gac cca gca ggc acc ccc aag gac aac 534
 Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala Gly Thr Pro Lys Asp Asn
 155 160 165
 cac gtc att cac cca tct cct aca gag atg tct gca gtc aag gag aat 582
 His Val Ile His Pro Ser Pro Thr Glu Met Ser Ala Val Lys Glu Asn
 170 175 180
 cag aca gcg ccc cag gtt tca ggg gat aaa act acc cca ggg gaa cac 630
 Gln Thr Ala Pro Gln Val Ser Gly Asp Lys Thr Thr Pro Gly Glu His
 185 190 195
 agg cac tca tcc gag aga cag cca ccc acg cag gac ccc agt ggg aag 678
 Arg His Ser Ser Glu Arg Gln Pro Pro Thr Gln Asp Pro Ser Gly Lys
 200 205 210
 gag aag gat cag gtg ttg gga ctg ggc cac ctc aat gac tcc tac aac 726
 Glu Lys Asp Gln Val Leu Gly Leu Gly His Leu Asn Asp Ser Tyr Asn
 215 220 225 230
 ttc agt ttc cac att gtg atc agc tcc agg gct gag gaa ggc cag tac 774
 Phe Ser Phe His Ile Val Ile Ser Ser Arg Ala Glu Glu Gly Gln Tyr
 235 240 245
 agc ctc aac ttc cac aac tgt cac aac tcc atc cca ggc cag gag cag 822
 Ser Leu Asn Phe His Asn Cys His Asn Ser Ile Pro Gly Gln Glu Gln
 250 255 260
 cca ttc gac ctc act gtg atg atc cgg gag aag aat cca gaa ggc ttc 870
 Pro Phe Asp Leu Thr Val Met Ile Arg Glu Lys Asn Pro Glu Gly Phe
 265 270 275
 ttg tca gca gcc gaa atc ccc ctc ttc aaa ctc tac ctg atc atg tct 918

Leu Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser
 280 285 290
 gcc tgc ttt ctg gcc gca gac atc ttc tgg gtg tcc gtg ctc tgc aag 966
 Ala Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys
 295 300 305 310
 aac aca tac agt gtc ttc aag atc cac tgg ctc atg gca gcc ctg gcg 1014
 Asn Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala
 315 320 325
 ttc acc aag agt gtc tcc cta ctc ttc cac agc atc aac tac tac ttc 1062
 Phe Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe
 330 335 340
 atc aac agc cag ggc cac ccc atc gaa ggc ctc gcg gtc atg cac tat 1110
 Ile Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr
 345 350 355
 atc aca cac ctg ctg aag ggc gcc ctt ctc ttc atc acc atc gcc ttg 1158
 Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu
 360 365 370
 atc ggc tca ggc tgg gcc ttt gtg aag tat atg ctg tcg gac aag gag 1206
 Ile Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu
 375 380 385 390
 aag aag att ttt ggc att gtg att ccc ctg cag gtc ctg gct aat gta 1254
 Lys Lys Ile Phe Gly Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val
 395 400 405
 gca tac att gtc att gag tcc cgt gag gag ggt gcc agc gac tat gga 1302
 Ala Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly
 410 415 420
 ctc tgg aag gag atc ttg ttc ctg gtg gat ctc atc tgc tgt ggt gcc 1350

Leu Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala
 425 430 435
 atc ctt ttc ccg gtg gtc tgg tcc att cgg cat ctg cag gat gca tcc 1398
 Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser
 440 445 450
 ggc act gat ggg aag gtg gca gtg aac ctg gcc agg ctg aag ctg ttc 1446
 Gly Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe
 455 460 465 470
 cga cat tac tac gtc atg gtc atc tgc tat atc tac ttt aca cgt atc 1494
 Arg His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile
 475 480 485
 atc gcc att ctg ctg caa gta gca gtg ccc ttc cag tgg cag tgg ctg 1542
 Ile Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu
 490 495 500
 tac cag ctc ttg gtg gag agt tcc aca ctg gcc ttc ttc gtg ctc act 1590
 Tyr Gln Leu Leu Val Glu Ser Ser Thr Leu Ala Phe Phe Val Leu Thr
 505 510 515
 ggc tac aag ttc cag ccg gct ggg gac aac cca tac ctg cag ctg cca 1638
 Gly Tyr Lys Phe Gln Pro Ala Gly Asp Asn Pro Tyr Leu Gln Leu Pro
 520 525 530
 cag gag gat gag gag gac gta cag atg gag caa gtg atg aca gac tct 1686
 Gln Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser
 535 540 545 550
 ggg ttt cgg gaa ggc ctg tcc aaa gtt aac aag aca gcc agt ggc cgg 1734
 Gly Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg
 555 560 565
 gag ctg ttg tgacttcct gtgtccagt agccgccctc agacctcctg 1783

Glu Leu Leu

cacctcgcac ccctacactt gtcccaagtg tgcagggagc tggaggggat gctgcggaca 1843
 aggcattccag gatgtggatc cccaaggagc cttcagaaaa gatgccctct cctcaccagg 1903
 gagcaagcag ttcagcctct tgtggtacaa taaggaccag tctcttgact tggagggttc 1963
 tgagtatcta cggcaggctg catttatgat ctcagttcac ggggtggcac gtgcctgtca 2023
 tcccattgct ctggagagcc cgggcttcat aaaccttga ttagtaaaca aataaagaaa 2083
 aagtggaatt ccagtgagg ggaggaccac ctgttgagct aaa 2126

<210> 166

<211> 569

<212> PRT

<213> Mus musculus

<400> 166

Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln

1 5 10 15

Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys

20 25 30

Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp

35 40 45

Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val

50 55 60

Glu Leu Ser Leu Leu Arg Leu Ser Leu Gln Glu Thr Glu Lys Lys Leu

65 70 75 80

Pro Lys Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Ser Val Arg

85 90 95

Ser Tyr Ser Arg Arg Asn Ser His Glu Cys Pro Leu Asp Arg Asn Ser

100 105 110

Ser Asn Phe Leu Val Leu Phe Leu Ile Asn Ile Lys Asp Leu Gln Val
 115 120 125
 Gln Val Arg Lys Tyr Gly Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu
 130 135 140
 Leu Pro Glu Ala Pro Thr Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala
 145 150 155 160
 Gly Thr Pro Lys Asp Asn His Val Ile His Pro Ser Pro Thr Glu Met
 165 170 175
 Ser Ala Val Lys Glu Asn Gln Thr Ala Pro Gln Val Ser Gly Asp Lys
 180 185 190
 Thr Thr Pro Gly Glu His Arg His Ser Ser Glu Arg Gln Pro Pro Thr
 195 200 205
 Gln Asp Pro Ser Gly Lys Glu Lys Asp Gln Val Leu Gly Leu Gly His
 210 215 220
 Leu Asn Asp Ser Tyr Asn Phe Ser Phe His Ile Val Ile Ser Ser Arg
 225 230 235 240
 Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe His Asn Cys His Asn Ser
 245 250 255
 Ile Pro Gly Gln Glu Gln Pro Phe Asp Leu Thr Val Met Ile Arg Glu
 260 265 270
 Lys Asn Pro Glu Gly Phe Leu Ser Ala Ala Glu Ile Pro Leu Phe Lys
 275 280 285
 Leu Tyr Leu Ile Met Ser Ala Cys Phe Leu Ala Ala Asp Ile Phe Trp
 290 295 300
 Val Ser Val Leu Cys Lys Asn Thr Tyr Ser Val Phe Lys Ile His Trp
 305 310 315 320
 Leu Met Ala Ala Leu Ala Phe Thr Lys Ser Val Ser Leu Leu Phe His

	325		330		335										
Ser	Ile	Asn	Tyr	Tyr	Phe	Ile	Asn	Ser	Gln	Gly	His	Pro	Ile	Glu	Gly
	340		345		350										
Leu	Ala	Val	Met	His	Tyr	Ile	Thr	His	Leu	Leu	Lys	Gly	Ala	Leu	Leu
	355		360		365										
Phe	Ile	Thr	Ile	Ala	Leu	Ile	Gly	Ser	Gly	Trp	Ala	Phe	Val	Lys	Tyr
	370		375		380										
Met	Leu	Ser	Asp	Lys	Glu	Lys	Lys	Ile	Phe	Gly	Ile	Val	Ile	Pro	Leu
385			390		395									400	
Gln	Val	Leu	Ala	Asn	Val	Ala	Tyr	Ile	Val	Ile	Glu	Ser	Arg	Glu	Glu
	405		410		415										
Gly	Ala	Ser	Asp	Tyr	Gly	Leu	Trp	Lys	Glu	Ile	Leu	Phe	Leu	Val	Asp
	420		425		430										
Leu	Ile	Cys	Cys	Gly	Ala	Ile	Leu	Phe	Pro	Val	Val	Trp	Ser	Ile	Arg
	435		440		445										
His	Leu	Gln	Asp	Ala	Ser	Gly	Thr	Asp	Gly	Lys	Val	Ala	Val	Asn	Leu
	450		455		460										
Ala	Arg	Leu	Lys	Leu	Phe	Arg	His	Tyr	Tyr	Val	Met	Val	Ile	Cys	Tyr
465			470		475									480	
Ile	Tyr	Phe	Thr	Arg	Ile	Ile	Ala	Ile	Leu	Leu	Gln	Val	Ala	Val	Pro
	485		490		495										
Phe	Gln	Trp	Gln	Trp	Leu	Tyr	Gln	Leu	Leu	Val	Glu	Ser	Ser	Thr	Leu
	500		505		510										
Ala	Phe	Phe	Val	Leu	Thr	Gly	Tyr	Lys	Phe	Gln	Pro	Ala	Gly	Asp	Asn
	515		520		525										
Pro	Tyr	Leu	Gln	Leu	Pro	Gln	Glu	Asp	Glu	Glu	Asp	Val	Gln	Met	Glu
	530		535		540										

Gln Val Met Thr Asp Ser Gly Phe Arg Glu Gly Leu Ser Lys Val Asn
 545 550 555 560

Lys Thr Ala Ser Gly Arg Glu Leu Leu
 565

<210> 167

<211> 1820

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1686)

<400> 167

atg gca gtg agc gag agg agg ggg ctc agc ggc gag agc cca acg cag	48
Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln	
1 5 10 15	
tgc cga tgg gga tac ttg tcg ctg ctg gtg ctg acg ctg agc ggc tgc	96
Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys	
20 25 30	
tca ggc cgt atc cac cgg ctg act ctc aca ggg gag aag cga gct gac	144
Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp	
35 40 45	
atc caa ctg aac agc ttc gga ttc tac acc aat ggt tcc ctg gaa gta	192
Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val	
50 55 60	
gag ctg agc tta ctg cga ctc agc ctc cag gag aca gaa aag aag ttg	240
Glu Leu Ser Leu Leu Arg Leu Ser Leu Gln Glu Thr Glu Lys Lys Leu	

65	70	75	80	
cca aag gtg ggg ttc agc ttg agc aga gtt cgg tct ggc agt gtc cgc	288			
Pro Lys Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Ser Val Arg				
85	90	95		
tcc tac tcg aga cgg aac tcc cat gaa tgc cct ctg gat aga aac agc	336			
Ser Tyr Ser Arg Arg Asn Ser His Glu Cys Pro Leu Asp Arg Asn Ser				
100	105	110		
agc aac ttc ctg gtc ctg ttc ctc atc aat atc aag gac ctg cag gtc	384			
Ser Asn Phe Leu Val Leu Phe Leu Ile Asn Ile Lys Asp Leu Gln Val				
115	120	125		
caa gtc cga aaa tat ggg gag cag aag ttg ttc atc tcc cct ggc ctt	432			
Gln Val Arg Lys Tyr Gly Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu				
130	135	140		
ctc cct gaa gct ccc acc cag tca ggt ccc ccg aaa cca gac cca gca	480			
Leu Pro Glu Ala Pro Thr Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala				
145	150	155	160	
ggc acc ccc aag gac aac cac gag atg tct gca gtc aag gag aat cag	528			
Gly Thr Pro Lys Asp Asn His Glu Met Ser Ala Val Lys Glu Asn Gln				
165	170	175		
aca gcg ccc cag gtt tca ggg gat aaa act acc cca ggg gaa cac agg	576			
Thr Ala Pro Gln Val Ser Gly Asp Lys Thr Thr Pro Gly Glu His Arg				
180	185	190		
cac tca tcc gag aga cag cca ccc acg cag gac ccc agt ggg aag gag	624			
His Ser Ser Glu Arg Gln Pro Pro Thr Gln Asp Pro Ser Gly Lys Glu				
195	200	205		
aag gat cag gtg ttg gga ctg ggc cac ctc aat gac tcc tac aac ttc	672			
Lys Asp Gln Val Leu Gly Leu Gly His Leu Asn Asp Ser Tyr Asn Phe				

210	215	220	
agt ttc cac att gtg atc agc tcc agg gct gag gaa ggc cag tac agc	720		
Ser Phe His Ile Val Ile Ser Ser Arg Ala Glu Glu Gly Gln Tyr Ser			
225	230	235	240
ctc aac ttc cac aac tgt cac aac tcc atc cca ggc cag gag cag cca	768		
Leu Asn Phe His Asn Cys His Asn Ser Ile Pro Gly Gln Glu Gln Pro			
245	250	255	
ttc gac ctc act gtg atg atc cgg gag aag aat cca gaa ggc ttc ttg	816		
Phe Asp Leu Thr Val Met Ile Arg Glu Lys Asn Pro Glu Gly Phe Leu			
260	265	270	
tca gca gcc gaa atc ccc ctc ttc aaa ctc tac ctg atc atg tct gcc	864		
Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser Ala			
275	280	285	
tgc ttt ctg gcc gca gac atc ttc tgg gtg tcc gtg ctc tgc aag aac	912		
Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys Asn			
290	295	300	
aca tac agt gtc ttc aag atc cac tgg ctc atg gca gcc ctg gcg ttc	960		
Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe			
305	310	315	320
acc aag agt gtc tcc cta ctc ttc cac agc atc aac tac tac ttc atc	1008		
Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile			
325	330	335	
aac agc cag ggc cac ccc atc gaa ggc ctc gcg gtc atg cac tat atc	1056		
Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr Ile			
340	345	350	
aca cac ctg ctg aag ggc gcc ctt ctc ttc atc acc atc gcc ttg atc	1104		
Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile			

355	360	365	
ggc tca ggc tgg gcc ttt gtg aag tat atg ctg tcg gac aag gag aag	1152		
Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu Lys			
370	375	380	
aag att ttt ggc att gtg att ccc ctg cat gtc ctg gct aat gta gca	1200		
Lys Ile Phe Gly Ile Val Ile Pro Leu His Val Leu Ala Asn Val Ala			
385	390	395	400
tac att gtt att gag tcc cgt gag gag ggt gcc agc gac tat gga ctc	1248		
Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly Leu			
	405	410	415
tgg aag gag atc ttg ttc ctg gtg gat ctc atc tgc tgt ggt gcc atc	1296		
Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile			
	420	425	430
ctt ttc ccg gtg gtc tgg tcc att cgg cat ctg cag gat gca tcc ggc	1344		
Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly			
	435	440	445
act gat ggg aag gtg gca gtg aac ctg gcc agg ctg aag ctg ttc cga	1392		
Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe Arg			
	450	455	460
cat tac tac gtc atg gtc atc tgc tat atc tac ttt aca cgt atc atc	1440		
His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile Ile			
465	470	475	480
gcc att ctg ctg caa gta gca gtg ccc ttc cag tgg cag tgg ctg tac	1488		
Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr			
	485	490	495
cag ctc ttg gtg gag agt tcc aca ctg gcc ttc ttc gtg ctc act ggc	1536		
Gln Leu Leu Val Glu Ser Ser Thr Leu Ala Phe Phe Val Leu Thr Gly			

500 505 510
 tac aag ttc cag ccg gct ggg gac aac cca tac ctg cag ctg cca cag 1584
 Tyr Lys Phe Gln Pro Ala Gly Asp Asn Pro Tyr Leu Gln Leu Pro Gln
 515 520 525
 gag gat gag gag gac gta cag atg gag caa gtg atg aca gac tct ggg 1632
 Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly
 530 535 540
 ttt cgg gaa ggc ctg tcc aaa gtt aac aag aca gcc agt ggc cgg gag 1680
 Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu
 545 550 555 560
 ctg ttg tgatctcagt tcacgggggtg gcacgtgcct gtcatcccat tgctctggag 1736
 Leu Leu
 agcccggggct tcataaaacc ttgattagta aacaaataaa gaaaaagtgg aattcccagt 1796
 gaggggagga ccacctgttg agct 1820

<210> 168

<211> 562

<212> PRT

<213> Mus musculus

<400> 168

Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln

1

5

10

15

Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys

20

25

30

Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp

35

40

45

Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val

50		55		60											
Glu	Leu	Ser	Leu	Leu	Arg	Leu	Ser	Leu	Gln	Glu	Thr	Glu	Lys	Lys	Leu
65				70				75							80
Pro	Lys	Val	Gly	Phe	Ser	Leu	Ser	Arg	Val	Arg	Ser	Gly	Ser	Val	Arg
			85					90						95	
Ser	Tyr	Ser	Arg	Arg	Asn	Ser	His	Glu	Cys	Pro	Leu	Asp	Arg	Asn	Ser
		100						105						110	
Ser	Asn	Phe	Leu	Val	Leu	Phe	Leu	Ile	Asn	Ile	Lys	Asp	Leu	Gln	Val
		115						120						125	
Gln	Val	Arg	Lys	Tyr	Gly	Glu	Gln	Lys	Leu	Phe	Ile	Ser	Pro	Gly	Leu
		130						135						140	
Leu	Pro	Glu	Ala	Pro	Thr	Gln	Ser	Gly	Pro	Pro	Lys	Pro	Asp	Pro	Ala
145					150						155				160
Gly	Thr	Pro	Lys	Asp	Asn	His	Glu	Met	Ser	Ala	Val	Lys	Glu	Asn	Gln
				165						170					175
Thr	Ala	Pro	Gln	Val	Ser	Gly	Asp	Lys	Thr	Thr	Pro	Gly	Glu	His	Arg
		180								185					190
His	Ser	Ser	Glu	Arg	Gln	Pro	Pro	Thr	Gln	Asp	Pro	Ser	Gly	Lys	Glu
		195								200					205
Lys	Asp	Gln	Val	Leu	Gly	Leu	Gly	His	Leu	Asn	Asp	Ser	Tyr	Asn	Phe
		210								215					220
Ser	Phe	His	Ile	Val	Ile	Ser	Ser	Arg	Ala	Glu	Glu	Gly	Gln	Tyr	Ser
225						230					235				240
Leu	Asn	Phe	His	Asn	Cys	His	Asn	Ser	Ile	Pro	Gly	Gln	Glu	Gln	Pro
				245							250				255
Phe	Asp	Leu	Thr	Val	Met	Ile	Arg	Glu	Lys	Asn	Pro	Glu	Gly	Phe	Leu
		260									265				270

Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser Ala
275 280 285
Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys Asn
290 295 300
Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe
305 310 315 320
Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile
325 330 335
Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr Ile
340 345 350
Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile
355 360 365
Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu Lys
370 375 380
Lys Ile Phe Gly Ile Val Ile Pro Leu His Val Leu Ala Asn Val Ala
385 390 395 400
Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly Leu
405 410 415
Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile
420 425 430
Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly
435 440 445
Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe Arg
450 455 460
His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile Ile
465 470 475 480
Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr

485 490 495
 Gln Leu Leu Val Glu Ser Ser Thr Leu Ala Phe Phe Val Leu Thr Gly
 500 505 510
 Tyr Lys Phe Gln Pro Ala Gly Asp Asn Pro Tyr Leu Gln Leu Pro Gln
 515 520 525
 Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly
 530 535 540
 Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu
 545 550 555 560
 Leu Leu

<210> 169

<211> 1914

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)..(1656)

<400> 169

ggagtcgggg aggaggtggc tccagag atg gca gtg agc gag agg agg ggg ctc 54

Met Ala Val Ser Glu Arg Arg Gly Leu

1

5

ggc cgc ggg agc ccc gcg gag tgg ggg cag cgg cta ctt ctg gtg ctg 102

Gly Arg Gly Ser Pro Ala Glu Trp Gly Gln Arg Leu Leu Leu Val Leu

10

15

20

25

ctg ttg ggt ggc tgc tcc ggg cgc atc cac cgg ctg gcg ctg acg ggg 150

Leu Leu Gly Gly Cys Ser Gly Arg Ile His Arg Leu Ala Leu Thr Gly

30	35	40	
gag aag cga gcg gac atc cag ctg aac agc ttc ggt ttc tac acc aat			198
Glu Lys Arg Ala Asp Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn			
45	50	55	
ggc tct ctg gag gtg gag ttg agc gtc ctg cgg ctg ggc ctc cgg gag			246
Gly Ser Leu Glu Val Glu Leu Ser Val Leu Arg Leu Gly Leu Arg Glu			
60	65	70	
gca gaa gag aag tcc ctg ctg gtg ggg ttc agt ctc agc cgg gtt cgg			294
Ala Glu Glu Lys Ser Leu Leu Val Gly Phe Ser Leu Ser Arg Val Arg			
75	80	85	
tct ggc aga gtt cgc tcc tat tca acc cgg gat ttc cag gac tgc cct			342
Ser Gly Arg Val Arg Ser Tyr Ser Thr Arg Asp Phe Gln Asp Cys Pro			
90	95	100	105
ctc cag aaa aac agt agc agt ttc ctg gtc ctg ttc ctc atc aac acc			390
Leu Gln Lys Asn Ser Ser Ser Phe Leu Val Leu Phe Leu Ile Asn Thr			
110	115	120	
aag gat ctg cag gtc cag gtg cgg aag tat gga gag cag aag acg ttg			438
Lys Asp Leu Gln Val Gln Val Arg Lys Tyr Gly Glu Gln Lys Thr Leu			
125	130	135	
ttt atc ttt ccc ggg ctc ctc ccg gaa gca ccc tcc aaa cca ggg ctc			486
Phe Ile Phe Pro Gly Leu Leu Pro Glu Ala Pro Ser Lys Pro Gly Leu			
140	145	150	
ccg aag cca cag gcc aca gtc ccc cgc aag gtg gat ggc gga ggg acc			534
Pro Lys Pro Gln Ala Thr Val Pro Arg Lys Val Asp Gly Gly Gly Thr			
155	160	165	
tct gca gcc agc aag ccc aag tca aca ccc gca gtg att cag ggt cct			582
Ser Ala Ala Ser Lys Pro Lys Ser Thr Pro Ala Val Ile Gln Gly Pro			

170	175	180	185	
agt ggg aag gac aag gac	ctg gtg ttg ggc	ctg agc cac ctc aac aac	630	
Ser Gly Lys Asp Lys Asp	Leu Val Leu Gly Leu Ser	His Leu Asn Asn		
	190	195	200	
tcc tac aac ttc agt ttc	cac gtg gtg atc ggc	tct cag gcg gaa gaa	678	
Ser Tyr Asn Phe Ser Phe	His Val Val Ile Gly Ser	Gln Ala Glu Glu		
	205	210	215	
ggc cag tac agc ctg aac	ttc cac aac tgc aac	aat tca gtg cca gga	726	
Gly Gln Tyr Ser Leu Asn	Phe His Asn Cys Asn	Asn Ser Val Pro Gly		
	220	225	230	
aag gag cat cca ttc gac	atc acg gtg atg atc	cgg gag aag aac ccc	774	
Lys Glu His Pro Phe Asp	Ile Thr Val Met Ile Arg	Glu Lys Asn Pro		
	235	240	245	
gat ggc ttc ctg tcg gca	gcg gag atg ccc ctt	ttc aag ctc tac atg	822	
Asp Gly Phe Leu Ser Ala	Ala Glu Met Pro Leu Phe	Lys Leu Tyr Met		
	250	255	260	265
gtc atg tcc gcc tgc ttc	ctg gcc gct ggc atc	ttc tgg gtg tcc atc	870	
Val Met Ser Ala Cys Phe	Leu Ala Ala Gly Ile Phe	Trp Val Ser Ile		
	270	275	280	
ctc tgc agg aac acg tac	agc gtc ttc aag atc	cac tgg ctc atg gcg	918	
Leu Cys Arg Asn Thr Tyr	Ser Val Phe Lys Ile His	Trp Leu Met Ala		
	285	290	295	
gcc ttg gcc ttc acc aag	agc atc tct ctc ctc	ttc cac agc atc aac	966	
Ala Leu Ala Phe Thr Lys	Ser Ile Ser Leu Leu Phe	His Ser Ile Asn		
	300	305	310	
tac tac ttc atc aac agc	cag ggc cac ccc atc	gaa ggc ctt gcc gtc	1014	
Tyr Tyr Phe Ile Asn Ser	Gln Gly His Pro Ile Glu	Gly Leu Ala Val		

315	320	325	
atg tac tac atc gca cac ctg ctg aag ggc gcc ctc ctc ttc atc acc			1062
Met Tyr Tyr Ile Ala His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr			
330	335	340	345
atc gcc ctg att ggc tca ggc tgg gcc ttc atc aag tac gtc ctg tcg			1110
Ile Ala Leu Ile Gly Ser Gly Trp Ala Phe Ile Lys Tyr Val Leu Ser			
350	355	360	
gat aag gag aag aag gtc ttt ggg atc gtg atc ccc atg cag gtc ctg			1158
Asp Lys Glu Lys Lys Val Phe Gly Ile Val Ile Pro Met Gln Val Leu			
365	370	375	
gcc aac gtg gcc tac atc atc atc gag tcc cgc gag gaa ggc gcc agc			1206
Ala Asn Val Ala Tyr Ile Ile Ile Glu Ser Arg Glu Glu Gly Ala Ser			
380	385	390	
gac tac gtg ctg tgg aag gag att ttg ttc ctg gtg gac ctc atc tgc			1254
Asp Tyr Val Leu Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys			
395	400	405	
tgt ggt gcc atc ctg ttc ccc gta gtc tgg tcc atc cgg cat ctc cag			1302
Cys Gly Ala Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln			
410	415	420	425
gat gcg tct ggc aca gac ggg aag gtg gca gtg aac ctg gcc aag ctg			1350
Asp Ala Ser Gly Thr Asp Gly Lys Val Ala Val Asn Leu Ala Lys Leu			
430	435	440	
aag ctg ttc cgg cat tac tat gtc atg gtc atc tgc tac gtc tac ttc			1398
Lys Leu Phe Arg His Tyr Tyr Val Met Val Ile Cys Tyr Val Tyr Phe			
445	450	455	
acc cgc atc atc gcc atc ctg ctg cag gtg gct gtg ccc ttt cag tgg			1446
Thr Arg Ile Ile Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp			

460 465 470
 cag tgg ctg tac cag ctc ttg gtg gag ggc tcc acc ctg gcc ttc ttc 1494
 Gln Trp Leu Tyr Gln Leu Leu Val Glu Gly Ser Thr Leu Ala Phe Phe
 475 480 485
 gtg ctc acg ggc tac aag ttc cag ccc aca gga aac aac ccg tac ctg 1542
 Val Leu Thr Gly Tyr Lys Phe Gln Pro Thr Gly Asn Asn Pro Tyr Leu
 490 495 500 505
 cag ctg ccc cag gag gac gag gag gat gtt cag atg gag caa gta atg 1590
 Gln Leu Pro Gln Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met
 510 515 520
 acg gac tct ggg ttc cgg gaa ggc ctc tcc aaa gtc aac aaa aca gcc 1638
 Thr Asp Ser Gly Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala
 525 530 535
 agc ggg cgg gaa ctg tta tgatcacctc cacatctcag accaaagggt 1686
 Ser Gly Arg Glu Leu Leu
 540
 cgtcctcccc cagcatttct cactcctgcc cttcttccac agcgtatgtg gggagggtgga 1746
 ggggggtccat gtggaccagg cgccagetc cccggggaccc cggttcccgg acaagcccat 1806
 ttggaagaag agtcccttcc tccccccaaa tattgggcag ccctgtcctt accccgggac 1866
 caccctccc ttccagctat gtgtacaata atgaccaatc tgtttggc 1914

<210> 170

<211> 543

<212> PRT

<213> Homo sapiens

<400> 170

Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu

1	5	10	15
Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly			
20	25	30	
Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln			
35	40	45	
Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu			
50	55	60	
Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu			
65	70	75	80
Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr			
85	90	95	
Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser			
100	105	110	
Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val			
115	120	125	
Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu			
130	135	140	
Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val			
145	150	155	160
Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys			
165	170	175	
Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu			
180	185	190	
Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His			
195	200	205	
Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe			
210	215	220	

His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile
 225 230 235 240
 Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala
 245 250 255
 Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu
 260 265 270
 Ala Ala Gly Ile Phe Trp Val Ser Ile Leu Cys Arg Asn Thr Tyr Ser
 275 280 285
 Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe Thr Lys Ser
 290 295 300
 Ile Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile Asn Ser Gln
 305 310 315 320
 Gly His Pro Ile Glu Gly Leu Ala Val Met Tyr Tyr Ile Ala His Leu
 325 330 335
 Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile Gly Ser Gly
 340 345 350
 Trp Ala Phe Ile Lys Tyr Val Leu Ser Asp Lys Glu Lys Lys Val Phe
 355 360 365
 Gly Ile Val Ile Pro Met Gln Val Leu Ala Asn Val Ala Tyr Ile Ile
 370 375 380
 Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Val Leu Trp Lys Glu
 385 390 395 400
 Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile Leu Phe Pro
 405 410 415
 Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly Thr Asp Gly
 420 425 430
 Lys Val Ala Val Asn Leu Ala Lys Leu Lys Leu Phe Arg His Tyr Tyr

435 440 445
 Val Met Val Ile Cys Tyr Val Tyr Phe Thr Arg Ile Ile Ala Ile Leu
 450 455 460
 Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr Gln Leu Leu
 465 470 475 480
 Val Glu Gly Ser Thr Leu Ala Phe Phe Val Leu Thr Gly Tyr Lys Phe
 485 490 495
 Gln Pro Thr Gly Asn Asn Pro Tyr Leu Gln Leu Pro Gln Glu Asp Glu
 500 505 510
 Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly Phe Arg Glu
 515 520 525
 Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu Leu Leu
 530 535 540

<210> 171

<211> 1881

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (361).. (1344)

<400> 171

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 cagtttctcat ggcttgcagg cggttgctgt gtcagaggga gttttcagat aaacggtgac 120
 tgaaagaaca tggcttccca aggtggaatt cagactgagg acgtcagtgc ttccctccgt 180
 gagctctgcg tgtgtgtgca ctgtccacag gggtaaacta aaagccacca gagctctctg 240
 tcctggaccc aacctgcctt gaaaacaacg aggaacacca aatctggcac ttctcctaa 300


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aacatcttcc atcttgcatg agacagactc tccgagcata ggaaaggctg acaggcagtt 360
atg gag cag gac aat ggc acc atc cag gct cca ggc ttg ccg ccc acc 408
Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr
      1              5              10              15
acc tgc gtc tac cgt gag gat ttc aag cga ctg ctg cta acc ccg gta 456
Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
      20              25              30
tac tcg gtg gtg ctg gtg gtc ggc ctg cca ctg aac atc tgc gtc att 504
Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
      35              40              45
gcc cag atc tgc gca tcc cgc cgg acc ctg acc cgt tcc gct gtg tac 552
Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
      50              55              60
acc ctg aac ctg gca ctg gcg gac ctg atg tat gcc tgt tca cta ccc 600
Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
      65              70              75              80
cta ctt atc tat aac tac gcc aga ggg gac cac tgg ccc ttc gga gac 648
Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
      85              90              95
ctc gcc tgc cgc ttt gta cgc ttc ctc ttc tat gcc aat cta cat ggc 696
Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
      100             105             110
agc atc ctg ttc ctc acc tgc att agc ttc cag cgc tac ctg ggc atc 744
Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
      115             120             125
tgc cac ccc ctg gct tcc tgg cac aag cgt gga ggt cgc cgt gct gct 792
Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala

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130	135	140	
tgg gta gtg tgt gga gtc gtg tgg ctg gct gtg aca gcc cag tgc ctg			840
Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu			
145	150	155	160
ccc acg gca gtc ttt gct gcc aca ggc atc cag cgc aac cgc act gtg			888
Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val			
	165	170	175
tgc tac gac ctg agc cca ccc atc ctg tct act cgc tac ctg ccc tat			936
Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr			
	180	185	190
ggc atg gcc ctc acg gtc atc ggc ttc ttg ctg ccc ttc ata gcc tta			984
Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu			
	195	200	205
ctg gct tgt tat tgt cgc atg gcc cgc cgc ctg tgt cgc cag gat ggc			1032
Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly			
	210	215	220
cca gca ggt cct gtg gcc caa gag cgg cgc agc aag gcg gct cgt atg			1080
Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met			
225	230	235	240
gct gtg gtg gtg gca gct gtc ttt gcc atc agc ttc ctg cct ttc cac			1128
Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His			
	245	250	255
atc acc aag aca gcc tac ttg gct gtg cgc tcc acg ccc ggt gtc tct			1176
Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser			
	260	265	270
tgc cct gtg ctg gag acc ttc gct gct gcc tac aaa ggc act cgg ccc			1224
Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro			

275 280 285
 ttc gcc agt gtc aac agt gtt ctg gac ccc att ctc ttc tac ttc aca 1272
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 caa cag aag ttc cgg cgg caa ccc cac gat ctc tta cag agg ctc aca 1320
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr
 305 310 315 320
 gcc aag tgg cag agg cag aga gtc tgaggcccca gaggaggccc tggggcactg 1374
 Ala Lys Trp Gln Arg Gln Arg Val
 325
 gctgcaatgt gtttgtcact ggggccatgg ttgaagcttt ctctcaatcc caaaccatac 1434
 agagaagtaa aacttggctc aacatgcctg ggcctccaga atttccacat caaccacaaa 1494
 actaagacac ctgtgatttg gcaactggctc aattcatgct tgttacattc agaactcagg 1554
 atgtttgtgac gagataacaa gttctgggtc agcctgggtc acacagtga accccactgt 1614
 gaaaccccat ctcagatgat caaggatctg ctagacatct caggatgtgc taggccctgg 1674
 aatagcaatg cagattccaa caaaggtctt ctccaccccc acccccaccc cacctttctt 1734
 gtgttttacag ggtggagggg actgctggtg cactgtcacg tgagggaag gtccctcctg 1794
 tccaagagcc cggaaagctc acgttcacat ccatttgcca agacttttgc ataagagaga 1854
 aataaatgtg tttttgtggt tgggtgtt 1881

<210> 172

<211> 328

<212> PRT

<213> Mus musculus

<400> 172

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr

1

5

10

15

Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
 20 25 30
 Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
 35 40 45
 Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
 50 55 60
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
 65 70 75 80
 Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
 85 90 95
 Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
 100 105 110
 Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
 115 120 125
 Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala
 130 135 140
 Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu
 145 150 155 160
 Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
 165 170 175
 Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr
 180 185 190
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu
 195 200 205
 Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly
 210 215 220
 Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met

225 230 235 240
 Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His
 245 250 255
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser
 260 265 270
 Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
 275 280 285
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr
 305 310 315 320
 Ala Lys Trp Gln Arg Gln Arg Val
 325

<210> 173

<211> 1829

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (543).. (1526)

<400> 173

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 cggaagaact ggttctgtgg aatttgtgct tatttcccat caaggatcaa ggacctgctc 120
 tggggctacc tcagggcccc acaggatgag gggctggttt tcagatgagt tttctgcttg 180
 cctgtcatct ggatagtgtc taaaaatttg caaactgcct tcttgtcagt gtcttgctca 240
 ttcttcatga cactcctgat atgtctctca gtttcctcat ctgctgctc tccagacttc 300

tgccagaaca ttgcacgcga cagtttcagg cacagaactg actggcagca ggggctgctc 360
 cacgagtggg aatttgctcc agcacttcac ggactgcaag cgaggcactt gctaactctt 420
 ggataacaag acctctgcc gaagaacat ggctttggaa ggcggagttc aggctgagga 480
 gatgggtgcg gtcctcagtg agccccctgcc tccctgaaca taggaaaccc acctgggcag 540
 cc atg gaa tgg gac aat ggc aca ggc cag gct ctg ggc ttg cca ccc 587
 Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro
 1 5 10 15
 acc acc tgt gtc tac cgc gag aac ttc aag caa ctg ctg ctg cca cct 635
 Thr Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro
 20 25 30
 gtg tat tcg gcg gtg ctg gcg gct ggc ctg ccg ctg aac atc tgt gtc 683
 Val Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val
 35 40 45
 att acc cag atc tgc acg tcc cgc cgg gcc ctg acc cgc acg gcc gtg 731
 Ile Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val
 50 55 60
 tac acc cta aac ctt gct ctg gct gac ctg cta tat gcc tgc tcc ctg 779
 Tyr Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu
 65 70 75
 ccc ctg ctc atc tac aac tat gcc caa ggt gat cac tgg ccc ttt ggc 827
 Pro Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly
 80 85 90 95
 gac ttc gcc tgc cgc ctg gtc cgc ttc ctc ttc tat gcc aac ctg cac 875
 Asp Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His
 100 105 110
 ggc agc atc ctc ttc ctc acc tgc atc agc ttc cag cgc tac ctg ggc 923
 Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly

115	120	125	
atc tgc cac ccg ctg gcc ccc tgg cac aaa cgt ggg ggc cgc cgg gct	971		
Ile Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala			
130	135	140	
gcc tgg cta gtg tgt gta gcc gtg tgg ctg gcc gtg aca acc cag tgc	1019		
Ala Trp Leu Val Cys Val Ala Val Trp Leu Ala Val Thr Thr Gln Cys			
145	150	155	
ctg ccc aca gcc atc ttc gct gcc aca ggc atc cag cgt aac cgc act	1067		
Leu Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr			
160	165	170	175
gtc tgc tat gac ctc agc ccg cct gcc ctg gcc acc cac tat atg ccc	1115		
Val Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro			
180	185	190	
tat ggc atg gct ctc act gtc atc ggc ttc ctg ctg ccc ttt gct gcc	1163		
Tyr Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala			
195	200	205	
ctg ctg gcc tgc tac tgt ctc ctg gcc tgc cgc ctg tgc cgc cag gat	1211		
Leu Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp			
210	215	220	
ggc ccg gca gag cct gtg gcc cag gag cgg cgt ggc aag gcg gcc cgc	1259		
Gly Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg			
225	230	235	
atg gcc gtg gtg gtg gct gct gcc ttt gcc atc agc ttc ctg cct ttt	1307		
Met Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe			
240	245	250	255
cac atc acc aag aca gcc tac ctg gca gtg cgc tcg acg ccg ggc gtc	1355		
His Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val			

260 265 270
 ccc tgc act gta ttg gag gcc ttt gca gcg gcc tac aaa ggc acg cgg 1403
 Pro Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg
 275 280 285
 ccg ttt gcc agt gcc aac agc gtg ctg gac ccc atc ctc ttc tac ttc 1451
 Pro Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe
 290 295 300
 acc cag aag aag ttc cgc cgg cga cca cat gag ctc cta cag aaa ctc 1499
 Thr Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu
 305 310 315
 aca gcc aaa tgg cag agg cag ggt cgc tgagtcctcc aggtcctggg 1546
 Thr Ala Lys Trp Gln Arg Gln Gly Arg
 320 325
 cagccttcat atttgccatt gtgtccgggg caccaggagc cccaccaacc ccaaaccatg 1606
 cggagaatta gagttcagct cagctgggca tggagttaag atccctcaca ggacccagaa 1666
 gctcaccaaaa aactatttct tcagcccctt ctctggccca gaccctgtgg gcatggagat 1726
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<210> 174

<211> 328

<212> PRT

<213> Homo sapiens

<400> 174

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr

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5

10

15

Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val

20	25	30
Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile		
35	40	45
Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr		
50	55	60
Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro		
65	70	75
Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp		
85	90	95
Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly		
100	105	110
Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile		
115	120	125
Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala		
130	135	140
Trp Leu Val Cys Val Ala Val Trp Leu Ala Val Thr Thr Gln Cys Leu		
145	150	155
Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val		
165	170	175
Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr		
180	185	190
Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu		
195	200	205
Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly		
210	215	220
Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met		
225	230	235
		240

Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe His
 245 250 255
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Pro
 260 265 270
 Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
 275 280 285
 Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr
 305 310 315 320
 Ala Lys Trp Gln Arg Gln Gly Arg
 325

<210> 175

<211> 1477

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (35)..(1003)

<400> 175

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Met Ala Ala Pro Lys Gly Lys

1

5

ctt tgg gtc cag gcc caa ctg ggg ctc ccg ccg ctg ctg ctg ttg act 103

Leu Trp Val Gln Ala Gln Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr

10

15

20

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atg gcg ctg gcc gga ggc tcg ggg act gca gcg gcc gaa gcc ttt gac 151
Met Ala Leu Ala Gly Gly Ser Gly Thr Ala Ala Ala Glu Ala Phe Asp
      25              30              35
tcg gtc ctg gga gac aca gcg tcc tgt cac cgg gcc tgt cag ctg acc 199
Ser Val Leu Gly Asp Thr Ala Ser Cys His Arg Ala Cys Gln Leu Thr
      40              45              50              55
tac ccc ttg cac acc tac ccg aag gaa gag gag tta tac gca tgc cag 247
Tyr Pro Leu His Thr Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln
              60              65              70
aga ggc tgc agg ctg ttt tca att tgc cag ttt gtg gat gat ggg ctt 295
Arg Gly Cys Arg Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Leu
              75              80              85
gat tta aat cgg acc aag ctg gaa tgt gaa tct gcg tgc aca gaa gca 343
Asp Leu Asn Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala
              90              95              100
tat tcc caa cct gat gag cag tat gct tgt cat ctt ggc tgc cag gat 391
Tyr Ser Gln Pro Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asp
      105              110              115
cag ttg cca ttt gct gaa ctg aga caa gaa caa ctc atg tcc ctg atg 439
Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met
      120              125              130              135
cca aga atg cat ctc ctc ttc cct ctg act ctg gtg agg tcg ttc tgg 487
Pro Arg Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp
              140              145              150
agt gac atg atg gac tct gca cag agc ttc ata acc tct tca tgg act 535
Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr
              155              160              165

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ttt tat ctt caa gcc gat gac gga aaa ata gtt ata ttc cag tct aag 583
 Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe Gln Ser Lys
 170 175 180
 cca gaa att cag tat gca ccg cag ttg gag cag gag cct aca aac ttg 631
 Pro Glu Ile Gln Tyr Ala Pro Gln Leu Glu Gln Glu Pro Thr Asn Leu
 185 190 195
 aga gaa tca tct tta agc aaa atg tcc tat ctg cag atg aga aac tca 679
 Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln Met Arg Asn Ser
 200 205 210 215
 caa gca cac agg aac tac ctt gaa gag gaa gaa agc gat ggc ttt tta 727
 Gln Ala His Arg Asn Tyr Leu Glu Glu Glu Glu Ser Asp Gly Phe Leu
 220 225 230
 aga tgt cta tct ctt aac tct gga tgg att tta acc aca acc ctt gtc 775
 Arg Cys Leu Ser Leu Asn Ser Gly Trp Ile Leu Thr Thr Thr Leu Val
 235 240 245
 ctc tcg gtg atg gtg ttg ctc tgg atc tgt tgt gca gct gtt gct aca 823
 Leu Ser Val Met Val Leu Leu Trp Ile Cys Cys Ala Ala Val Ala Thr
 250 255 260
 gct gta gaa cag tat gtt ccc cct gag aag ctg agt atc tat ggt gac 871
 Ala Val Glu Gln Tyr Val Pro Pro Glu Lys Leu Ser Ile Tyr Gly Asp
 265 270 275
 ttg gaa ttt atg aat gaa caa aag ctg agc aga tac cca gct cct tct 919
 Leu Glu Phe Met Asn Glu Gln Lys Leu Ser Arg Tyr Pro Ala Pro Ser
 280 285 290 295
 ctt gtg att gtt agg tct cag act gaa gaa cat gag gag gca ggg ccc 967
 Leu Val Ile Val Arg Ser Gln Thr Glu Glu His Glu Glu Ala Gly Pro
 300 305 310

ctg ccc acc aag gtg aac ctt gct cac tca gaa atc taagcttttt 1013

Leu Pro Thr Lys Val Asn Leu Ala His Ser Glu Ile

315

320

aaaagagtcg tggacacata aacttccatt cctcatagag ctttttaaga tggtttcatt 1073

ggacataggc cttaagaaat cactataaaa tgcaataaaa gttaccaaac tctgtgaaga 1133

ctttatttgc tgtgacttta cctgtatttt tctagtcatt taagatggac attgggttgt 1193

atttttatatt tactaatatc tgtagctact tagttagttg cattgggtttt ggtttttttc 1253

ctctcttcgc caaattctat gagctgatca ttgtggcccc gccctgcca tgccccccgt 1313

cagtcattctc acttaataac cgaaacctta ggggtgtgatg cttctgcccc gaaatggcct 1373

ccaaactgtc ctctggatta tagcagaaat gttatttaat gacactacat tttcagttgt 1433

attgaattga aatcattaaa atctatttga ataattatgt tctg 1477

<210> 176

<211> 323

<212> PRT

<213> Mus musculus

<400> 176

Met Ala Ala Pro Lys Gly Lys Leu Trp Val Gln Ala Gln Leu Gly Leu

1

5

10

15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr

20

25

30

Ala Ala Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys

35

40

45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu

50

55

60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys

65

70

75

80

Gln Phe Val Asp Asp Gly Leu Asp Leu Asn Arg Thr Lys Leu Glu Cys
85 90 95
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Pro Asp Glu Gln Tyr Ala
100 105 110
Cys His Leu Gly Cys Gln Asp Gln Leu Pro Phe Ala Glu Leu Arg Gln
115 120 125
Glu Gln Leu Met Ser Leu Met Pro Arg Met His Leu Leu Phe Pro Leu
130 135 140
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
145 150 155 160
Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
165 170 175
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro Gln Leu
180 185 190
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
195 200 205
Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Tyr Leu Glu Glu
210 215 220
Glu Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp
225 230 235 240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile
245 250 255
Cys Cys Ala Ala Val Ala Thr Ala Val Glu Gln Tyr Val Pro Pro Glu
260 265 270
Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys Leu
275 280 285
Ser Arg Tyr Pro Ala Pro Ser Leu Val Ile Val Arg Ser Gln Thr Glu

290 295 300
Glu His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala His
305 310 315 320
Ser Glu Ile

<210> 177

<211> 1696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

$\langle 222 \rangle$ (251).. (1219)

<400> 177

aggccccgct tcgcgctaac gcttgcgatg gttgaattcc cctcctcacg ccagcctagg 60
agaagaagtt cgtagtccca gaggtgaggc aggaggcggc agtttctggc gggtgagggc 120
ggagctgaag tgacagcgga ggcggaagca acggtcggtg gggcggagaa gggggctggc 180
cccaggagga ggaggaaacc cttccgagaa aacagcaaca agctgagctg ctgtgacaga 240
ggggaacaag atg gcg gcg ccg aag ggg agc ctc tgg gtg agg acc caa 289

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln

1 5 10

ctg ggg ctc ccg ccg ctg ctg ctg ctg acc atg gcc ttg gcc gga ggt 337
Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly

15 20 25

tcg ggg acc gct tcg gct gaa gca ttt gac tcg gtc ttg ggt gat acg 385
Ser Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr

30 35 40 45

gcg tct tgc cac cgg gcc tgt cag ttg acc tac ccc ttg cac acc tac 433

Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr	
50 55 60	
cct aag gaa gag gag ttg tac gca tgt cag aga ggt tgc agg ctg ttt	481
Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe	
65 70 75	
tca att tgt cag ttt gtg gat gat gga att gac tta aat cga act aaa	529
Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys	
80 85 90	
ttg gaa tgt gaa tct gca tgt aca gaa gca tat tcc caa tct gat gag	577
Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu	
95 100 105	
caa tat gct tgc cat ctt ggt tgc cag aat cag ctg cca ttc gct gaa	625
Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu	
110 115 120 125	
ctg aga caa gaa caa ctt atg tcc ctg atg cca aaa atg cac cta ctc	673
Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu	
130 135 140	
ttt cct cta act ctg gtg agg tca ttc tgg agt gac atg atg gac tcc	721
Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser	
145 150 155	
gca cag agc ttc ata acc tct tca tgg act ttt tat ctt caa gcc gat	769
Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp	
160 165 170	
gac gga aaa ata gtt ata ttc cag tct aag cca gaa atc cag tac gca	817
Asp Gly Lys Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala	
175 180 185	
cca cat ttg gag cag gag cct aca aat ttg aga gaa tca tct cta agc	865

Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser
 190 195 200 205
 aaa atg tcc tat ctg caa atg aga aat tca caa gcg cac agg aat ttt 913
 Lys Met Ser Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe
 210 215 220
 ctt gaa gat gga gaa agt gat ggc ttt tta aga tgc ctc tct ctt aac 961
 Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn
 225 230 235
 tct ggg tgg att tta act aca act ctt gtc ctc tcg gtg atg gta ttg 1009
 Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu
 240 245 250
 ctt tgg att tgt tgt gca act gtt gct aca gct gtg gag cag tat gtt 1057
 Leu Trp Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val
 255 260 265
 ccc tct gag aag ctg agt atc tat ggt gac ttg gag ttt atg aat gaa 1105
 Pro Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu
 270 275 280 285
 caa aag cta aac aga tat cca gct tct tct ctt gtg gtt gtt aga tct 1153
 Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser
 290 295 300
 aaa act gaa gat cat gaa gaa gca ggg cct cta cct aca aaa gtg aat 1201
 Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn
 305 310 315
 ctt gct cat tct gaa att taagcatttt tcttttaaaa gacaagtgtg 1249
 Leu Ala His Ser Glu Ile
 320
 atagacatct aaaattccac tctcataga gcttttaaaa tggtttcatt ggatataggc 1309

cttagaat cactataaaa tgcaaataaa gttactcaaa tctgtgaaga ctgtatttgc 1369
 tataacttta ttggtattgt tttttagta atttaagagg tggatgtttg ggattgtatt 1429
 attatatttac taatatctgt agctattttg ttttttgctt tggttattgt ttttttcct 1489
 tttcttagct atgagctgat cattgctcct tctcacctcc tgccatgata ctgtcagtta 1549
 ccttagttaa caagctgaat atttagtaga aatgatgctt ctgctcagga atggcccaca 1609
 aatctgtaat ttgaaattta gcaggaaatg acctttaatg acactacatt ttcaggaact 1669
 gaaatcatta aaattttatt tgaataa 1696

<210> 178

<211> 323

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu

1 5 10 15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr

20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys

35 40 45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu

50 55 60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys

65 70 75 80

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys

85 90 95

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala

100 105 110

Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175
 Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
 180 185 190
 Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
 195 200 205
 Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp
 210 215 220
 Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp
 225 230 235 240
 Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile
 245 250 255
 Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser Glu
 260 265 270
 Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys Leu
 275 280 285
 Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr Glu
 290 295 300
 Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala His
 305 310 315 320
 Ser Glu Ile

<210> 179

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18).. (989)

<400> 179

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ggggagaggg gaacaag atg gcg gcg ccg aag ggg agc ctc tgg gtg agg      50
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              1              5              10
acc caa ctg ggg ctc ccg ccg ctg ctg ctg ctg acc atg gcc ttg gcc      98
Thr Gln Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala
              15              20              25
gga ggt tcg ggg acc gct tcg gct gaa gca ttt gac tcg gtc ttg ggt      146
Gly Gly Ser Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly
              30              35              40
gat acg gcg tct tgc cac ccg gcc tgt cag ttg acc tac ccc ttg cac      194
Asp Thr Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His
              45              50              55
acc tac cct aag gaa gag gag ttg tac gca tgt cag aga ggt tgc agg      242
Thr Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
              60              65              70              75
ctg ttt tca att tgt cag ttt gtg gat gat gga att gac tta aat cga      290
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg

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80	85	90	
act aaa ttg gaa tgt gaa tct gca tgt aca gaa gca tat tcc caa tct			338
Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser			
95	100	105	
gat gag caa tat gct tgc cat ctt ggt tgc cag aat cag ctg cca ttc			386
Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe			
110	115	120	
gct gaa ctg aga caa gaa caa ctt atg tcc ctg atg cca aaa atg cac			434
Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His			
125	130	135	
cta ctc ttt cct cta act ctg gtg agg tca ttc tgg agt gac atg atg			482
Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met			
140	145	150	155
gac tcc gca cag agc ttc ata acc tct tca tgg act ttt tat ctt caa			530
Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln			
160	165	170	
gcc gat gac gga aaa ata gtt ata ttc cag tct aag cca gaa atc cag			578
Ala Asp Asp Gly Lys Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln			
175	180	185	
tac gca cca cat ttg gag cag gag cct aca aat ttg aga gaa tca tct			626
Tyr Ala Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser			
190	195	200	
cta agc aaa atg tcc tca gat ctg caa atg aga aat tca caa gcg cac			674
Leu Ser Lys Met Ser Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His			
205	210	215	
agg aat ttt ctt gaa gat gga gaa agt gat ggc ttt tta aga tgc ctc			722
Arg Asn Phe Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu			

220 225 230 235
 tct ctt aac tct ggg tgg att tta act aca act ctt gtc ctc tcg gtg 770
 Ser Leu Asn Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val
 240 245 250
 atg gta ttg ctt tgg att tgt tgt gca act gtt gct aca gct gtg gag 818
 Met Val Leu Leu Trp Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu
 255 260 265
 cag tat gtt ccc tct gag aag ctg agt atc tat ggt gac ttg gag ttt 866
 Gln Tyr Val Pro Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe
 270 275 280
 atg aat gaa caa aag cta aac aga tat cca gct tct tct ctt gtg gtt 914
 Met Asn Glu Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val
 285 290 295
 gtt aga tct aaa act gaa gat cat gaa gaa gca ggg cct cta cct aca 962
 Val Arg Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr
 300 305 310 315
 aaa gtg aat ctt gct cat tct gaa att taagcatttt tcttttaaaa 1009
 Lys Val Asn Leu Ala His Ser Glu Ile
 320
 gacaagtgta atagacatct aaaattccac tctcataga gcttttaaaa tggtttcatt 1069
 ggatataggc cttaagaaat cactataaaa tgcaaataaa gttactcaaa tctgtgaaga 1129
 ctgtatttgc tataacttta ttggtattgt tttttagta atttaagagg tggatgtttg 1189
 ggattgtatt attattttac taatatctgt agctattttg ttttttgctt tggttattgt 1249
 ttttttcct tttcttagct atgagctgat cattgctcct tctcacctcc tgccatgata 1309
 ctgtcagtta ccttagtta caagctgaat atttagtaga aatgatgctt ctgctcagga 1369
 atggcccaca aatctgtaat ttgaaattta gcaggaaatg acctttaatg aactacatt 1429
 ttcaggaact gaaatcatta aaattttatt tgaataa 1466

<210> 180

<211> 324

<212> PRT

<213> Homo sapiens

<400> 180

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
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 Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20 25 30
 Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
 35 40 45
 His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 50 55 60
 Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65 70 75 80
 Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
 85 90 95
 Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110
 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys

	165	170	175
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu			
	180	185	190
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser			
	195	200	205
Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu			
	210	215	220
Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly			
225	230	235	240
Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp			
	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser			
	260	265	270
Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys			
	275	280	285
Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr			
	290	295	300
Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala			
305	310	315	320
His Ser Glu Ile			

<210> 181

<211> 1831

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (226).. (1359)

<400> 181

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 ctgctaggtg tccactggag tgtgtttacat ctctgggacct ttagaggaat tctggagtgcg 120
 gggctgtggc tgctgtctcc ccattcagaa gccacttgct agtagctact gaaaggctct 180
 tcattgtctc ttctgtcca ggaacaccgg tctaggaagc agaag atg cca tac tcc 237

Met Pro Tyr Ser

1

aac ctg cat cca gcc atc cca cgg ccc aga ggt cac cgc tcc aaa tat 285
 Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His Arg Ser Lys Tyr
 5 10 15 20
 gta gcc ctc atc ttt ctg gtg gcc agc ctg atg atc ctt tgg gtg gca 333
 Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile Leu Trp Val Ala
 25 30 35
 aag gat cca cca aat cac act ctg aag tac cta gca ctt cac cta gcc 381
 Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala Leu His Leu Ala
 40 45 50
 tcg cac gaa ctt gga cta ctg ttg aaa aac ctc tgc tgt ctg gct gaa 429
 Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys Cys Leu Ala Glu
 55 60 65
 gag ctg tgc cat gtc cag tcc agg tac cag ggc agc tac tgg aag gct 477
 Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser Tyr Trp Lys Ala
 70 75 80
 gtg cgc gcc tgc ctg gga tgc ccc atc cac tgt atg gct atg att cta 525
 Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met Ala Met Ile Leu
 85 90 95 100
 cta tcg tct tat ttc tat ttc ctc caa aac act gct gac ata tac ctc 573

Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala Asp Ile Tyr Leu	
105 110 115	
agt tgg atg ttt ggc ctt ctg gtc ctc tat aag tcc cta agc atg ctc	621
Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser Leu Ser Met Leu	
120 125 130	
ctg ggc ctt cag agc ttg act cca gcg gaa gtc tct gca gtc tgt gaa	669
Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser Ala Val Cys Glu	
135 140 145	
gaa aag aag tta aat gtt gcc cac ggg ctg gcc tgg tca tac tac att	717
Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile	
150 155 160	
ggg tac ttg cgg ttg atc tta cca ggg ctc cag gcc cgg atc cga atg	765
Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala Arg Ile Arg Met	
165 170 175 180	
ttc aat cag cta cat aac aac atg ctc agt ggt gca ggg agc cga aga	813
Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala Gly Ser Arg Arg	
185 190 195	
ctg tac atc ctc ttt cca ttg gac tgt ggg gtg cct gac aac ctg agt	861
Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser	
200 205 210	
gta gtt gac ccc aac att cga ttc cga gat atg ctg ccc cag caa aac	909
Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu Pro Gln Gln Asn	
215 220 225	
atc gac cgt gct ggc atc aag aat cgg gtt tat tcc aac agc gtc tac	957
Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser Asn Ser Val Tyr	
230 235 240	
gag att ctg gag aac gga cag cca gca ggc gtc tgt atc ctg gag tac	1005

Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys Ile Leu Glu Tyr
 245 250 255 260
 gcc acc ccc ttg cag acc ctg ttt gcc atg tca cag gat gcc aaa gct 1053
 Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Asp Ala Lys Ala
 265 270 275
 ggc ttc agt cgg gag gat cgg ctt gag cag gct aaa ctc ttc tgc cgg 1101
 Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg
 280 285 290
 aca ctt gag gaa atc ctg gaa gat gtc ccc gag tct cga aat aac tgc 1149
 Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser Arg Asn Asn Cys
 295 300 305
 cgc ctc att gtc tac caa gaa ccc aca gac gga aac agt ttc tca ctg 1197
 Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn Ser Phe Ser Leu
 310 315 320
 tct cag gag gtg ctc cgg cac att cgt cag gaa gaa aag gag gag gtt 1245
 Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu Lys Glu Glu Val
 325 330 335 340
 acc atg aat gcc ccc atg acc tca gtg gca cct cct ccc tcc gta ctg 1293
 Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro Pro Ser Val Leu
 345 350 355
 tcc caa gag cca aga ctc ctc atc agt ggt atg gat cag cct ctc cca 1341
 Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp Gln Pro Leu Pro
 360 365 370
 ctc cgc act gac ctc atc tgaggcatgg gacagccttg tctgggctct 1389
 Leu Arg Thr Asp Leu Ile
 375
 agtgatcctt tagcctcctg actgagcctt ccttcaatgg ttgggggcct cagagacttc 1449

acatctccag atgagtccca cattcctggg caagccattt atttcacctc tctgagcctc 1509
 aaccaaccct actatgaaag gaggtcataa tgcgttccct gcccagccaa aggattttat 1569
 atatgtagaa gttggtgtca atgcctggta aacttgagag aaaggccaag tacttcccgt 1629
 ggatgctgca gacattccct gctctctgtt gacctgtgtg gatggtacca gcagacttcc 1689
 aacctccag cttctggtca cgtgtgttca atgggagctt aagtagatgg cgagagggag 1749
 aaggaacatt tgttctgtta gctgtataca atcacagtgg gctggcctgt caactgcctt 1809
 cttataaaac acatctattc tc 1831

<210> 182

<211> 378

<212> PRT

<213> Mus musculus

<400> 182

Met Pro Tyr Ser Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His

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Arg Ser Lys Tyr Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile

20 25 30

Leu Trp Val Ala Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala

35 40 45

Leu His Leu Ala Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys

50 55 60

Cys Leu Ala Glu Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser

65 70 75 80

Tyr Trp Lys Ala Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met

85 90 95

Ala Met Ile Leu Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala

100 105 110

Asp Ile Tyr Leu Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser
115 120 125
Leu Ser Met Leu Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser
130 135 140
Ala Val Cys Glu Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp
145 150 155 160
Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala
165 170 175
Arg Ile Arg Met Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala
180 185 190
Gly Ser Arg Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro
195 200 205
Asp Asn Leu Ser Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu
210 215 220
Pro Gln Gln Asn Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser
225 230 235 240
Asn Ser Val Tyr Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys
245 250 255
Ile Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln
260 265 270
Asp Ala Lys Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys
275 280 285
Leu Phe Cys Arg Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser
290 295 300
Arg Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn
305 310 315 320
Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu

325 330 335
 Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro
 340 345 350
 Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp
 355 360 365
 Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile
 370 375

<210> 183

<211> 2109

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (243).. (1379)

<400> 183

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 ggaacccgct gttcagagct gtgactgcgg ctgcactcag agaagctgcc cttggctgct 180
 cgtagcgccg ggccttctct cctcgtcatc atccagagca gccagtgtcc gggaggcaga 240
 ag atg ccc cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt 287

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly

1 5 10 15
 cac ggg gcc cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg 335
 His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
 20 25 30
 acc ctt tgg ggg cta gga gag cca cca gag cac act ctc cgg tac ctg 383

Thr	Leu	Trp	Gly	Leu	Gly	Glu	Pro	Pro	Glu	His	Thr	Leu	Arg	Tyr	Leu	
			35					40					45			
gtc	ctc	cac	cta	gcc	tcc	ctg	cag	ctg	gga	ctg	ctg	tta	aac	ggg	gtc	431
Val	Leu	His	Leu	Ala	Ser	Leu	Gln	Leu	Gly	Leu	Leu	Leu	Asn	Gly	Val	
		50					55					60				
tgc	agc	ctg	gct	gag	gag	ctg	cgc	cac	atc	cac	tcc	agg	tac	cgg	ggc	479
Cys	Ser	Leu	Ala	Glu	Glu	Leu	Arg	His	Ile	His	Ser	Arg	Tyr	Arg	Gly	
		65				70					75					
agc	tac	tgg	agg	act	gtg	cgg	gcc	tgc	ctg	ggc	tgc	ccc	ctc	cgc	cgt	527
Ser	Tyr	Trp	Arg	Thr	Val	Arg	Ala	Cys	Leu	Gly	Cys	Pro	Leu	Arg	Arg	
80					85				90					95		
ggg	gcc	ctg	ttg	ctg	ctg	tcc	atc	tat	ttc	tac	tac	tcc	ctc	cca	aat	575
Gly	Ala	Leu	Leu	Leu	Leu	Ser	Ile	Tyr	Phe	Tyr	Tyr	Ser	Leu	Pro	Asn	
			100					105				110				
gcg	gtc	ggc	ccg	ccc	ttc	act	tgg	atg	ctt	gcc	ctc	ctg	ggc	ctc	tcg	623
Ala	Val	Gly	Pro	Pro	Phe	Thr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	
			115					120				125				
cag	gca	ctg	aac	atc	ctc	ctg	ggc	ctc	aag	ggc	ctg	gcc	cca	gct	gag	671
Gln	Ala	Leu	Asn	Ile	Leu	Leu	Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	
		130				135					140					
atc	tct	gca	gtg	tgt	gaa	aaa	ggg	aat	ttc	aac	gtg	gcc	cat	ggg	ctg	719
Ile	Ser	Ala	Val	Cys	Glu	Lys	Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	
		145				150					155					
gca	tgg	tca	tat	tac	atc	gga	tat	ctg	cgg	ctg	atc	ctg	cca	gag	ctc	767
Ala	Trp	Ser	Tyr	Tyr	Ile	Gly	Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	
160					165				170					175		
cag	gcc	cgg	att	cga	act	tac	aat	cag	cat	tac	aac	aac	ctg	cta	cgg	815

Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg
 180 185 190
 ggt gca gtg agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg 863
 Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly
 195 200 205
 gtg cct gat aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat 911
 Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp
 210 215 220
 aaa ctg ccc cag cag acc ggt gac cgt gct ggc atc aag gat cgg gtt 959
 Lys Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val
 225 230 235
 tac agc aac agc atc tat gag ctt ctg gag aac ggg cag cgg gcg ggc 1007
 Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly
 240 245 250 255
 acc tgt gtc ctg gag tac gcc acc ccc ttg cag act ttg ttt gcc atg 1055
 Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met
 260 265 270
 tca caa tac agt caa gct ggc ttt agc cgg gag gat agg ctt gag cag 1103
 Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln
 275 280 285
 gcc aaa ctc ttc tgc cgg aca ctt gag gac atc ctg gca gat gcc cct 1151
 Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro
 290 295 300
 gag tct cag aac aac tgc cgc ctc att gcc tac cag gaa cct gca gat 1199
 Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp
 305 310 315
 gac agc agc ttc tcg ctg tcc cag gag gtt ctc cgg cac ctg cgg cag 1247

Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln
 320 325 330 335
 gag gaa aag gaa gag gtt act gtg ggc agc ttg aag acc tca gcg gtg 1295
 Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val
 340 345 350
 ccc agt acc tcc acg atg tcc caa gag cct gag ctc ctc atc agt gga 1343
 Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly
 355 360 365
 atg gaa aag ccc ctc cct ctc cgc acg gat ttc tct tgagaccag 1389
 Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 370 375
 ggtcaccagg ccagagcctc cagtgggtctc caagcctctg gactgggggc tctcttcagt 1449
 ggctgaatgt ccagcagagc tatttccttc cacagggggc cttgcaggga aggggtccagg 1509
 acttgacatc ttaagatgog tcttgteccc ttgggccagt catttcccct ctctgagcct 1569
 cgggtgtcttc aacctgtgaa atgggatcat aatcaactgcc ttacctccct cacggttggtt 1629
 gtgaggactg agtgtgtgga agtttttcat aaactttgga tgctagtgtgta cttaggggggt 1689
 gtgccagggtg tctttcatgg ggccttcag acccaactccc cacccttctc cccttccttt 1749
 gcccgggggac gccgaactct ctcaatggta tcaacagget ccttcgccct ctggctcctg 1809
 gtcatgttcc attattgggg agccccagca gaagaatgga gaggaggagg aggctgagtt 1869
 tgggggtattg aatcccccggt cttccaccct gcagcatcaa ggttgctatg gactctcctg 1929
 ccgggcaact cttgcgtaat catgactatc tctaggattc tggcaccact tccttcctg 1989
 gcccttaag cctagctgtg tatcggcacc cccacccac tagagtactc cctctcactt 2049
 gcggtttcct tatactccac ccctttctca acggtccttt tttaaagcac atctcagatt 2109

<210> 184

<211> 379

<212> PRT

<213> Homo sapiens

<400> 184

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
1 5 10 15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
20 25 30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
35 40 45
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
50 55 60
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
65 70 75 80
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
85 90 95
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
100 105 110
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
115 120 125
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
130 135 140
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
145 150 155 160
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
165 170 175
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
180 185 190
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

195	200	205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys		
210	215	220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr		
225	230	235
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr		
245	250	255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser		
260	265	270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala		
275	280	285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu		
290	295	300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp		
305	310	315
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu		
325	330	335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro		
340	345	350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met		
355	360	365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser		
370	375	

<210> 185

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)..(1482)

<400> 185

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atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc	105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr	
1 5 10 15	
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt	153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu	
20 25 30	
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac	201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp	
35 40 45	
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt	249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser	
50 55 60	
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc	297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe	
65 70 75 80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc	345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly	
85 90 95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc	393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr	
100 105 110	

gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg	441
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg	
115 120 125	
gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc	489
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala	
130 135 140	
atc ttc atg gtg ata act gca ctg gtg aag gtg gac act tcc tcc tgg	537
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp	
145 150 155 160	
acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc	585
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser	
165 170 175	
ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc	633
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser	
180 185 190	
ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc	681
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly	
195 200 205	
ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt	729
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser	
210 215 220	
gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc acc atc ttc	777
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	
225 230 235 240	
ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat	825
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr	
245 250 255	

gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt	873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly	
260 265 270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275 280 285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290 295 300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser	
305 310 315 320	
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt	1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly	
325 330 335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc	1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe	
340 345 350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg	1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp	
355 360 365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc	1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu	
370 375 380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc	1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro	
385 390 395 400	

cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca 1305
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
 405 410 415
 ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
 420 425 430
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
 435 440 445
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly
 450 455 460
 tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga 1502
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile
 465 470 475
 cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggctg ggggccatgg 1562
 aggaaaggcc taaagtttca ctggtggaca gagagcagag cacactcggg cctcatccct 1622
 cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcat 1682
 attaacagaa cactcctgag acagttgaag aagaaatagc acaaatacagg ggtactccct 1742
 tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtgtt 1802
 cgccctagag ttattacaaa gccagtgcca aaaccagcc atgggctctt tgcaacctcc 1862
 cagctgcgct cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1922
 gaaggggtct ccttgaatg gaagtccct ggcattgtca gtctcaggc ccaagactca 1982
 agtgtgcaca gaccctgtg ttctgtgggt gaacaactgc ccactaacca gactggaaaa 2042
 ccagaaaga tgggccttcc atgaatgctt cattccagag ggaccagagg gcctccctgt 2102
 gcaagggatc aagcatgtct ggcctgggtt ttcaaaaaa gagggatcct catgacctgg 2162
 tgggtctatgg cctgggtcaa gatgagggtc ttttagtgtt cctgtttaca acatgtcaaa 2222

gccattgggtt caagggcgta ataaatactt gcgtattcaa

2262

<210> 186

<211> 475

<212> PRT

<213> Homo sapiens

<400> 186

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

1 5 10 15

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

20 25 30

Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp

35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser

50 55 60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe

65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly

85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr

100 105 110

Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg

115 120 125

Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala

130 135 140

Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp

145 150 155 160

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser
165 170 175
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser
180 185 190
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly
195 200 205
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser
210 215 220
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
225 230 235 240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr
245 250 255
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly
260 265 270
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser
275 280 285
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys
290 295 300
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser
305 310 315 320
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly
325 330 335
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe
340 345 350
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp
355 360 365
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu

370 375 380
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro
 385 390 395 400
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
 405 410 415
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
 420 425 430
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
 435 440 445
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly
 450 455 460
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile
 465 470 475

<210> 187

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)..(1482)

<400> 187

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 atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc 105
 Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr
 1 5 10 15
 tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt 153

Tyr	Arg	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	Leu	Leu				
20								25				30							
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac																201			
Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	Pro	Glu	Asp				
35				40				45											
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt																249			
Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	Gly	Ile	Gly	Ser				
50				55				60											
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc																297			
Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	Glu	Tyr	Trp	Met	Phe				
65				70				75				80							
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc																345			
Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	Gly	Glu	Asp	Pro	Glu	Gly				
				85				90				95							
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc																393			
Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	Tyr	Leu	Ala	Val	Ala	Ser	Thr				
100				105				110											
gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg																441			
Val	Pro	Ser	Met	Leu	Cys	Leu	Val	Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg				
115				120				125											
gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc																489			
Val	Ala	Val	His	Ile	Arg	Val	Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala				
130				135				140											
atc ttc atg gtg ata act gca ctg gtg aag gtg gac act ttc tcc tgg																537			
Ile	Phe	Met	Val	Ile	Thr	Ala	Leu	Val	Lys	Val	Asp	Thr	Phe	Ser	Trp				
145				150				155				160							
acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc																585			

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser	
165	170
175	
ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc	633
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser	
180	185
190	
ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc	681
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly	
195	200
205	
ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt	729
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser	
210	215
220	
gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc acc atc ttc	777
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	
225	230
235	240
ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat	825
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr	
245	250
255	
gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt	873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly	
260	265
270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275	280
285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290	295
300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017

Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser
 305 310 315 320
 ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt 1065
 Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly
 325 330 335
 tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc 1113
 Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe
 340 345 350
 ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg 1161
 Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp
 355 360 365
 atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc 1209
 Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu
 370 375 380
 ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc 1257
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro
 385 390 395 400
 cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca 1305
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
 405 410 415
 ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
 420 425 430
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
 435 440 445
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449

Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly

450

455

460

tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggagg gacacaagga 1502

Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile

465

470

475

cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggtg ggggccatgg 1562

aggaaaggcc taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1622

cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcatt 1682

attaacagaa cactcctgag acagttgaag aagaaatagc acaaatacagg ggtactccct 1742

tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtggt 1802

cggcctagag ttattacaaa gccagtgcca aaaccagcc atgggctctt tgcaacctcc 1862

cagctgcgt cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1922

gaaggggtct ccctggaatg gaagtcccct ggcatgggtca gtccctcagge ccaagactca 1982

agtgtgcaca gaccctgtg ttctgtgggt gaacaactgc ccactaacca gactggaaaa 2042

cccagaaaga tgggccttcc atgaatgctt cattccagag ggaccagagg gcctccctgt 2102

gcaagggatc aagcatgtct ggcctgggtt ttcaaaaaaa gagggatcct catgacctgg 2162

tggtctatgg cctgggtcaa gatgagggtc ttttagtggt cctgtttaca acatgtcaaa 2222

gccattgggt caagggcgta ataaatactt gcgtattcaa 2262

<210> 188

<211> 475

<212> PRT

<213> Homo sapiens

<400> 188

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

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5

10

15

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

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Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp		
35	40	45
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser		
50	55	60
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe		
65	70	75
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly		
85	90	95
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr		
100	105	110
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg		
115	120	125
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala		
130	135	140
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp		
145	150	155
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser		
165	170	175
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser		
180	185	190
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly		
195	200	205
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser		
210	215	220
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe		
225	230	235
		240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr
245 250 255
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly
260 265 270
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser
275 280 285
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys
290 295 300
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser
305 310 315 320
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly
325 330 335
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe
340 345 350
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp
355 360 365
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu
370 375 380
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro
385 390 395 400
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
405 410 415
Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
420 425 430
Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
435 440 445
Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly

450	455	460	
Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile			
465	470	475	
<210>	189		
<211>	2262		
<212>	DNA		
<213>	Homo sapiens		
<220>			
<221>	CDS		
<222>	(58)..(1482)		
<400>	189		
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atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc			105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr			
1	5	10	15
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt			153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu			
	20	25	30
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac			201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp			
35	40	45	
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt			249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser			
50	55	60	
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc			297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe			

65	70	75	80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc				345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly				
	85	90	95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc				393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr				
	100	105	110	
gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg				441
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg				
	115	120	125	
gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc				489
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala				
	130	135	140	
atc ttc atg gtg ata act gca ctg gtg aag gtg gac act tcc tcc tgg				537
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp				
	145	150	155	160
acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc				585
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser				
	165	170	175	
ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc				633
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser				
	180	185	190	
ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc				681
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly				
	195	200	205	
ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt				729
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser				

210	215	220	
gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc act gtc ttc			777
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe			
225	230	235	240
ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat			825
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr			
245	250	255	
gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt			873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly			
260	265	270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc			921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser			
275	280	285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag			969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys			
290	295	300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc			1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser			
305	310	315	320
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt			1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly			
325	330	335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc			1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe			
340	345	350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg			1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp			

355	360	365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc			1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu			
370	375	380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc			1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro			
385	390	395	400
cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca			1305
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala			
405	410	415	
ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg			1353
Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu			
420	425	430	
gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc			1401
Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala			
435	440	445	
acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc			1449
Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly			
450	455	460	
tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga			1502
Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile			
465	470	475	
cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggtg ggggccatgg			1562
aggaaaggcc taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct			1622
ccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtc			1682
attaacagaa cactcctgag acagttgaag aagaaatagc acaaatcagg ggtactccct			1742
tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtgtt			1802

cgccctagag	ttattacaaa	gccagtgcc	aaaccagcc	atgggctctt	tgcaacctcc	1862
cagctgcgct	cattccagct	gacagcgaga	tgcaagcaaa	tgctcagctc	tccttaccct	1922
gaaggggtct	ccctggaatg	gaagtcccct	ggcatggtca	gtcctcaggc	ccaagactca	1982
agtgtgcaca	gacccctgtg	ttctgtgggt	gaacaactgc	ccactaacca	gactggaaaa	2042
cccagaaaga	tgggccttcc	atgaatgctt	cattccagag	ggaccagagg	gcctccctgt	2102
gcaagggatc	aagcatgtct	ggcctggggt	ttcaaaaaaa	gagggatcct	catgacctgg	2162
tggtctatgg	cctgggtcaa	gatgagggtc	ttttagtgtt	cctgtttaca	acatgtcaaa	2222
gccattggtt	caagggcgta	ataaataactt	gcgtattcaa			2262

<210> 190

<211> 475

<212> PRT

<213> Homo sapiens

<400> 190

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

1 5 10 15

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

20 25 30

Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp

35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser

50 55 60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe

65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly

85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr

100	105	110	
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg			
115	120	125	
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala			
130	135	140	
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp			
145	150	155	160
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser			
165	170	175	
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser			
180	185	190	
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly			
195	200	205	
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser			
210	215	220	
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe			
225	230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr			
245	250	255	
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly			
260	265	270	
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser			
275	280	285	
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys			
290	295	300	
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser			
305	310	315	320

Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly
 325 330 335
 Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe
 340 345 350
 Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp
 355 360 365
 Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu
 370 375 380
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro
 385 390 395 400
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala
 405 410 415
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
 420 425 430
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
 435 440 445
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly
 450 455 460
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile
 465 470 475

<210> 191

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58).. (1482)

<400> 191

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atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc	105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr	
1 5 10 15	
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt	153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu	
20 25 30	
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac	201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp	
35 40 45	
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt	249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser	
50 55 60	
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc	297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe	
65 70 75 80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc	345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly	
85 90 95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc	393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr	
100 105 110	
gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg	441
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg	
115 120 125	

gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc 489
 Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala
 130 135 140
 atc ttc atg gtg ata act gca ctg gtg aag gtg gac act ttc tcc tgg 537
 Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp
 145 150 155 160
 acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc 585
 Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser
 165 170 175
 ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc 633
 Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser
 180 185 190
 ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc 681
 Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly
 195 200 205
 ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt 729
 Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser
 210 215 220
 gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc act gtc ttc 777
 Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe
 225 230 235 240
 ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat 825
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr
 245 250 255
 gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt 873
 Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly
 260 265 270

gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275 280 285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290 295 300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser	
305 310 315 320	
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt	1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly	
325 330 335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc	1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe	
340 345 350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg	1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp	
355 360 365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc	1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu	
370 375 380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc	1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro	
385 390 395 400	
cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca	1305
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala	
405 410 415	

ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu
 420 425 430
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala
 435 440 445
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly
 450 455 460
 tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga 1502
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile
 465 470 475
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<210> 192

<211> 475

<212> PRT

<213> Homo sapiens

<400> 192

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20 25 30

Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp

35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser

50 55 60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe

65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly

85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr

100 105 110

Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg

115 120 125

Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala

130 135 140

Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp

145 150 155 160

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser

165 170 175

Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser

180	185	190
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly		
195	200	205
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser		
210	215	220
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe		
225	230	235
240		
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr		
245	250	255
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly		
260	265	270
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser		
275	280	285
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys		
290	295	300
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser		
305	310	315
320		
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly		
325	330	335
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe		
340	345	350
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp		
355	360	365
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu		
370	375	380
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro		
385	390	395
400		

Arg	Val	His	Leu	Lys	Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala		
				405						410						415	
Leu	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu		
				420						425						430	
Ala	Leu	Leu	Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala		
				435						440						445	
Thr	Gly	Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly		
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Ser	Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile							
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<210> 193

<211> 3535

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (105).. (1682)

<400> 193

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tagggtcagc ggtgacatcc caaaggggcag gcccggcagc cgcc atg gtg gcc aag 116

Met Val Ala Lys

1

gat tac ccc ttc tac ctc acg gtc aag aga gcg aac tgc agc ctg gag 164

Asp Tyr Pro Phe Tyr Leu Thr Val Lys Arg Ala Asn Cys Ser Leu Glu

5 10 15 20

cta ccc ccg gcc agc ggt ccg gcc aag gac gct gag gag cct agt aat 212

Leu Pro Pro Ala Ser Gly Pro Ala Lys Asp Ala Glu Glu Pro Ser Asn
 25 30 35
 aaa cgg gtc aaa ccc ctt tcc cga gtc acg tcg cta gca aac ctc atc 260
 Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile
 40 45 50
 ccg ccc gtg aag gcc acg cca tta aag cgc ttc agt caa acc ctg cag 308
 Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln
 55 60 65
 cgc tcc att agc ttc cgc agt gag agc cgc cct gac atc ctc gcc ccc 356
 Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro Asp Ile Leu Ala Pro
 70 75 80
 cga ccc tgg tcc aga aat gcc gcc ccc tcg agc acg aaa cgg aga gat 404
 Arg Pro Trp Ser Arg Asn Ala Ala Pro Ser Ser Thr Lys Arg Arg Asp
 85 90 95 100
 agc aag ctg tgg agt gag acc ttc gat gtg tgc gtc aat cag atg ctt 452
 Ser Lys Leu Trp Ser Glu Thr Phe Asp Val Cys Val Asn Gln Met Leu
 105 110 115
 aca tcc aag gaa atc aaa cgt cag gag gcg atc ttt gag ctt tcc caa 500
 Thr Ser Lys Glu Ile Lys Arg Gln Glu Ala Ile Phe Glu Leu Ser Gln
 120 125 130
 gga gaa gaa gac ttg ata gaa gac ttg aaa tta gca aaa aag gcc tat 548
 Gly Glu Glu Asp Leu Ile Glu Asp Leu Lys Leu Ala Lys Lys Ala Tyr
 135 140 145
 cat gac ccc atg ctg aaa ctc tcc ata atg aca gaa caa gag ttg aat 596
 His Asp Pro Met Leu Lys Leu Ser Ile Met Thr Glu Gln Glu Leu Asn
 150 155 160
 caa att ttt gga aca ctg gac tct cta att cct cta cat gaa gag ctc 644

Gln	Ile	Phe	Gly	Thr	Leu	Asp	Ser	Leu	Ile	Pro	Leu	His	Glu	Glu	Leu		
165					170					175					180		
ctt	agt	cag	ctt	cga	gat	gtt	agg	aag	cct	gat	ggc	tcg	act	gaa	cat	692	
Leu	Ser	Gln	Leu	Arg	Asp	Val	Arg	Lys	Pro	Asp	Gly	Ser	Thr	Glu	His		
				185						190					195		
gtt	ggt	ccc	atc	ctc	gtg	ggc	tgg	ctc	cct	tgc	ctc	agc	tcc	tat	gat	740	
Val	Gly	Pro	Ile	Leu	Val	Gly	Trp	Leu	Pro	Cys	Leu	Ser	Ser	Tyr	Asp		
				200						205					210		
agc	tac	tgc	agc	aat	caa	gta	gcc	gcc	aaa	gct	ctg	ctg	gac	cac	aaa	788	
Ser	Tyr	Cys	Ser	Asn	Gln	Val	Ala	Ala	Lys	Ala	Leu	Leu	Asp	His	Lys		
				215						220					225		
aag	caa	gat	cac	cga	gtc	cag	gat	ttc	cta	cag	cga	tgt	tta	gaa	tcc	836	
Lys	Gln	Asp	His	Arg	Val	Gln	Asp	Phe	Leu	Gln	Arg	Cys	Leu	Glu	Ser		
				230						235					240		
ccc	ttt	agc	cgc	aaa	cta	gat	ctc	tgg	aat	ttc	ctc	gat	att	cca	aga	884	
Pro	Phe	Ser	Arg	Lys	Leu	Asp	Leu	Trp	Asn	Phe	Leu	Asp	Ile	Pro	Arg		
245					250					255					260		
agc	cgc	ctg	gta	aaa	tac	cct	ctg	ctt	ctc	cga	gaa	atc	ttg	agg	cac	932	
Ser	Arg	Leu	Val	Lys	Tyr	Pro	Leu	Leu	Leu	Arg	Glu	Ile	Leu	Arg	His		
				265						270					275		
aca	cca	aat	gat	aat	cca	gat	cag	cag	cac	ttg	gaa	gaa	gct	ata	aat	980	
Thr	Pro	Asn	Asp	Asn	Pro	Asp	Gln	Gln	His	Leu	Glu	Glu	Ala	Ile	Asn		
				280						285					290		
atc	att	cag	gga	att	gtg	gca	gaa	atc	aac	acc	aag	act	ggt	gaa	tct	1028	
Ile	Ile	Gln	Gly	Ile	Val	Ala	Glu	Ile	Asn	Thr	Lys	Thr	Gly	Glu	Ser		
				295						300					305		
gaa	tgc	cgc	tat	tat	aaa	gag	cgg	ctt	ctt	tac	ttg	gaa	gaa	ggc	cag	1076	

Glu Cys Arg Tyr Tyr Lys Glu Arg Leu Leu Tyr Leu Glu Glu Gly Gln	
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aaa gac tcc ctg atc gac agc tct cga gtc ttg tgt tgt cat ggt gaa	1124
Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys Cys His Gly Glu	
325	330
ctg aag aac aat cgg ggc gtg aaa ctg cat gtt ttc ctg ttc caa gaa	1172
Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe Leu Phe Gln Glu	
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gtg ctt gtg atc act cga gcc gtc acc cac aat gag cag ctt tgc tac	1220
Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu Gln Leu Cys Tyr	
360	365
cag ctg tac cgt cag cca atc ccc gtg aaa gac ctc ctg ctg gaa gac	1268
Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu Leu Leu Glu Asp	
375	380
ctc cag gat gga gaa gtg agg ctg ggt ggc tcc ctg cga ggg gca ttc	1316
Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu Arg Gly Ala Phe	
390	395
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Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val Ser Phe Lys Asn	
405	410
gga tcc caa agt cag acc cac tcg cta caa gcc aat gac act ttc aac	1412
Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn Asp Thr Phe Asn	
425	430
aaa cag cag tgg ctt aac tgt att cgt caa gcc aaa gaa aca gtt ttg	1460
Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys Glu Thr Val Leu	
440	445
tgt gct gcc ggg caa gct ggg gtg ctt gac tcc gag gga tcg ttc cta	1508

Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu Gly Ser Phe Leu
 455 460 465
 aat ccc acc acc ggg agc aga gag cta cag gga gaa aca aaa ctt gag 1556
 Asn Pro Thr Thr Gly Ser Arg Glu Leu Gln Gly Glu Thr Lys Leu Glu
 470 475 480
 cag atg gac caa tcg gac agt gag tca gac tgt agt atg gac acg agt 1604
 Gln Met Asp Gln Ser Asp Ser Glu Ser Asp Cys Ser Met Asp Thr Ser
 485 490 495 500
 gag gtc agc ctc gac tgt gag cgc atg gaa cag aca gac tct tcc tgt 1652
 Glu Val Ser Leu Asp Cys Glu Arg Met Glu Gln Thr Asp Ser Ser Cys
 505 510 515
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 Gly Asn Ser Arg His Gly Glu Ser Asn Val
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<210> 194

<211> 526

<212> PRT

<213> Homo sapiens

<400> 194

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Val	Lys	Pro	Leu	Ser	Arg
Val	Thr	Ser	Leu		
	35		40		45
Ala	Asn	Leu	Ile	Pro	Pro
Val	Lys	Ala	Thr	Pro	Leu
Lys	Arg	Phe	Ser		
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Gln	Thr	Leu	Gln	Arg	Ser
Ile	Ser	Phe	Arg	Ser	Glu
Ser	Arg	Pro	Asp		
	65		70		75
Ile	Leu	Ala	Pro	Arg	Pro
Trp	Ser	Arg	Asn	Ala	Ala
Pro	Ser	Ser	Thr		
	85		90		95
Lys	Arg	Arg	Asp	Ser	Lys
Leu	Trp	Ser	Glu	Thr	Phe
Asp	Val	Cys	Val		
	100		105		110
Asn	Gln	Met	Leu	Thr	Ser
Lys	Glu	Ile	Lys	Arg	Gln
Glu	Ala	Ile	Phe		
	115		120		125
Glu	Leu	Ser	Gln	Gly	Glu
Glu	Asp	Leu	Lys	Leu	Ala
	130		135		140
Lys	Lys	Ala	Tyr	His	Asp
Pro	Met	Leu	Lys	Leu	Ser
Ile	Met	Thr	Glu		
	145		150		155
Gln	Glu	Leu	Asn	Gln	Ile
Phe	Gly	Thr	Leu	Asp	Ser
Leu	Ile	Pro	Leu		
	165		170		175
His	Glu	Glu	Leu	Leu	Ser
Gln	Leu	Arg	Asp	Val	Arg
Lys	Pro	Asp	Gly		
	180		185		190
Ser	Thr	Glu	His	Val	Gly
Pro	Ile	Leu	Val	Gly	Trp
Leu	Pro	Cys	Leu		
	195		200		205
Ser	Ser	Tyr	Asp	Ser	Tyr
Cys	Ser	Asn	Gln	Val	Ala
Ala	Lys	Ala	Leu		
	210		215		220
Leu	Asp	His	Lys	Lys	Gln
Asp	His	Arg	Val	Gln	Asp
Phe	Leu	Gln	Arg		
	225		230		235
					240

Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp Leu Trp Asn Phe Leu
 245 250 255
 Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro Leu Leu Leu Arg Glu
 260 265 270
 Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp Gln Gln His Leu Glu
 275 280 285
 Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala Glu Ile Asn Thr Lys
 290 295 300
 Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu Arg Leu Leu Tyr Leu
 305 310 315 320
 Glu Glu Gly Gln Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys
 325 330 335
 Cys His Gly Glu Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe
 340 345 350
 Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu
 355 360 365
 Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu
 370 375 380
 Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu
 385 390 395 400
 Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val
 405 410 415
 Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn
 420 425 430
 Asp Thr Phe Asn Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys
 435 440 445
 Glu Thr Val Leu Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu

450 455 460
 Gly Ser Phe Leu Asn Pro Thr Thr Gly Ser Arg Glu Leu Gln Gly Glu
 465 470 475 480
 Thr Lys Leu Glu Gln Met Asp Gln Ser Asp Ser Glu Ser Asp Cys Ser
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<210> 195

<211> 3375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (199).. (1131)

<400> 195

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 ctccggggcg ggggcgccag cggcgaagcc ccctccccgg ggaggcggga cctgggggag 180
 cggcggcggc cgggaacg atg cat cag aag ctg ctg aag agc gcg cat tac 231

Met His Gln Lys Leu Leu Lys Ser Ala His Tyr

1

5

10

atc gag ctg ggc agc tac cag tac tgg ccg gtc ctg gtg ccc cgt ggc 279
 Ile Glu Leu Gly Ser Tyr Gln Tyr Trp Pro Val Leu Val Pro Arg Gly

15

20

25

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 Ile Arg Leu Tyr Thr Tyr Glu Gln Ile Pro Gly Ser Leu Lys Asp Asn
 30 35 40
 ccg tac atc acc gac ggc tac cgg gcc tac ctg ccg tcc agg ctg tgt 375
 Pro Tyr Ile Thr Asp Gly Tyr Arg Ala Tyr Leu Pro Ser Arg Leu Cys
 45 50 55
 atc aaa agt ttg ttt att tta tct aat gag aca gta aac atc tgg agt 423
 Ile Lys Ser Leu Phe Ile Leu Ser Asn Glu Thr Val Asn Ile Trp Ser
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 cat ttg ctg ggt ttc ttt ctc ttc ttc acc ctg gga ata tat gac atg 471
 His Leu Leu Gly Phe Phe Leu Phe Phe Thr Leu Gly Ile Tyr Asp Met
 80 85 90
 aca tct gtg tta cct tca gca agt gcg tcc aga gaa gat ttt gta att 519
 Thr Ser Val Leu Pro Ser Ala Ser Ala Ser Arg Glu Asp Phe Val Ile
 95 100 105
 tgt tct att tgt ctt ttc tgc ttc cag gtc tgt atg ctt tgc tct gtg 567
 Cys Ser Ile Cys Leu Phe Cys Phe Gln Val Cys Met Leu Cys Ser Val
 110 115 120
 ggc tat cat ctt ttt tcc tgc cat cgg tca gaa aaa aca tgt cga aga 615
 Gly Tyr His Leu Phe Ser Cys His Arg Ser Glu Lys Thr Cys Arg Arg
 125 130 135
 tgg atg gca tta gat tat gca gga att tct att gga ata ctg ggc tgc 663
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 140 145 150 155
 tat gtc tca gga gta ttt tac gca ttt tat tgt aat aac tac tgg cgt 711
 Tyr Val Ser Gly Val Phe Tyr Ala Phe Tyr Cys Asn Asn Tyr Trp Arg
 160 165 170

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Gln Val Tyr Leu Ile Thr Val Leu Ala Met Ile Leu Ala Val Phe Phe	
175 180 185	
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Ala Gln Ile His Pro Asn Tyr Leu Thr Gln Gln Trp Gln Arg Leu Arg	
190 195 200	
tct atc atc ttt tgt tct gtt tcg gga tat gga gtg att cct act ctt	855
Ser Ile Ile Phe Cys Ser Val Ser Gly Tyr Gly Val Ile Pro Thr Leu	
205 210 215	
cac tgg gtt tgg ctc aat gga gga att ggt gct cct att gta cag gac	903
His Trp Val Trp Leu Asn Gly Gly Ile Gly Ala Pro Ile Val Gln Asp	
220 225 230 235	
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Phe Ala Pro Arg Val Ile Val Met Tyr Met Ile Ala Leu Leu Ala Phe	
240 245 250	
cta ttc tac att tcc aaa gtc cca gag cgg tac ttt cca gga caa cta	999
Leu Phe Tyr Ile Ser Lys Val Pro Glu Arg Tyr Phe Pro Gly Gln Leu	
255 260 265	
aac tac ctc gga tca agc cac caa ata tgg cat atc ctt gca gta gtg	1047
Asn Tyr Leu Gly Ser Ser His Gln Ile Trp His Ile Leu Ala Val Val	
270 275 280	
atg tta tat tgg tgg cat cag tca aca gtg tat gtc atg cag tac aga	1095
Met Leu Tyr Trp Trp His Gln Ser Thr Val Tyr Val Met Gln Tyr Arg	
285 290 295	
cat agc aag cct tgt cct gac tat gtt tca cat ttg tgaattaggt	1141
His Ser Lys Pro Cys Pro Asp Tyr Val Ser His Leu	
300 305 310	

atggccacct ggtgagttca gttgttaagc aatatataat ggggaattgt atacccact 1201
atttctaaga ttccattag tttcccttt ttccttttta atatgagtaa tgctttataa 1261
aaatgggaaa aaaagtatac ttaaggatct gtagtaataa ctgctttaca aaatccttaa 1321
aactactaat ttgctgcttg tacagaaagt gaaaattagt tggcaatcat aagaaacatc 1381
tgaataacaa cgataaatgg gaaactagt ttgaaatagg attcatttta cttagcacca 1441
gcttaatttc cttaggaagg gctcatctcc attagaaaat ggagtcactt tatgtgctta 1501
attattttca gttaattgtc aagtttaagt gcctaataca ggcaagtgtt gtttcagcct 1561
atgcttaatg caagctagga tagtgatttt aaataatcac taaaatcact agatttaaat 1621
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tgcagtaagt tgagagaagg gttgagaaga ggaaaagaac ttctcatttt ctatcagata 1801
agaatcacat tagaaactaa gtacaagatt agacaacaaa ttatgtggtc aaataatata 1861
gtcattagct acctaaacat ttaattcca gatattattt aattccatat aataactgaa 1921
ttcttgtgag tggattacag gtttttgatc caaaattcc agagctttca actctctgaa 1981
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cctctcattt tttcactgct atgatatact tattataaaa tagggaatga atgaatgaat 3241
atggattgct gttaactaga aacacttctg tatgtcagtc agcatttaat gaccacctac 3301
tgtgtgcaca gcactactgg taaaattttg aagacattgt taacattaaa aaatatttta 3361
aagttgtcta caaa 3375

<210> 196

<211> 311

<212> PRT

<213> Homo sapiens

<400> 196

Met His Gln Lys Leu Leu Lys Ser Ala His Tyr Ile Glu Leu Gly Ser

1 5 10 15

Tyr Gln Tyr Trp Pro Val Leu Val Pro Arg Gly Ile Arg Leu Tyr Thr

20 25 30

Tyr Glu Gln Ile Pro Gly Ser Leu Lys Asp Asn Pro Tyr Ile Thr Asp

35 40 45

Gly Tyr Arg Ala Tyr Leu Pro Ser Arg Leu Cys Ile Lys Ser Leu Phe

50 55 60

Ile Leu Ser Asn Glu Thr Val Asn Ile Trp Ser His Leu Leu Gly Phe

65 70 75 80

Phe Leu Phe Phe Thr Leu Gly Ile Tyr Asp Met Thr Ser Val Leu Pro
 85 90 95
 Ser Ala Ser Ala Ser Arg Glu Asp Phe Val Ile Cys Ser Ile Cys Leu
 100 105 110
 Phe Cys Phe Gln Val Cys Met Leu Cys Ser Val Gly Tyr His Leu Phe
 115 120 125
 Ser Cys His Arg Ser Glu Lys Thr Cys Arg Arg Trp Met Ala Leu Asp
 130 135 140
 Tyr Ala Gly Ile Ser Ile Gly Ile Leu Gly Cys Tyr Val Ser Gly Val
 145 150 155 160
 Phe Tyr Ala Phe Tyr Cys Asn Asn Tyr Trp Arg Gln Val Tyr Leu Ile
 165 170 175
 Thr Val Leu Ala Met Ile Leu Ala Val Phe Phe Ala Gln Ile His Pro
 180 185 190
 Asn Tyr Leu Thr Gln Gln Trp Gln Arg Leu Arg Ser Ile Ile Phe Cys
 195 200 205
 Ser Val Ser Gly Tyr Gly Val Ile Pro Thr Leu His Trp Val Trp Leu
 210 215 220
 Asn Gly Gly Ile Gly Ala Pro Ile Val Gln Asp Phe Ala Pro Arg Val
 225 230 235 240
 Ile Val Met Tyr Met Ile Ala Leu Leu Ala Phe Leu Phe Tyr Ile Ser
 245 250 255
 Lys Val Pro Glu Arg Tyr Phe Pro Gly Gln Leu Asn Tyr Leu Gly Ser
 260 265 270
 Ser His Gln Ile Trp His Ile Leu Ala Val Val Met Leu Tyr Trp Trp
 275 280 285
 His Gln Ser Thr Val Tyr Val Met Gln Tyr Arg His Ser Lys Pro Cys

290 295 300
 Pro Asp Tyr Val Ser His Leu
 305 310

<210> 197
 <211> 1210
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (644).. (937)
 <400> 197

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 ggggagggtc ttgctgcctg tacccacctc tgacatttgc actccttagac aacatagccg 120
 ctaatttggtt ggaaaggcgt taaaagaaaa aaaaaaaagt gctattttacc gcctccctct 180
 ttgacagaag actgtctgtc aaagtaacct cgccccaagt gacttttttaa ggggtggctc 240
 accaggaggg agtcagagca gaacttggac tgagtcctgc aggacacagg tattagcttt 300
 tctcttttat ttgctttatg tttcatttac ttctttggat cgaatagctc caattgtatt 360
 gctgttattt ggtttttcat tttgttgttg ggttttttga tgtgggtgtt ttttgttttg 420
 ttttgtttct ttttgtcttt ttagaaagag ggtttcctc tattgccctg gctggagtac 480
 agtggtgga tcaactgttca ctacagcctc caacttattc ctgggctcaa gcaatccttc 540
 tgtctccatc tcctgagcag ctgggactct aggcatttgc caccgtgcc aatttttttt 600
 taattccttt ttaaaaatat tttaatcctt tccggaaaaa aat atg ttt tcc atg 655
 Met Phe Ser Met
 1
 gac ttg ctt att tcc ttt ata cag tcc att gtc gtt gaa ttc tta ttt 703
 Asp Leu Leu Ile Ser Phe Ile Gln Ser Ile Val Val Glu Phe Leu Phe

5	10	15	20	
gaa ttt gtg ata cac cct ctc ata ggg aac ata aca aat ttc ctc cca				751
Glu Phe Val Ile His Pro Leu Ile Gly Asn Ile Thr Asn Phe Leu Pro				
25	30	35		
cag caa tta atg acg agt gcg atg aga agc ata atg aca atg att aac				799
Gln Gln Leu Met Thr Ser Ala Met Arg Ser Ile Met Thr Met Ile Asn				
40	45	50		
ttg ata att aaa aat cta atc aac caa ctg ttg atg att gta cta aac				847
Leu Ile Ile Lys Asn Leu Ile Asn Gln Leu Leu Met Ile Val Leu Asn				
55	60	65		
aaa ata att tca ttt tta cac aac cag ttg tat gtg aac tat gtt gaa				895
Lys Ile Ile Ser Phe Leu His Asn Gln Leu Tyr Val Asn Tyr Val Glu				
70	75	80		
aac agg atg cat gac tgg cgg cca gaa caa aga agt ttg gtt				937
Asn Arg Met His Asp Trp Arg Pro Glu Gln Arg Ser Leu Val				
85	90	95		
taatttctat ctatacaccc agtaaaatat ctgtaatacc actggaaaac cttaaaatac				997
attatctatt tcttgtaaaa gaatgatgaa atgtgaattt gaacagcata aatatgtaca				1057
agtatctctt ctcaacggaa aaaattatgt ttgtggatga aatatgaacc gagtttgtgg				1117
atgaaatatg agcagcatga ataagcacag atatctctcc tcaatggaaa aaatcacgta				1177
caaaatataa gaaccagtt tgtggatgcg tga				1210

<210> 198

<211> 98

<212> PRT

<213> Homo sapiens

<400> 198

Met Phe Ser Met Asp Leu Leu Ile Ser Phe Ile Gln Ser Ile Val Val
 1 5 10 15
 Glu Phe Leu Phe Glu Phe Val Ile His Pro Leu Ile Gly Asn Ile Thr
 20 25 30
 Asn Phe Leu Pro Gln Gln Leu Met Thr Ser Ala Met Arg Ser Ile Met
 35 40 45
 Thr Met Ile Asn Leu Ile Ile Lys Asn Leu Ile Asn Gln Leu Leu Met
 50 55 60
 Ile Val Leu Asn Lys Ile Ile Ser Phe Leu His Asn Gln Leu Tyr Val
 65 70 75 80
 Asn Tyr Val Glu Asn Arg Met His Asp Trp Arg Pro Glu Gln Arg Ser
 85 90 95
 Leu Val

<210> 199

<211> 990

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99).. (665)

<400> 199

gacgcgccgc ggtccccgcc tgccgctgct ccgccgcagt cgccgctcca gtctatccgg 60

cactaggaac agccccgagc ggcgagacgg tccccgcc atg tct gcg gcc atg agg 116

Met Ser Ala Ala Met Arg

1 5

gag agg ttc gac cgg ttc ctg cac gag aag aac tgc atg act gac ctt 164

Glu Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu	
10 15 20	
ctg gcc aag ctc gag gcc aaa acc ggc gtg aac agg agc ttc atc gct	212
Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala	
25 30 35	
ctt ggt gtc atc gga ctg gtg gcc ttg tac ctg gtg ttc ggt tat gga	260
Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly	
40 45 50	
gcc tct ctc ctc tgc aac ctg ata gga ttt ggc tac cca gcc tac atc	308
Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile	
55 60 65 70	
tca att aaa gct ata gag agt ccc aac aaa gaa gat gat acc cag tgg	356
Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp	
75 80 85	
ctg acc tac tgg gta gtg tat ggt gtg ttc agc att gct gaa ttc ttc	404
Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe	
90 95 100	
tct gat atc ttc ctg tca tgg ttc ccc ttc tac tac atg ctg aag tgt	452
Ser Asp Ile Phe Leu Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys	
105 110 115	
ggc ttc ctg ttg tgg tgc atg gcc ccg agc cct tct aat ggg gct gaa	500
Gly Phe Leu Leu Trp Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu	
120 125 130	
ctg ctc tac aag cgc atc atc cgt cct ttc ttc ctg aag cac gag tcc	548
Leu Leu Tyr Lys Arg Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser	
135 140 145 150	
cag atg gac agt gtg gtc aag gac ctt aaa gac aag gcc aaa gag act	596

Gln Met Asp Ser Val Val Lys Asp Leu Lys Asp Lys Ala Lys Glu Thr
 155 160 165
 gca gat gcc atc act aaa gaa gcg aag aaa gct acc gtg aat tta ctg 644
 Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu
 170 175 180
 ggt gaa gaa aag aag agc acc taaaccagac tggatggaaa cttcctgccc 695
 Gly Glu Glu Lys Lys Ser Thr
 185
 tctctgtacc ttctactgg agcttgatgt tatattaggg actgtggtat aattatttta 755
 ataatgttgc cttggaaaca tttttgagat attaaagatt ggaatgtgtt gtaagtttct 815
 ttgcttactt ttactgtcta tatatatagg gagcacttta aacttaatgc agtgggcagt 875
 gtccacgttt ttggaaaatg tattttgcct ctgggtagga aaagatgtat gttgctatcc 935
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<210> 200

<211> 189

<212> PRT

<213> Homo sapiens

<400> 200

Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg Phe Leu His Glu Lys
 1 5 10 15
 Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val
 20 25 30
 Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr
 35 40 45
 Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe
 50 55 60

606/861

aagtatttgt ggtaataacc cttaccggga gtttactga agctactctc cagagagacc	180
ggatcttcaa acattttacc aggaagcgcc aaagggt atg cga agg cga gtc cac	236
Met Arg Arg Arg Val His	
1 5	
cag atc aat gga cac aag ttc atg gcc acg tat ctg agg cag ccc acc	284
Gln Ile Asn Gly His Lys Phe Met Ala Thr Tyr Leu Arg Gln Pro Thr	
10 15 20	
tac tgc tct cac tgc agg gag ttt atc tgg gga gtg ttt ggg aaa cag	332
Tyr Cys Ser His Cys Arg Glu Phe Ile Trp Gly Val Phe Gly Lys Gln	
25 30 35	
ggt tat cag tgc caa gtg tgc acc tgt gtc gtc cat aaa cgc tgc cat	380
Gly Tyr Gln Cys Gln Val Cys Thr Cys Val Val His Lys Arg Cys His	
40 45 50	
cat cta att gtt aca gcc tgt act tgc caa aac aat att aac aaa gtg	428
His Leu Ile Val Thr Ala Cys Thr Cys Gln Asn Asn Ile Asn Lys Val	
55 60 65 70	
gat tca aag att gca gaa cag agg ttc ggg atc aac atc cca cac aag	476
Asp Ser Lys Ile Ala Glu Gln Arg Phe Gly Ile Asn Ile Pro His Lys	
75 80 85	
ttc agc atc cac aac tac aaa gtg cca aca ttc tgc gat cac tgt ggc	524
Phe Ser Ile His Asn Tyr Lys Val Pro Thr Phe Cys Asp His Cys Gly	
90 95 100	
tca ctg ctc tgg gga ata atg cga caa gga ctt cag tgt aaa ata tgt	572
Ser Leu Leu Trp Gly Ile Met Arg Gln Gly Leu Gln Cys Lys Ile Cys	
105 110 115	
aaa atg aat gtg cat att cga tgt caa gcg aac gtg gcc cct aac tgt	620
Lys Met Asn Val His Ile Arg Cys Gln Ala Asn Val Ala Pro Asn Cys	

120	125	130	
ggg gta aat gcg gtg gaa ctt gcc aag acc ctg gca ggg atg ggt ctc			668
Gly Val Asn Ala Val Glu Leu Ala Lys Thr Leu Ala Gly Met Gly Leu			
135	140	145	150
caa ccc gga aat att tct cca acc tcg aaa ctc gtt tcc aga tcg acc			716
Gln Pro Gly Asn Ile Ser Pro Thr Ser Lys Leu Val Ser Arg Ser Thr			
	155	160	165
cta aga cga cag gga aag gag agc agc aaa gaa gga aat ggg att ggg			764
Leu Arg Arg Gln Gly Lys Glu Ser Ser Lys Glu Gly Asn Gly Ile Gly			
	170	175	180
gtt aat tct tcc aac cga ctt ggt atc gac aac ttt gag ttc atc cga			812
Val Asn Ser Ser Asn Arg Leu Gly Ile Asp Asn Phe Glu Phe Ile Arg			
	185	190	195
gtg ttg ggg aag ggg agt ttt ggg aag gtg atg ctt gca aga gta aaa			860
Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Arg Val Lys			
200	205	210	
gaa aca gga gac ctc tat gct gtg aag gtg ctg aag aag gac gtg att			908
Glu Thr Gly Asp Leu Tyr Ala Val Lys Val Leu Lys Lys Asp Val Ile			
215	220	225	230
ctg cag gat gat gat gtg gaa tgc acc atg acc gag aaa agg atc ctg			956
Leu Gln Asp Asp Asp Val Glu Cys Thr Met Thr Glu Lys Arg Ile Leu			
	235	240	245
tct ctg gcc cgc aat cac ccc ttc ctc act cag ttg ttc tgc tgc ttt			1004
Ser Leu Ala Arg Asn His Pro Phe Leu Thr Gln Leu Phe Cys Cys Phe			
	250	255	260
cag acc ccc gat cgt ctg ttt ttt gtg atg gag ttt gtg aat ggg ggt			1052
Gln Thr Pro Asp Arg Leu Phe Phe Val Met Glu Phe Val Asn Gly Gly			

265	270	275	
gac ttg atg ttc cac att cag aag tct cgt cgt ttt gat gaa gca cga			1100
Asp Leu Met Phe His Ile Gln Lys Ser Arg Arg Phe Asp Glu Ala Arg			
280	285	290	
gct cgc ttc tat gct gca gaa atc att tcg gct ctc atg ttc ctc cat			1148
Ala Arg Phe Tyr Ala Ala Glu Ile Ile Ser Ala Leu Met Phe Leu His			
295	300	305	310
gat aaa gga atc atc tat aga gat ctg aaa ctg gac aat gtc ctg ttg			1196
Asp Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu			
315	320	325	
gac cac gag ggt cac tgt aaa ctg gca gac ttc gga atg tgc aag gag			1244
Asp His Glu Gly His Cys Lys Leu Ala Asp Phe Gly Met Cys Lys Glu			
330	335	340	
ggg att tgc aat ggt gtc acc acg gcc aca ttc tgt ggc acg cca gac			1292
Gly Ile Cys Asn Gly Val Thr Thr Ala Thr Phe Cys Gly Thr Pro Asp			
345	350	355	
tat atc gct cca gag atc ctc cag gaa atg ctg tac ggg cct gca gta			1340
Tyr Ile Ala Pro Glu Ile Leu Gln Glu Met Leu Tyr Gly Pro Ala Val			
360	365	370	
gac tgg tgg gca atg ggc gtg ttg ctc tat gag atg ctc tgt ggt cac			1388
Asp Trp Trp Ala Met Gly Val Leu Leu Tyr Glu Met Leu Cys Gly His			
375	380	385	390
gcg cct ttt gag gca gag aat gaa gat gac ctc ttt gag gcc ata ctg			1436
Ala Pro Phe Glu Ala Glu Asn Glu Asp Asp Leu Phe Glu Ala Ile Leu			
395	400	405	
aat gat gag gtg gtc tac cct acc tgg ctc cat gaa gat gcc aca ggg			1484
Asn Asp Glu Val Val Tyr Pro Thr Trp Leu His Glu Asp Ala Thr Gly			

410	415	420	
atc cta aaa tct ttc atg acc aag aac ccc acc atg cgc ttg ggc agc			1532
Ile Leu Lys Ser Phe Met Thr Lys Asn Pro Thr Met Arg Leu Gly Ser			
425	430	435	
ctg act cag gga ggc gag cac gcc atc ttg aga cat cct ttt ttt aag			1580
Leu Thr Gln Gly Gly Glu His Ala Ile Leu Arg His Pro Phe Phe Lys			
440	445	450	
gaa atc gac tgg gcc cag ctg aac cat cgc caa ata gaa ccg cct ttc			1628
Glu Ile Asp Trp Ala Gln Leu Asn His Arg Gln Ile Glu Pro Pro Phe			
455	460	465	470
aga ccc aga atc aaa tcc cga gaa gat gtc agt aat ttt gac cct gac			1676
Arg Pro Arg Ile Lys Ser Arg Glu Asp Val Ser Asn Phe Asp Pro Asp			
475	480	485	
ttc ata aag gaa gag cca gtt tta act cca att gat gag gga cat ctt			1724
Phe Ile Lys Glu Glu Pro Val Leu Thr Pro Ile Asp Glu Gly His Leu			
490	495	500	
cca atg att aac cag gat gag ttt aga aac ttt tcc tat gtg tct cca			1772
Pro Met Ile Asn Gln Asp Glu Phe Arg Asn Phe Ser Tyr Val Ser Pro			
505	510	515	
gaa ttg caa cca tagccttatg gggagtgaga gagagggcac gagaacccaa			1824
Glu Leu Gln Pro			
520			
agggaataga gattctccag gaatttcttc tatgggacct tcccagcatc agccttagaa			1884
caagaacctt accttcaagg agcaagtga gaactctgtg aaggatggaa ctttcagata			1944
tcaactat tt agagtccaga gggagccatg gcactagaaa tagttgataa tgaaatgaga			2004
ttttatgaag tataccgctc cacctatgag cgtctgtctc tgtgggcttg ggatgttaac			2064
aggagccaaa aggagggaaa gtgtgaagaa taaagtagat ctgagaaatt ctgagccaat			2124

caggcttctt aattcaagag acaaaccaag acgttctgtc aactgtgctg tgctcttctt 2184
 taagccaatg aacccaatt cctggcagtc tacaagaagt ctcttaatgc taatgaagaa 2244
 tttaaaggtc tttttaagga aatgaagggc tttccaaata gaatgattta ctctgaagaa 2304
 acaaacaatg gtatctctga aactcacaac ctaaagccca atcttgaaaa tatgttgtgc 2364
 accaagacga ctgcttcagc ttcttctctt atccttactt tctttaatag atatttatta 2424
 aactgtccag tgaaaagggt ccacaatgcc cagtattgta aacaacaggt ttgcattcat 2484
 gaagctttca ttcattctgg agtctactaa tttacctgaa tgggtgttgc attctgtgaa 2544
 atgcctctcc acgttgcata tgtcacactt ttgtctgcac ataactcttt tttcacaaga 2604
 agggtcactg ccacaacagc acagtcagcg ggtgaattac aggtgcctgc tgcctgccta 2664
 cctgggtaat ctgatcttgt ctgtatcgcc gtgtgctcat cactgaggaa ttgcaggcca 2724
 ctcatgtcag tgaccagatt tgtggcttat aaacattagc agtttatatta tgttttaaga 2784
 tgcaaagatg tgtgtttgat attcacttta ataattagaa atggatcttg taaacagggc 2844
 atatatcaaa gatgacctta taatatgtac ccgaatatac agttcaagaa ttttgtctga 2904
 ctggaaataa atgcattttg tagcaaaa 2932

<210> 202

<211> 522

<212> PRT

<213> Homo sapiens

<400> 202

Met Arg Arg Arg Val His Gln Ile Asn Gly His Lys Phe Met Ala Thr

1 5 10 15

Tyr Leu Arg Gln Pro Thr Tyr Cys Ser His Cys Arg Glu Phe Ile Trp

20 25 30

Gly Val Phe Gly Lys Gln Gly Tyr Gln Cys Gln Val Cys Thr Cys Val

35 40 45

Val His Lys Arg Cys His His Leu Ile Val Thr Ala Cys Thr Cys Gln

50 55 60
Asn Asn Ile Asn Lys Val Asp Ser Lys Ile Ala Glu Gln Arg Phe Gly
65 70 75 80
Ile Asn Ile Pro His Lys Phe Ser Ile His Asn Tyr Lys Val Pro Thr
85 90 95
Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Ile Met Arg Gln Gly
100 105 110
Leu Gln Cys Lys Ile Cys Lys Met Asn Val His Ile Arg Cys Gln Ala
115 120 125
Asn Val Ala Pro Asn Cys Gly Val Asn Ala Val Glu Leu Ala Lys Thr
130 135 140
Leu Ala Gly Met Gly Leu Gln Pro Gly Asn Ile Ser Pro Thr Ser Lys
145 150 155 160
Leu Val Ser Arg Ser Thr Leu Arg Arg Gln Gly Lys Glu Ser Ser Lys
165 170 175
Glu Gly Asn Gly Ile Gly Val Asn Ser Ser Asn Arg Leu Gly Ile Asp
180 185 190
Asn Phe Glu Phe Ile Arg Val Leu Gly Lys Gly Ser Phe Gly Lys Val
195 200 205
Met Leu Ala Arg Val Lys Glu Thr Gly Asp Leu Tyr Ala Val Lys Val
210 215 220
Leu Lys Lys Asp Val Ile Leu Gln Asp Asp Asp Val Glu Cys Thr Met
225 230 235 240
Thr Glu Lys Arg Ile Leu Ser Leu Ala Arg Asn His Pro Phe Leu Thr
245 250 255
Gln Leu Phe Cys Cys Phe Gln Thr Pro Asp Arg Leu Phe Phe Val Met
260 265 270

Glu Phe Val Asn Gly Gly Asp Leu Met Phe His Ile Gln Lys Ser Arg
275 280 285
Arg Phe Asp Glu Ala Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ile Ser
290 295 300
Ala Leu Met Phe Leu His Asp Lys Gly Ile Ile Tyr Arg Asp Leu Lys
305 310 315 320
Leu Asp Asn Val Leu Leu Asp His Glu Gly His Cys Lys Leu Ala Asp
325 330 335
Phe Gly Met Cys Lys Glu Gly Ile Cys Asn Gly Val Thr Thr Ala Thr
340 345 350
Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Leu Gln Glu Met
355 360 365
Leu Tyr Gly Pro Ala Val Asp Trp Trp Ala Met Gly Val Leu Leu Tyr
370 375 380
Glu Met Leu Cys Gly His Ala Pro Phe Glu Ala Glu Asn Glu Asp Asp
385 390 395 400
Leu Phe Glu Ala Ile Leu Asn Asp Glu Val Val Tyr Pro Thr Trp Leu
405 410 415
His Glu Asp Ala Thr Gly Ile Leu Lys Ser Phe Met Thr Lys Asn Pro
420 425 430
Thr Met Arg Leu Gly Ser Leu Thr Gln Gly Gly Glu His Ala Ile Leu
435 440 445
Arg His Pro Phe Phe Lys Glu Ile Asp Trp Ala Gln Leu Asn His Arg
450 455 460
Gln Ile Glu Pro Pro Phe Arg Pro Arg Ile Lys Ser Arg Glu Asp Val
465 470 475 480
Ser Asn Phe Asp Pro Asp Phe Ile Lys Glu Glu Pro Val Leu Thr Pro

485 490 495
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 203

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 gcgcttgga gggacggctg ggcttccccg gcccgctgag ggctaggcgg cgggctcccc 180
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 cccccggggc cggggcagcg gcgccggc atg tgc tct ggc acc atg aag ttc 412

Met Ser Ser Gly Thr Met Lys Phe

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 Asn Gly Tyr Leu Arg Val Arg Ile Gly Glu Ala Val Gly Leu Gln Pro
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 acc cgc tgg tcc ctg cgc cac tgc ctc ttc aag aag ggc cac cag ctg 508

Ile	Asn	Gly	His	Lys	Phe	Met	Ala	Thr	Tyr	Leu	Arg	Gln	Pro	Thr	Tyr		
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tgc	tct	cac	tgc	agg	gag	ttt	atc	tgg	gga	gtg	ttt	ggg	aaa	cag	ggt	988	
Cys	Ser	His	Cys	Arg	Glu	Phe	Ile	Trp	Gly	Val	Phe	Gly	Lys	Gln	Gly		
185					190						195			200			
tat	cag	tgc	caa	gtg	tgc	acc	tgt	gtc	gtc	cat	aaa	cgc	tgc	cat	cat	1036	
Tyr	Gln	Cys	Gln	Val	Cys	Thr	Cys	Val	Val	His	Lys	Arg	Cys	His	His		
				205					210					215			
cta	att	gtt	aca	gcc	tgt	act	tgc	caa	aac	aat	att	aac	aaa	gtg	gat	1084	
Leu	Ile	Val	Thr	Ala	Cys	Thr	Cys	Gln	Asn	Asn	Ile	Asn	Lys	Val	Asp		
				220					225					230			
tca	aag	att	gca	gaa	cag	agg	ttc	ggg	atc	aac	atc	cca	cac	aag	ttc	1132	
Ser	Lys	Ile	Ala	Glu	Gln	Arg	Phe	Gly	Ile	Asn	Ile	Pro	His	Lys	Phe		
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agc	atc	cac	aac	tac	aaa	gtg	cca	aca	ttc	tgc	gat	cac	tgt	ggc	tca	1180	
Ser	Ile	His	Asn	Tyr	Lys	Val	Pro	Thr	Phe	Cys	Asp	His	Cys	Gly	Ser		
				250					255					260			
ctg	ctc	tgg	gga	ata	atg	cga	caa	gga	ctt	cag	tgt	aaa	ata	tgt	aaa	1228	
Leu	Leu	Trp	Gly	Ile	Met	Arg	Gln	Gly	Leu	Gln	Cys	Lys	Ile	Cys	Lys		
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Met	Asn	Val	His	Ile	Arg	Cys	Gln	Ala	Asn	Val	Ala	Pro	Asn	Cys	Gly		
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gta	aat	gcg	gtg	gaa	ctt	gcc	aag	acc	ctg	gca	ggg	atg	ggt	ctc	caa	1324	
Val	Asn	Ala	Val	Glu	Leu	Ala	Lys	Thr	Leu	Ala	Gly	Met	Gly	Leu	Gln		
				300							305			310			
ccc	gga	aat	att	tct	cca	acc	tcg	aaa	ctc	gtt	tcc	aga	tcg	acc	cta	1372	

Pro Gly Asn Ile Ser Pro Thr Ser Lys Leu Val Ser Arg Ser Thr Leu	
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aga cga cag gga aag gag agc agc aaa gaa gga aat ggg att ggg gtt	1420
Arg Arg Gln Gly Lys Glu Ser Ser Lys Glu Gly Asn Gly Ile Gly Val	
330 335 340	
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Asn Ser Ser Asn Arg Leu Gly Ile Asp Asn Phe Glu Phe Ile Arg Val	
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Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Arg Val Lys Glu	
365 370 375	
aca gga gac ctc tat gct gtg aag gtg ctg aag aag gac gtg att ctg	1564
Thr Gly Asp Leu Tyr Ala Val Lys Val Leu Lys Lys Asp Val Ile Leu	
380 385 390	
cag gat gat gat gtg gaa tgc acc atg acc gag aaa agg atc ctg tct	1612
Gln Asp Asp Asp Val Glu Cys Thr Met Thr Glu Lys Arg Ile Leu Ser	
395 400 405	
ctg gcc cgc aat cac ccc ttc ctc act cag ttg ttc tgc tgc ttt cag	1660
Leu Ala Arg Asn His Pro Phe Leu Thr Gln Leu Phe Cys Cys Phe Gln	
410 415 420	
acc ccc gat cgt ctg ttt ttt gtg atg gag ttt gtg aat ggg ggt gac	1708
Thr Pro Asp Arg Leu Phe Phe Val Met Glu Phe Val Asn Gly Gly Asp	
425 430 435 440	
ttg atg ttc cac att cag aag tct cgt cgt ttt gat gaa gca cga gct	1756
Leu Met Phe His Ile Gln Lys Ser Arg Arg Phe Asp Glu Ala Arg Ala	
445 450 455	
cgc ttc tat gct gca gaa atc att tcg gct ctc atg ttc ctc cat gat	1804

Arg Phe Tyr Ala Ala Glu Ile Ile Ser Ala Leu Met Phe Leu His Asp
 460 465 470
 aaa gga atc atc tat aga gat ctg aaa ctg gac aat gtc ctg ttg gac 1852
 Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp
 475 480 485
 cac gag ggt cac tgt aaa ctg gca gac ttc gga atg tgc aag gag ggg 1900
 His Glu Gly His Cys Lys Leu Ala Asp Phe Gly Met Cys Lys Glu Gly
 490 495 500
 att tgc aat ggt gtc acc acg gcc aca ttc tgt ggc acg cca gac tat 1948
 Ile Cys Asn Gly Val Thr Thr Ala Thr Phe Cys Gly Thr Pro Asp Tyr
 505 510 515 520
 atc gct cca gag atc ctc cag gaa atg ctg tac ggg cct gca gta gac 1996
 Ile Ala Pro Glu Ile Leu Gln Glu Met Leu Tyr Gly Pro Ala Val Asp
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 tgg tgg gca atg ggc gtg ttg ctc tat gag atg ctc tgt ggt cac gcg 2044
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 cct ttt gag gca gag aac gaa gat gac ctc ttt gag gcc ata ctg aat 2092
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 gat gag gtg gtc tac cct acc tgg ctc cat gaa gat gcc aca ggg atc 2140
 Asp Glu Val Val Tyr Pro Thr Trp Leu His Glu Asp Ala Thr Gly Ile
 570 575 580
 cta aaa tct ttc atg acc aag aac ccc acc atg cgc ttg ggc agc ctg 2188
 Leu Lys Ser Phe Met Thr Lys Asn Pro Thr Met Arg Leu Gly Ser Leu
 585 590 595 600
 act cag gga ggc gag cac gcc atc ttg aga cat cct ttt ttt aag gaa 2236

Thr Gln Gly Gly Glu His Ala Ile Leu Arg His Pro Phe Phe Lys Glu
 605 610 615
 atc gac tgg gcc cag ctg aac cat cgc caa ata gaa ccg cct ttc aga 2284
 Ile Asp Trp Ala Gln Leu Asn His Arg Gln Ile Glu Pro Pro Phe Arg
 620 625 630
 ccc aga atc aaa tcc cga gaa gat gtc agt aat ttt gac cct gac ttc 2332
 Pro Arg Ile Lys Ser Arg Glu Asp Val Ser Asn Phe Asp Pro Asp Phe
 635 640 645
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 Ile Lys Glu Glu Pro Val Leu Thr Pro Ile Asp Glu Gly His Leu Pro
 650 655 660
 atg att aac cag gat gag ttt aga aac ttt tcc tat gtg tct cca gaa 2428
 Met Ile Asn Gln Asp Glu Phe Arg Asn Phe Ser Tyr Val Ser Pro Glu
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 ttg caa cca tagccttatg gggagtgaga gagagggcac gagaacccaa 2477
 Leu Gln Pro
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<212> PRT

<213> Homo sapiens

<400> 204

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 35 40 45
 Val Asp Gln Val Arg Val Gly Gln Thr Ser Thr Lys Gln Lys Thr Asn
 50 55 60
 Lys Pro Thr Tyr Asn Glu Glu Phe Cys Ala Asn Val Thr Asp Gly Gly
 65 70 75 80
 His Leu Glu Leu Ala Val Phe His Glu Thr Pro Leu Gly Tyr Asp His
 85 90 95
 Phe Val Ala Asn Cys Thr Leu Gln Phe Gln Glu Leu Leu Arg Thr Thr

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Gly Ala Ser Asp Thr Phe Glu Gly Trp Val Asp Leu Glu Pro Glu Gly			
115	120	125	
Lys Val Phe Val Val Ile Thr Leu Thr Gly Ser Phe Thr Glu Ala Thr			
130	135	140	
Leu Gln Arg Asp Arg Ile Phe Lys His Phe Thr Arg Lys Arg Gln Arg			
145	150	155	160
Ala Met Arg Arg Arg Val His Gln Ile Asn Gly His Lys Phe Met Ala			
165	170	175	
Thr Tyr Leu Arg Gln Pro Thr Tyr Cys Ser His Cys Arg Glu Phe Ile			
180	185	190	
Trp Gly Val Phe Gly Lys Gln Gly Tyr Gln Cys Gln Val Cys Thr Cys			
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Val Val His Lys Arg Cys His His Leu Ile Val Thr Ala Cys Thr Cys			
210	215	220	
Gln Asn Asn Ile Asn Lys Val Asp Ser Lys Ile Ala Glu Gln Arg Phe			
225	230	235	240
Gly Ile Asn Ile Pro His Lys Phe Ser Ile His Asn Tyr Lys Val Pro			
245	250	255	
Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Ile Met Arg Gln			
260	265	270	
Gly Leu Gln Cys Lys Ile Cys Lys Met Asn Val His Ile Arg Cys Gln			
275	280	285	
Ala Asn Val Ala Pro Asn Cys Gly Val Asn Ala Val Glu Leu Ala Lys			
290	295	300	
Thr Leu Ala Gly Met Gly Leu Gln Pro Gly Asn Ile Ser Pro Thr Ser			
305	310	315	320

Lys Leu Val Ser Arg Ser Thr Leu Arg Arg Gln Gly Lys Glu Ser Ser
325 330 335

Lys Glu Gly Asn Gly Ile Gly Val Asn Ser Ser Asn Arg Leu Gly Ile
340 345 350

Asp Asn Phe Glu Phe Ile Arg Val Leu Gly Lys Gly Ser Phe Gly Lys
355 360 365

Val Met Leu Ala Arg Val Lys Glu Thr Gly Asp Leu Tyr Ala Val Lys
370 375 380

Val Leu Lys Lys Asp Val Ile Leu Gln Asp Asp Asp Val Glu Cys Thr
385 390 395 400

Met Thr Glu Lys Arg Ile Leu Ser Leu Ala Arg Asn His Pro Phe Leu
405 410 415

Thr Gln Leu Phe Cys Cys Phe Gln Thr Pro Asp Arg Leu Phe Phe Val
420 425 430

Met Glu Phe Val Asn Gly Gly Asp Leu Met Phe His Ile Gln Lys Ser
435 440 445

Arg Arg Phe Asp Glu Ala Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ile
450 455 460

Ser Ala Leu Met Phe Leu His Asp Lys Gly Ile Ile Tyr Arg Asp Leu
465 470 475 480

Lys Leu Asp Asn Val Leu Leu Asp His Glu Gly His Cys Lys Leu Ala
485 490 495

Asp Phe Gly Met Cys Lys Glu Gly Ile Cys Asn Gly Val Thr Thr Ala
500 505 510

Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Leu Gln Glu
515 520 525

Met Leu Tyr Gly Pro Ala Val Asp Trp Trp Ala Met Gly Val Leu Leu

530 535 540
Tyr Glu Met Leu Cys Gly His Ala Pro Phe Glu Ala Glu Asn Glu Asp
545 550 555 560
Asp Leu Phe Glu Ala Ile Leu Asn Asp Glu Val Val Tyr Pro Thr Trp
565 570 575
Leu His Glu Asp Ala Thr Gly Ile Leu Lys Ser Phe Met Thr Lys Asn
580 585 590
Pro Thr Met Arg Leu Gly Ser Leu Thr Gln Gly Gly Glu His Ala Ile
595 600 605
Leu Arg His Pro Phe Phe Lys Glu Ile Asp Trp Ala Gln Leu Asn His
610 615 620
Arg Gln Ile Glu Pro Pro Phe Arg Pro Arg Ile Lys Ser Arg Glu Asp
625 630 635 640
Val Ser Asn Phe Asp Pro Asp Phe Ile Lys Glu Glu Pro Val Leu Thr
645 650 655
Pro Ile Asp Glu Gly His Leu Pro Met Ile Asn Gln Asp Glu Phe Arg
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<211> 2874

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (160).. (1272)

<400> 205

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cttatcttag agccacactg agattggaac ccgcaaaat atg cca gga aac gcc 174

Met Pro Gly Asn Ala

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acc cca gtg acc acc act gcc ccg tgg gcc tcc ctg ggc ctc tcc gcc 222

Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser Leu Gly Leu Ser Ala

10

15

20

aag acc tgc aac aac gtg tcc ttc gaa gag agc agg ata gtc ctg gtc 270

Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser Arg Ile Val Leu Val

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gtg gtg tac agc gcg gtg tgc acg ctg ggg gtg ccg gcc aac tgc ctg 318

Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu

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45

50

act gcg tgg ctg gcg ctg ctg cag gta ctg cag ggc aac gtg ctg gcc 366

Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala

55

60

65

gtc tac ctg ctc tgc ctg gca ctc tgc gag ctg ctg tac aca ggc acg 414

Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr

70

75

80

85

ctg cca ctc tgg gtc atc tat atc cgc aac cag cac cgc tgg acc cta 462

Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu

90

95

100

ggc ctg ctg gcc tgc aag gtg acc gcc tac atc ttc ttc tgc aac atc 510

Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile

105

110

115

624/861

tac gtc agc atc ctc ttc ctg tgc tgc atc tcc tgc gac cgc ttc gtg	558
Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val	
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gcc gtg gtg tac gcg ctg gag agt cgg ggc cgc cgc cgc cgg agg acc	606
Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr	
135 140 145	
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Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His	
150 155 160 165	
tac ccg gtg ttc cag acg gaa gac aag gag acc tgc ttt gac atg ctg	702
Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu	
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Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val	
185 190 195	
ggc ttt gcc atc cct ctc tcc atc atc gcc ttc acc aac cac cgg att	798
Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile	
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ttc agg agc atc aag cag agc atg ggc tta agc gct gcc cag aag gcc	846
Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala	
215 220 225	
aag gtg aag cac tcg gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc	894
Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys	
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Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser	
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Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu	
265 270 275	
tac aca gcc tct gtg gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg	1038
Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val	
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gct gac ccc att atc tac gtg ctg gcc acg gac cat tcc cgc caa gaa	1086
Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu	
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Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp	
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Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro	
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Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro	
345 350 355	
ggg tca cca tgc cct gca aag agg ctg att gag gag tcc tgc	1272
Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys	
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<211> 371

<212> PRT

<213> Homo sapiens

<400> 206

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 Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val
 35 40 45
 Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln
 50 55 60
 Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu
 65 70 75 80
 Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln
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 His Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile
 100 105 110
 Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser
 115 120 125
 Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg
 130 135 140
 Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu
 145 150 155 160
 Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr
 165 170 175
 Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr
 180 185 190
 Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe
 195 200 205
 Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser

210 215 220
 Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val
 225 230 235 240
 Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
 245 250 255
 Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
 260 265 270
 Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
 275 280 285
 Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
 290 295 300
 His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp
 305 310 315 320
 Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
 325 330 335
 Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
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 Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
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 Glu Ser Cys
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<211> 2588

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (901).. (2040)

<400> 207

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cacactgaga ttggaacccg caaaatatgc cagggaggaa ggtgagcaag ggacacgaca   180
ctcaccogga taaaccaaac aagcgcagcg aggctgtggg gaaaccggan ccctgcacac   240
cgccggggga aggtgggcn cgcaccac cgtggaagaa cagcgcggan gcacccacg   300
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atg tgc cca atg cta ctg aaa aac ggt tac aat gga aac gcc acc cca   948
Met Cys Pro Met Leu Leu Lys Asn Gly Tyr Asn Gly Asn Ala Thr Pro
1           5           10          15
gtg acc acc act gcc ccg tgg gcc tcc ctg ggc ctc tcc gcc aag acc   996
Val Thr Thr Thr Ala Pro Trp Ala Ser Leu Gly Leu Ser Ala Lys Thr
          20          25          30
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Cys Asn Asn Val Ser Phe Glu Glu Ser Arg Ile Val Leu Val Val Val
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Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu Thr Ala	
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Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala Val Tyr	
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Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr Leu Pro	
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ctc tgg gtc atc tat atc cgc aac cag cac cgc tgg acc cta ggc ctg	1236
Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu Gly Leu	
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ctg gcc tgc aag gtg acc gcc tac atc ttc ttc tgc aac atc tac gtc	1284
Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile Tyr Val	
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Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val Ala Val	
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Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr Ala Ile	
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Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His Tyr Pro	
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Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu Gln Met	
180 185 190	

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Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe	
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gcc atc cct ctc tcc atc atc gcc ttc acc aac cac cgg att ttc agg	1572
Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg	
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agc atc aag cag agc atg ggc tta agc gct gcc cag aag gcc aag gtg	1620
Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val	
225 230 235 240	
aag cac tcg gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc ttc gcc	1668
Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala	
245 250 255	
ccg tac cac ctg gtt ctc ctc gtc aaa gcc gct gcc ttt tcc tac tac	1716
Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr	
260 265 270	
aga gga gac agg aac gcc atg tgc ggc ttg gag gaa agg ctg tac aca	1764
Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr	
275 280 285	
gcc tct gtg gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg gct gac	1812
Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp	
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ccc att atc tac gtg ctg gcc acg gac cat tcc cgc caa gaa gtg tcc	1860
Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser	
305 310 315 320	
aga atc cat aag ggg tgg aaa gag tgg tcc atg aag aca gac gtc acc	1908
Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr	
325 330 335	

agg ctc acc cac agc agg gac acc gag gag ctg cag tcg ccc gtg gcc 1956
 Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala
 340 345 350

ctt gca gac cac tac acc ttc tcc agg ccc gtg cac cca cca ggg tca 2004
 Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser
 355 360 365

cca tgc cct gca aag agg ctg att gag gag tcc tgc tgagcccact 2050
 Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys
 370 375 380

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<211> 380

<212> PRT

<213> Homo sapiens

<400> 208

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Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu Thr Ala		
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Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala Val Tyr		
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80		
Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr Leu Pro		
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Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu Gly Leu		
100	105	110
Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile Tyr Val		
115	120	125
Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val Ala Val		
130	135	140
Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr Ala Ile		
145	150	155
160		
Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His Tyr Pro		
165	170	175
Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu Gln Met		
180	185	190
Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe		
195	200	205
Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg		
210	215	220
Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val		
225	230	235
240		

Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala
245 250 255
Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr
260 265 270
Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr
275 280 285
Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp
290 295 300
Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser
305 310 315 320
Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr
325 330 335
Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala
340 345 350
Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser
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Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys
370 375 380

<210> 209

<211> 3347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1175)..(1750)

<400> 209

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Met Leu Gln Met Asp Ser Arg

1

5

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 Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe Ala Ile Pro
 10 15 20
 ctc tcc atc atc gcc ttc acc aac cac cgg att ttc agg agc atc aag 1291
 Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg Ser Ile Lys

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Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val Lys His Ser			
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gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc ttc gcc ccg tac cac			1387
Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala Pro Tyr His			
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Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp			
75	80	85	
agg aac gcc atg tgc ggc ttg gag gaa agg ctg tac aca gcc tct gtg			1483
Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val			
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gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg gct gac ccc att atc			1531
Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp Pro Ile Ile			
105	110	115	
tac gtg ctg gcc acg gac cat tcc cgc caa gaa gtg tcc aga atc cat			1579
Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser Arg Ile His			
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aag ggg tgg aaa gag tgg tcc atg aag aca gac gtc acc agg ctc acc			1627
Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr Arg Leu Thr			
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cac agc agg gac acc gag gag ctg cag tcg ccc gtg gcc ctt gca gac			1675
His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala Leu Ala Asp			
155	160	165	
cac tac acc ttc tcc agg ccc gtg cac cca cca ggg tca cca tgc cct			1723
His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser Pro Cys Pro			

170	175	180	
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Ala Lys Arg Leu Ile Glu Glu Ser Cys			
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<212> PRT

<213> Homo sapiens

<400> 210

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 35 40 45
 Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu
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 Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala
 65 70 75 80
 Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu
 85 90 95
 Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn
 100 105 110
 Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg
 115 120 125
 Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys

130	135	140
Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln		
145	150	155
Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His		
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Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys		
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<211> 2304

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<213> Homo sapiens

<220>

<221> CDS

<222> (362).. (1729)

<400> 211

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ggactcagtt tgtttctgct gattacaccc gtgcccagga gcttgacgcc ttagataaca	180
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actttaagaa aggaatgaac atgtatttaa ccaagttcca acaaaagaat gctgccgcag	360
g atg gac gtg gta gag gtc gcg ggc agt tgg tgg gca caa gag cga gag	409
Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu	
1 5 10 15	
gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag	457
Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu	

20	25	30	
gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat			505
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His			
35	40	45	
ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag			553
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu			
50	55	60	
gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat			601
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp			
65	70	75	80
atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat			649
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp			
85	90	95	
cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca			697
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser			
100	105	110	
gtc ctc ctg aac act gag gaa atg aag ttg aaa aac ccc gga aga tac			745
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr			
115	120	125	
cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc			793
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg			
130	135	140	
atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg			841
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg			
145	150	155	160
gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca			889
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala			

165	170	175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac			937
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His			
180	185	190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg			985
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp			
195	200	205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt			1033
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe			
210	215	220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag			1081
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu			
225	230	235	240
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag			1129
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys			
245	250	255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata			1177
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile			
260	265	270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg			1225
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val			
275	280	285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc			1273
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala			
290	295	300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg			1321
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro			

305	310	315	320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag				1369
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu				
325	330	335		
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga				1417
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg				
340	345	350		
aag cag ggg gac ctg caa ccc cca gcc aaa ccc gag caa ggg tcg tcg				1465
Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser				
355	360	365		
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag				1513
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys				
370	375	380		
ggg gac agg cag gcc cct cca ggc cca ttt ggt cag ctt ccc cgc cac				1561
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His				
385	390	395	400	
ggg cac ctc gtt ctt cca cac cct gtc ctg gtg ggg ctg tcc ggg aag				1609
Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys				
405	410	415		
aca cct acc ctg tgg gca ctc agg gtg tgc cca gcc cgg ccc tgg ctc				1657
Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu				
420	425	430		
agg gag gac ctc agg gtt cct gga gat tcc tgc agt gga act cca tgc				1705
Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys				
435	440	445		
ccc gcc tcc caa cgg acc tgg acg tagagggccc ttggttccgc cattatgatt				1759
Pro Ala Ser Gln Arg Thr Trp Thr				

450 455
 tcagacagag ctgctgggtc cgtgccatat cccaggagga ccagctggcc ccctgctggc 1819
 aggctgaaca ccctgcgag cgggtgagat cggttttcgc tgcaccacgc actgattccg 1879
 accagggcac ccccttcaga gctagggacg aacagccgtg tgctcccacc tcagggcctt 1939
 gcctctgcgg cctccacttg gaaagtcttc agttccctcc aggcttctag aagcatctgg 1999
 gccagggctc atggctggat aatttccta ggcttaacaa cccaagcaag cttcgcatcc 2059
 tcgttttatt tttggttaaa cttatgaaaa tgtattaaga aagagtgcag ctcgagagag 2119
 attcagagat ggaacacacc agacccaga tcacaaagcc aaccatgcc agcccctccc 2179
 agcaccacca gcccacgac catcgttctg aattctgacg acaccgtgag cctgcctttg 2239
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 aatga 2304

<210> 212

<211> 456

<212> PRT

<213> Homo sapiens

<400> 212

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 20 25 30
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
 180 185 190
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
 195 200 205
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
 210 215 220
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
 225 230 235 240
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys
 245 250 255
 Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile
 260 265 270
 Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val
 275 280 285
 Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala

290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
305	310	315 320
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
325	330	335
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
340	345	350
Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
355	360	365
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His		
385	390	395 400
Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys		
405	410	415
Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu		
420	425	430
Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys		
435	440	445
Pro Ala Ser Gln Arg Thr Trp Thr		
450	455	

<210> 213

<211> 2304

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (362).. (1729)

<400> 213

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ggactcagtt tgtttctgct gattacaccc gtgccagga gcttgacgcc ttagataaca      180
gccatcctat tgaagtcagt gtgggccatc catctgaggt tgatgagata tttgatgcta      240
tatcatatag caaaggtgca tctgtcatcc gaatgctgca tgactacatt ggggataagg      300
actttaagaa aggaatgaac atgtatttaa ccaagttcca acaaaagaat gctgccgcag      360
g atg gac gtg gta gag gtc gcg ggc agt tgg tgg gca caa gag cga gag      409
Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu
1           5           10           15
gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag      457
Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
20           25           30
gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat      505
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35           40           45
ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag      553
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50           55           60
gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat      601
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65           70           75           80
atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat      649
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85           90           95

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cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca	697
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser	
100 105 110	
gtc ctc ctg aac act gag gaa atg aag ttg aaa aac ccc gga aga tac	745
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr	
115 120 125	
cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc	793
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg	
130 135 140	
atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg	841
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg	
145 150 155 160	
gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca	889
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala	
165 170 175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac	937
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His	
180 185 190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg	985
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	1033
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	1081
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	

cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	1129
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	1177
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	1225
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	1273
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	1321
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro	
305 310 315 320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag	1369
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu	
325 330 335	
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga	1417
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg	
340 345 350	
aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa ggg tcg tcg	1465
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser	
355 360 365	
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag	1513
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys	
370 375 380	

ggg gac agg cag gcc cct cca ggc cca ttt ggt cag ctt ccc cgc cac 1561
 Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His
 385 390 395 400
 ggg cac ctc gtt ctt cca cac cct gtc ctg gtg ggg ctg tcc ggg aag 1609
 Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys
 405 410 415
 aca cct acc ctg tgg gca ctc agg gtg tgc cca gcc cgg ccc tgg ctc 1657
 Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu
 420 425 430
 agg gag gac ctc agg gtt cct gga gat tcc tgc agt gga act cca tgc 1705
 Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys
 435 440 445
 ccc gcc tcc caa cgg acc tgg acg tagagggcc ttggttcgc cattatgatt 1759
 Pro Ala Ser Gln Arg Thr Trp Thr
 450 455
 tcagacagag ctgctgggtc cgtgccatat cccaggagga ccagctggcc ccctgctggc 1819
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 agcaccceca gcccacgac catcgttctg aattctgacg acaccgtgag cctgcctttg 2239
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 aatga 2304

<210> 214

<211> 456

<212> PRT

<213> Homo sapiens

<400> 214

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

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Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu

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25

30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His

35

40

45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50

55

60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp

65

70

75

80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp

85

90

95

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser

100

105

110

Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr

115

120

125

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg

130

135

140

Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg

145

150

155

160

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala

165

170

175

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His

180	185	190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp		
195	200	205
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe		
210	215	220
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu		
225	230	235
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys		
245	250	255
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile		
260	265	270
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val		
275	280	285
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala		
290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
305	310	315
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
325	330	335
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
340	345	350
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
355	360	365
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His		
385	390	395
		400

Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys
 405 410 415
 Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu
 420 425 430
 Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys
 435 440 445
 Pro Ala Ser Gln Arg Thr Trp Thr
 450 455

<210> 215

<211> 1964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1647)

<400> 215

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 1 5 10 15
 gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag 96
 Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
 20 25 30
 gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat 144
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag 192

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50

55

60

gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat 240

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp

65

70

75

80

atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat 288

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp

85

90

95

cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca 336

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser

100

105

110

gtc ctc ctg aac att gag gaa atg aag ttg aaa aac ccc gga aga tac 384

Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr

115

120

125

cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc 432

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg

130

135

140

atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg 480

Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg

145

150

155

160

gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca 528

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala

165

170

175

tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac 576

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His

180

185

190

atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg 624

Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	672
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	720
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	768
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	816
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	864
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	912
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	960
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro	
305 310 315 320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag	1008
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu	
325 330 335	
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga	1056

Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg	
340	345
aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa ggg tcg tcg	1104
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser	
355	360
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag	1152
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys	
370	375
ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc ccg cgg ccc	1200
Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro	
385	390
att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc aca ccc tgt	1248
Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys	
405	410
cct ggt ggg gct gtc ccg gaa gac acc tac cct gtg ggc act cag ggt	1296
Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly	
420	425
gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt tcc tgg aga	1344
Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg	
435	440
ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac ctg gac gta	1392
Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val	
450	455
gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc tgc tgg gtc	1440
Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val	
465	470
cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg cag gct gaa	1488

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
 485 490 495
 cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc agc act gat 1536
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
 500 505 510
 tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag ccg tgt gct 1584
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
 515 520 525
 ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa agt tct cag 1632
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
 530 535 540
 ttc cct cca ggc ttc tagaagcatc tgggccaggg ctcatggctg gataatttcc 1687
 Phe Pro Pro Gly Phe
 545
 ctaggcttaa caacccaagc aagcttcgcg tctctgtttt atttttgggtt aaacttatga 1747
 aaatgtatta agaaagagtg cagctcgaga gagattcaga gatggaacac accagacccc 1807
 agatcacaaa gccaaccatg cccagcccct cccagcaccc ccagccccac gaccatcggt 1867
 ctgaattctg acgacaccgt gagcctgcct ttgtacttta aactcatgga aggataacta 1927
 ccttcacgtt ttgaaataaa tgtttcctgt tgaaatg 1964

<210> 216

<211> 549

<212> PRT

<213> Homo sapiens

<400> 216

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 20 25 30
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
 180 185 190
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
 195 200 205
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
 210 215 220
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu

659/861

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
 450 455 460
 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
 465 470 475 480
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
 485 490 495
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
 500 505 510
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
 515 520 525
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
 530 535 540
 Phe Pro Pro Gly Phe
 545

<210> 217

<211> 1964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1647)

<400> 217

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 gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag 96

Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
 20 25 30
 gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat 144
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag 192
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat 240
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat 288
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca 336
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 gtc ctc ctg aac att gag gaa atg aag ttg aaa aac ccc gga aga tac 384
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc 432
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg 480
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca 528

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala	
165 170 175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac	576
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His	
180 185 190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg	624
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	672
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	720
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	768
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	816
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	864
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	912
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	960

Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro
 305 310 315 320
 tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag 1008
 Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu
 325 330 335
 gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga 1056
 Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg
 340 345 350
 aag cag ggg gac ctg caa ccc cca gcc aaa ccc gag caa ggg tcg tcg 1104
 Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser
 355 360 365
 gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag 1152
 Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys
 370 375 380
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 Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro
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 att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc aca ccc tgt 1248
 Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys
 405 410 415
 cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc act cag ggt 1296
 Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly
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 Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
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Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
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 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
 465 470 475 480
 cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg cag gct gaa 1488
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
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 cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc agc act gat 1536
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
 500 505 510
 tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag ccg tgt gct 1584
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
 515 520 525
 ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa agt tct cag 1632
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
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 Phe Pro Pro Gly Phe
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<211> 549

<212> PRT

<213> Homo sapiens

<400> 218

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 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His

180	185	190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp		
195	200	205
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe		
210	215	220
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu		
225	230	235
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys		
245	250	255
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile		
260	265	270
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val		
275	280	285
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala		
290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
305	310	315
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
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Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
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Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
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Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro		
385	390	395
		400

Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys
 405 410 415
 Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly
 420 425 430
 Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
 435 440 445
 Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
 450 455 460
 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
 465 470 475 480
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
 485 490 495
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
 500 505 510
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
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 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
 530 535 540
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<210> 219

<211> 2647

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (755).. (2335)

<400> 219

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 aatgggtggac tccacagtcc ctccgcgaga gacgtggttt ccatgcgtac aatagatctt 180
 cctcatcccc caaacccaac accctcctgc tcaacaggcg ttattcctaa agtggcttca 240
 ctgttcagac tgaagagcca cggtagccaa agtgatgagc ggagtagaac cgagcagtcg 300
 ggagagatct tgttccctgt aggaaactgg gcatcgctga ggccctgagc atcccaggag 360
 gccgattgca cagagacctc tggtcgctga cccagtcctg cctccacatc cctggaatag 420
 cccatcatgg gcccttcacc ctgggcaggt ggaaaccatt caacctgctg gggccggtgt 480
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 gtgggccact gggctctggcc cttttttccc tgggggcggc ggtggaatgg gggttacgca 660
 gccagccagc atctgggagc ccggcgagag cggttcaggt gttctccgaa gccgccgcgt 720
 acggtgtgac cttagacaa ttctgtctca cagg atg gac gtg gta gag gtc gcg 775

Met Asp Val Val Glu Val Ala

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ggc agt tgg tgg gca caa gag cga gag gac atc att atg aaa tac gaa 823
 Gly Ser Trp Trp Ala Gln Glu Arg Glu Asp Ile Ile Met Lys Tyr Glu

10

15

20

aag gga cac cga gct ggg ctg cca gag gac aag ggg cct aag cct ttt 871
 Lys Gly His Arg Ala Gly Leu Pro Glu Asp Lys Gly Pro Lys Pro Phe

25

30

35

cga agc tac aac aac aac gtc gat cat ttg ggg att gta cat gag acg 919
 Arg Ser Tyr Asn Asn Asn Val Asp His Leu Gly Ile Val His Glu Thr

40

45

50

55

gag ctg cct cct ctg act gcg cgg gag gcg aag caa att cgg cgg gag 967

Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln Ile Arg Arg Glu	
60 65 70	
atc agc cga aag agc aag tgg gtg gat atg ctg gga gac tgg gag aaa	1015
Ile Ser Arg Lys Ser Lys Trp Val Asp Met Leu Gly Asp Trp Glu Lys	
75 80 85	
tac aaa agc agc aga aag ctc ata gat cga gcg tac aag gga atg ccc	1063
Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr Lys Gly Met Pro	
90 95 100	
atg aac atc cgg ggc ccg atg tgg tca gtc ctc ctg aac act gag gaa	1111
Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu Asn Thr Glu Glu	
105 110 115	
atg aag ttg aaa aac ccc gga aga tac cag atc atg aag gag aag ggc	1159
Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met Lys Glu Lys Gly	
120 125 130 135	
aag agg tca tct gag cac atc cag cgc atc gac cgg gac gta agc ggg	1207
Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg Asp Val Ser Gly	
140 145 150	
aca tta agg aag cat ata ttc ttc agg gat cga tac gga acc aag cag	1255
Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr Gly Thr Lys Gln	
155 160 165	
cgg gaa cta ctc cac atc ctc ctg gca tat gag gag tat aac ccg gag	1303
Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu Tyr Asn Pro Glu	
170 175 180	
gtg ggc tac tgc agg gac ctg agc cac atc gcc gcc ttg ttc ctc ctc	1351
Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala Leu Phe Leu Leu	
185 190 195	
tat ctt cct gag gag gat gca ttc tgg gca ctg gtg cag ctg ctg gcc	1399

Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala Leu Val Gln Leu Leu Ala
 200 205 210 215
 agt gag agg cac tcc ctg cag gga ttt cac agc cca aat ggc ggg acc 1447
 Ser Glu Arg His Ser Leu Gln Gly Phe His Ser Pro Asn Gly Gly Thr
 220 225 230
 gtc cag ggg ctc caa gac caa cag gag cat gtg gta gcc acg tca caa 1495
 Val Gln Gly Leu Gln Asp Gln Gln Glu His Val Val Ala Thr Ser Gln
 235 240 245
 ccc aag acc atg ggg cat cag atc tct ctc ggg ctc acc ctg cgc ctg 1543
 Pro Lys Thr Met Gly His Gln Ile Ser Leu Gly Leu Thr Leu Arg Leu
 250 255 260
 tgg gac gtg tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca 1591
 Trp Asp Val Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr
 265 270 275
 aga atc gcc ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg 1639
 Arg Ile Ala Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg
 280 285 290 295
 tgt ggc ccg tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc 1687
 Cys Gly Pro Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala
 300 305 310
 agg gat gag gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa 1735
 Arg Asp Glu Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys
 315 320 325
 cta aca aga aag cag ggg gac ctg caa ccc cca gcc aaa ccc gag caa 1783
 Leu Thr Arg Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln
 330 335 340
 ggg tcg tcg gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc 1831

Gly Ser Ser Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr	
345 350 355	
ctc tgc aag ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc	1879
Leu Cys Lys Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe	
360 365 370 375	
ccg cgg ccc att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc	1927
Pro Arg Pro Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser	
380 385 390	
aca ccc tgt cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc	1975
Thr Pro Cys Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly	
395 400 405	
act cag ggt gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt	2023
Thr Gln Gly Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly	
410 415 420	
tcc tgg aga ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac	2071
Ser Trp Arg Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp	
425 430 435	
ctg gac gta gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc	2119
Leu Asp Val Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser	
440 445 450 455	
tgc tgg gtc cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg	2167
Cys Trp Val Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp	
460 465 470	
cag gct gaa cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc	2215
Gln Ala Glu His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro	
475 480 485	
agc act gat tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag	2263

Ser Thr Asp Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln
 490 495 500
 ccg tgt gct ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa 2311
 Pro Cys Ala Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu
 505 510 515
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 Ser Ser Gln Phe Pro Pro Gly Phe
 520 525
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<211> 527

<212> PRT

<213> Homo sapiens

<400> 220

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 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
 180 185 190
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
 195 200 205
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
 210 215 220
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
 225 230 235 240
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Ile Ser
 245 250 255
 Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr Leu Val Glu Gly Glu
 260 265 270
 Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys Val Gln Gln Lys

275	280	285
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Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr Val Leu Lys His		
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Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly Asp Leu Gln		
325	330	335
Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg Pro Val Pro		
340	345	350
Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg Gln Ala Pro		
355	360	365
Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp Ser Ala Ser Pro		
370	375	380
Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly Gly Ala Val Arg		
385	390	395
Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser Pro Ala Leu		
405	410	415
Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Gln Trp Asn Ser		
420	425	430
Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly Pro Trp Phe Arg		
435	440	445
His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala Ile Ser Gln Glu		
450	455	460
Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro Ala Glu Arg Val		
465	470	475
Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln Gly Thr Pro		
485	490	495

Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr Ser Gly Pro Cys

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Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro Pro Gly Phe

515

520

525

<210> 221

<211> 2647

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (755).. (2335)

<400> 221

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cctcatcccc caaacccaac accctcctgc tcaacaggcg ttattcctaa agtggcttca      240
ctgttcagac tgaagagcca cggtagccaa agtgatgagc ggagtagaac cgagcagtcg      300
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Met Asp Val Val Glu Val Ala

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Gly Ser Trp Trp Ala Gln Glu Arg Glu Asp Ile Ile Met Lys Tyr Glu			
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aag gga cac cga gct ggg ctg cca gag gac aag ggg cct aag cct ttt			871
Lys Gly His Arg Ala Gly Leu Pro Glu Asp Lys Gly Pro Lys Pro Phe			
25	30	35	
cga agc tac aac aac aac gtc gat cat ttg ggg att gta cat gag acg			919
Arg Ser Tyr Asn Asn Asn Val Asp His Leu Gly Ile Val His Glu Thr			
40	45	50	55
gag ctg cct cct ctg act gcg cgg gag gcg aag caa att cgg cgg gag			967
Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln Ile Arg Arg Glu			
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Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr Lys Gly Met Pro			
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Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu Asn Thr Glu Glu			
105	110	115	
atg aag ttg aaa aac ccc gga aga tac cag atc atg aag gag aag ggc			1159
Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met Lys Glu Lys Gly			
120	125	130	135
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Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg Asp Val Ser Gly			

140	145	150	
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Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr Gly Thr Lys Gln			
155	160	165	
cgg gaa cta ctc cac atc ctc ctg gca tat gag gag tat aac ccg gag			1303
Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu Tyr Asn Pro Glu			
170	175	180	
gtg ggc tac tgc agg gac ctg agc cac atc gcc gcc ttg ttc ctc ctc			1351
Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala Leu Phe Leu Leu			
185	190	195	
tat ctt cct gag gag gat gca ttc tgg gca ctg gtg cag ctg ctg gcc			1399
Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala Leu Val Gln Leu Leu Ala			
200	205	210	215
agt gag agg cac tcc ctg cag gga ttt cac agc cca aat ggc ggg acc			1447
Ser Glu Arg His Ser Leu Gln Gly Phe His Ser Pro Asn Gly Gly Thr			
220	225	230	
gtc cag ggg ctc caa gac caa cag gag cat gtg gta gcc acg tca caa			1495
Val Gln Gly Leu Gln Asp Gln Gln Glu His Val Val Ala Thr Ser Gln			
235	240	245	
ccc aag acc atg ggg cat cag atc tct ctc ggg ctc acc ctg cgc ctg			1543
Pro Lys Thr Met Gly His Gln Ile Ser Leu Gly Leu Thr Leu Arg Leu			
250	255	260	
tgg gac gtg tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca			1591
Trp Asp Val Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr			
265	270	275	
aga atc gcc ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg			1639
Arg Ile Ala Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg			

280	285	290	295	
tgt ggc ccg tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc	1687			
Cys Gly Pro Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala				
300	305	310		
agg gat gag gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa	1735			
Arg Asp Glu Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys				
315	320	325		
cta aca aga aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa	1783			
Leu Thr Arg Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln				
330	335	340		
ggg tcg tcg gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc	1831			
Gly Ser Ser Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr				
345	350	355		
ctc tgc aag ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc	1879			
Leu Cys Lys Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe				
360	365	370	375	
ccg cgg ccc att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc	1927			
Pro Arg Pro Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser				
380	385	390		
aca ccc tgt cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc	1975			
Thr Pro Cys Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly				
395	400	405		
act cag ggt gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt	2023			
Thr Gln Gly Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly				
410	415	420		
tcc tgg aga ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac	2071			
Ser Trp Arg Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp				

425	430	435	
ctg gac gta gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc			2119
Leu Asp Val Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser			
440	445	450	455
tgc tgg gtc cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg			2167
Cys Trp Val Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp			
460	465	470	
cag gct gaa cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc			2215
Gln Ala Glu His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro			
475	480	485	
agc act gat tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag			2263
Ser Thr Asp Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln			
490	495	500	
ccg tgt gct ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa			2311
Pro Cys Ala Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu			
505	510	515	
agt tct cag ttc cct cca ggc ttc tagaagcatc tgggccaggg ctcatggctg			2365
Ser Ser Gln Phe Pro Pro Gly Phe			
520	525		
gataatttcc ctaggcttaa caaccgaagc aagcttcgca tcctcgtttt atttttggtt			2425
aaacttatga aaatgtatta agaaagagtg cagctcgaga gagattcaga gatggaacac			2485
accagacccc agatcacaaa gccaaaccatg cccagcccct cccagcacc cccagcccccac			2545
gaccatcggt ctgaattctg acgacaccgt gagcctgcct ttgtacttca aactcatgga			2605
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<210> 222

<211> 527

<212> PRT

<213> Homo sapiens

<400> 222

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           20           25           30
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
           35           40           45
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
           50           55           60
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65           70           75           80
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
           85           90           95
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
           100          105          110
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
           115          120          125
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
           130          135          140
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
145          150          155          160
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
           165          170          175
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
           180          185          190

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Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
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 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
 210 215 220
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
 225 230 235 240
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Ile Ser
 245 250 255
 Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr Leu Val Glu Gly Glu
 260 265 270
 Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys Val Gln Gln Lys
 275 280 285
 Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro Trp Ala Arg Phe Cys Asn
 290 295 300
 Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr Val Leu Lys His
 305 310 315 320
 Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly Asp Leu Pro
 325 330 335
 Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg Pro Val Pro
 340 345 350
 Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg Gln Ala Pro
 355 360 365
 Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp Ser Ala Ser Pro
 370 375 380
 Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly Gly Ala Val Arg
 385 390 395 400
 Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser Pro Ala Leu

405	410	415
Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Gln Trp Asn Ser		
420	425	430
Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly Pro Trp Phe Arg		
435	440	445
His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala Ile Ser Gln Glu		
450	455	460
Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro Ala Glu Arg Val		
465	470	475
Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln Gly Thr Pro		
485	490	495
Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr Ser Gly Pro Cys		
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Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro Pro Gly Phe		
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<210> 223

<211> 1817

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (119)..(415)

<400> 223

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atg ggg gct gct gtg ttt ttc gga tgc acc ttc gtc gcg ttc ggc cca	166

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro
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atc atc ctg gtg gcg gga gcc ttt ttc tgg ctg gtc tcc ctg ctc ttg 262
Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35 40 45
gct tct gtg gtc tgg ttc atc ttg gtc cac gtg aca gac cga tca gat 310
Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60
gca cgg ctc cag tat ggc ctc ctg att ttt ggt gct gct gtc tct gtc 358
Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80
ctt cta cag gaa gtg ttc cgt ttt gct tac tac aag ctc ctt aag cag 406
Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Gln
85 90 95
atg agg gct tagcatcact gaggtaggac ggaagatcac ccatctccat 455
Met Arg Ala
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tatcaatatt ttggctgatg cacttgggcc aggtgtgggtt gggatccatg gagactcacc 575
ctattacttc ctgacttcag cttttctgac agcagccatt atcctgctcc acaccttttg 635
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<210> 224

<211> 99

<212> PRT

<213> Mus musculus

<400> 224

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 20 25 30
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
 35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp

50

55

60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val

65

70

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80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Gln

85

90

95

Met Arg Ala

<210> 225

<211> 1997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136)..(876)

<400> 225

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cccacctgac cagcc atg ggg gct gcg gtg ttt ttc ggc tgc act ttc gtc 171

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val

1

5

10

gcg ttc ggc ccg gcc ttc gcg ctt ttc ttg atc act gtg gct ggg gac 219

Ala Phe Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp

15

20

25

ccg ctt cgc gtt atc atc ctg gtc gca ggg gca ttt ttc tgg ctg gtc 267

Pro Leu Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val

30

35

40

tcc	ctg	ctc	ctg	gcc	tct	gtg	gtc	tgg	ttc	atc	ttg	gtc	cat	gtg	acc	315
Ser	Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	
45					50					55					60	
gac	cgg	tca	gat	gcc	cgg	ctc	cag	tac	ggc	ctc	ctg	att	ttt	ggg	gct	363
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	
				65					70					75		
gct	gtc	tct	gtc	ctt	cta	cag	gag	gtg	ttc	cgc	ttt	gcc	tac	tac	aag	411
Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	
				80					85					90		
ctg	ctt	aag	aag	gca	gat	gag	ggg	tta	gca	tcg	ctg	agt	gag	gac	gga	459
Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	
				95					100					105		
aga	tca	ccc	atc	tcc	atc	cgc	cag	atg	gcc	tat	gtt	tct	ggg	ctc	tcc	507
Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	
				110					115					120		
ttc	ggg	atc	atc	agt	ggg	gtc	ttc	tct	gtt	atc	aat	att	ttg	gct	gat	555
Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	
125					130					135					140	
gca	ctt	ggg	cca	ggg	gtg	gtt	ggg	atc	cat	gga	gac	tca	ccc	tat	tac	603
Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	
				145					150					155		
ttc	ctg	act	tca	gcc	ttt	ctg	aca	gca	gcc	att	atc	ctg	ctc	cat	acc	651
Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	
				160					165					170		
ttt	tgg	gga	gtt	gtg	ttc	ttt	gat	gcc	tgt	gag	agg	aga	cgg	tac	tgg	699
Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	
				175					180					185		

gct ttg ggc ctg gtg gtt ggg agt cac cta ctg aca tcg gga ctg aca 747
 Ala Leu Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr
 190 195 200
 ttc ctg aac ccc tgg tat gag gcc agc ctg ctg ccc atc tat gca gtc 795
 Phe Leu Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val
 205 210 215 220
 act gtt tcc atg ggg ctc tgg gcc ttc atc aca gct gga ggg tcc ctc 843
 Thr Val Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu
 225 230 235
 cga agt att cag cgc agc ctc ttg tgt aag gac tgactacctg gactgatcgc 896
 Arg Ser Ile Gln Arg Ser Leu Leu Cys Lys Asp
 240 245
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<210> 226

<211> 247

<212> PRT

<213> Homo sapiens

<400> 226

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35 40 45
Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60
Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80
Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95
Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110
Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125
Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro

130 135 140
 Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
 145 150 155 160
 Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
 165 170 175
 Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
 180 185 190
 Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
 195 200 205
 Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
 210 215 220
 Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
 225 230 235 240
 Arg Ser Leu Leu Cys Lys Asp
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<210> 227

<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190).. (984)

<400> 227

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 ccagctggcg cgcccctccc atttgctgt cctggtcagg cccccacccc ctttcccacc 180

tgaccagcc atg ggg gct gcg gtg ttt ttc ggc tgc act ttc gtc gcg ttc 231
 Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe
 1 5 10
 ggc ccg gcc ttc gcg ctt ttc ttg atc act gtg gct ggg gac ccg ctt 279
 Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu
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 Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu
 35 40 45
 ctc ctg gcc tct gtg gtc tgg ttc atc ttg gtc cat gtg acc gac cgg 375
 Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg
 50 55 60
 tca gat gcc cgg ctc cag tac ggc ctc ctg att ttt ggt gct gct gtc 423
 Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val
 65 70 75
 tct gtc ctt cta cag gag gtg ttc cgc ttt gcc tac tac aag ctg ctt 471
 Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu
 80 85 90
 aag aag gca gat gag ggg tta gca tcg ctg agt gag gac gga aga tca 519
 Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser
 95 100 105 110
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 Pro Ile Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly
 115 120 125
 atc atc agt ggt gtc ttc tct gtt atc aat att ttg gct gat gca ctt 615
 Ile Ile Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu
 130 135 140

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 Gly Pro Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu
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 Thr Ser Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp
 160 165 170
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 Gly Val Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu
 175 180 185 190
 ggc ctg gtg gtt ggg agt cac cta ctg aca tcg gga ctg aca ttc ctg 807
 Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu
 195 200 205
 aac ccc tgg tat gag gcc agc ctg ctg ccc atc tat gca gtc act gtt 855
 Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val
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 Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser
 225 230 235
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 Ile Gln Arg Ser Leu Leu Cys Arg Arg Gln Glu Asp Ser Arg Val Met
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 Val Tyr Ser Ala Leu Arg Ile Pro Pro Glu Asp
 255 260 265
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<211> 265

<212> PRT

<213> Homo sapiens

<400> 228

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Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
           35           40           45
Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
           50           55           60
Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65           70           75           80
Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
           85           90           95

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Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110
Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125
Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140
Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160
Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
165 170 175
Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190
Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205
Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
210 215 220
Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
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Ser Ala Leu Arg Ile Pro Pro Glu Asp
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<211> 2212

<212> DNA

<213> Mus musculus

<220>

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<222> (43).. (813)

<400> 229

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Gly Val Asp Glu Arg Ser Pro Leu Leu Ser Ala Ser His Ser Gly Asn

5 10 15 20

gtc act ccc aca gcc ccg ccg tac ttg cag gaa agc agc ccc aga gct 150

Val Thr Pro Thr Ala Pro Pro Tyr Leu Gln Glu Ser Ser Pro Arg Ala

25 30 35

gaa ctc cca cct ccg tat aca gcc atc gcc agt cca gga aca agt ggt 198

Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro Gly Thr Ser Gly

40 45 50

att ccc gtg atc aac tgt cgt gtg tgc caa tct cta atc aac ctg gat 246

Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu Ile Asn Leu Asp

55 60 65

ggt aaa ctt cac cag cat gtg gtt aag tgc aca gtt tgc aat gaa gct 294

Gly Lys Leu His Gln His Val Val Lys Cys Thr Val Cys Asn Glu Ala

70 75 80

acg cca atc aaa acc ccc cca aca ggg aag aaa tat gtt aga tgc cct 342

Thr Pro Ile Lys Thr Pro Pro Thr Gly Lys Lys Tyr Val Arg Cys Pro

85 90 95 100

tgt aat tgt cta ctc att tgt aag gat aca tct cgg cga ata gga tgt 390

Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg Arg Ile Gly Cys

105	110	115	
ccg aga ccc aac tgt cga cgc ata att aac ctt ggc ccc gta atg ctc			438
Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly Pro Val Met Leu			
120	125	130	
att tct gaa gag caa cca gcc caa cct gca ttg ccg atc cag cca gaa			486
Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro Ile Gln Pro Glu			
135	140	145	
ggc aca agg gta gtg tgc ggg cac tgc ggg aac aca ttc ctg tgg atg			534
Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr Phe Leu Trp Met			
150	155	160	
gaa ctg agg ttc aac act ctg gca aaa tgc cca cac tgc aaa aaa atc			582
Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His Cys Lys Lys Ile			
165	170	175	180
tcc tcg gta ggt agc gcc ctt ccc cgg aga cgc tgc tgt gcg tat gtc			630
Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys Cys Ala Tyr Val			
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acc atc gga atg ata tgt att ttc att gca gtt gga tta act gtt ggc			678
Thr Ile Gly Met Ile Cys Ile Phe Ile Ala Val Gly Leu Thr Val Gly			
200	205	210	
aca caa gat ttt tca agg cga ttt cat gca acc tat gtg tct tgg gca			726
Thr Gln Asp Phe Ser Arg Arg Phe His Ala Thr Tyr Val Ser Trp Ala			
215	220	225	
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Ile Ala Tyr Leu Leu Gly Leu Ile Cys Leu Ile Arg Ala Cys Tyr Trp			
230	235	240	
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Gly Ala Ile Arg Val Ser Tyr Pro Glu His Gly Phe Ala			

245	250	255	
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<211> 257

<212> PRT

<213> Mus musculus

<400> 230

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His Ser Gly Asn Val Thr Pro Thr Ala Pro Pro Tyr Leu Gln Glu Ser

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Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro

35 40 45

Gly Thr Ser Gly Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu

50 55 60

Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val Lys Cys Thr Val

65 70 75 80

Cys Asn Glu Ala Thr Pro Ile Lys Thr Pro Pro Thr Gly Lys Lys Tyr

85 90 95

Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg

100 105 110

Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly

115 120 125

Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro

130 135 140

Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr

145 150 155 160

Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His

165 170 175

Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys

180 185 190
 Cys Ala Tyr Val Thr Ile Gly Met Ile Cys Ile Phe Ile Ala Val Gly
 195 200 205
 Leu Thr Val Gly Thr Gln Asp Phe Ser Arg Arg Phe His Ala Thr Tyr
 210 215 220
 Val Ser Trp Ala Ile Ala Tyr Leu Leu Gly Leu Ile Cys Leu Ile Arg
 225 230 235 240
 Ala Cys Tyr Trp Gly Ala Ile Arg Val Ser Tyr Pro Glu His Gly Phe
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<211> 2255

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (77)..(847)

<400> 231

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 Met Ala Ala Asp Gly Val Asp Glu Arg Ser Pro Leu
 1 5 10
 ctg tca gca tcc cac tcc gga aat gtc act ccc acc gcc cca ccg tac 160
 Leu Ser Ala Ser His Ser Gly Asn Val Thr Pro Thr Ala Pro Pro Tyr
 15 20 25
 ttg caa gaa agc agc ccc aga gcg gag ctc cca cct cca tat aca gcc 208

Leu Gln Glu Ser Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala
 30 35 40
 att gcc agt cca gac gcc agt ggt att cca gta ata aac tgc cgt gtg 256
 Ile Ala Ser Pro Asp Ala Ser Gly Ile Pro Val Ile Asn Cys Arg Val
 45 50 55 60
 tgc caa tca cta atc aat ttg gat ggc aag ctt cac cag cat gtg gtt 304
 Cys Gln Ser Leu Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val
 65 70 75
 aag tgc aca gtt tgc aat gaa gct acg cca atc aaa aac ccc cca aca 352
 Lys Cys Thr Val Cys Asn Glu Ala Thr Pro Ile Lys Asn Pro Pro Thr
 80 85 90
 ggc aag aaa tat gtt aga tgc cct tgt aat tgt ctt ctc att tgt aag 400
 Gly Lys Lys Tyr Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys
 95 100 105
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 Asp Thr Ser Arg Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile
 110 115 120
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 Ile Asn Leu Gly Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln
 125 130 135 140
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 Pro Ala Leu Pro Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His
 145 150 155
 tgt gga aac aca ttc ctg tgg atg gaa ctg agg ttc aac act ctg gca 592
 Cys Gly Asn Thr Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala
 160 165 170
 aaa tgc cca cac tgc aaa aaa atc tcc tca gtg ggt agt gca ctt cca 640

Lys Cys Pro His Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro
 175 180 185
 cga aga cgc tgc tgt gca tat att acc att gga atg ata tgt att ttc 688
 Arg Arg Arg Cys Cys Ala Tyr Ile Thr Ile Gly Met Ile Cys Ile Phe
 190 195 200
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 Ile Gly Val Gly Leu Thr Val Gly Thr Pro Asp Phe Ala Arg Arg Phe
 205 210 215 220
 cga gca acc tat gtt tct tgg gca att gct tat ctc cta gga ttg atc 784
 Arg Ala Thr Tyr Val Ser Trp Ala Ile Ala Tyr Leu Leu Gly Leu Ile
 225 230 235
 tgc ctt atc cga gct tgt tat tgg gga gcc ata aga gtc agt tat cca 832
 Cys Leu Ile Arg Ala Cys Tyr Trp Gly Ala Ile Arg Val Ser Tyr Pro
 240 245 250
 gaa cac agt ttt gca taagcttggt tatgattcag taatgcaggt gagagtgtct 887
 Glu His Ser Phe Ala
 255
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<211> 257

<212> PRT

<213> Homo sapiens

<400> 232

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           20           25           30
Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro
           35           40           45
Asp Ala Ser Gly Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu
           50           55           60

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Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val Lys Cys Thr Val
 65 70 75 80
 Cys Asn Glu Ala Thr Pro Ile Lys Asn Pro Pro Thr Gly Lys Lys Tyr
 85 90 95
 Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg
 100 105 110
 Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly
 115 120 125
 Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro
 130 135 140
 Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr
 145 150 155 160
 Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His
 165 170 175
 Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys
 180 185 190
 Cys Ala Tyr Ile Thr Ile Gly Met Ile Cys Ile Phe Ile Gly Val Gly
 195 200 205
 Leu Thr Val Gly Thr Pro Asp Phe Ala Arg Arg Phe Arg Ala Thr Tyr
 210 215 220
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<210> 233

<211> 1915

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (80)..(1297)

<400> 233

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          Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg
                1                5                10
cgc ata gca atg agt aag gat cag cac aat gga agt ctc aca gac ccc 160
Arg Ile Ala Met Ser Lys Asp Gln His Asn Gly Ser Leu Thr Asp Pro
                15                20                25
tct tca gtt cat gag aag aag aga agg gat cgg gaa gaa aga cag aat 208
Ser Ser Val His Glu Lys Lys Arg Arg Asp Arg Glu Glu Arg Gln Asn
                30                35                40
att gtc ctg tgg aga cag cca ctc att acc ttg cag tat ttc tct ctg 256
Ile Val Leu Trp Arg Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu
                45                50                55
gaa act ctt gta gtt ttg aag gaa tgg acc tca aaa ttg tgg cat cgt 304
Glu Thr Leu Val Val Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg
                60                65                70                75
caa agc att gtg gtg tcc ttt tta ctg ctg ctt gct gcg ctt gta gct 352
Gln Ser Ile Val Val Ser Phe Leu Leu Leu Leu Ala Ala Leu Val Ala
                80                85                90
acg tat tat gtg gaa gga gcg cac caa cag tat gtg cag cgg ata gag 400

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Lys Gln Phe Leu Leu Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser	
110 115 120	
tct gtt ggt ctt gga aca gga ctg cac acc ttt ctg ctt tat ctg ggc	496
Ser Val Gly Leu Gly Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly	
125 130 135	
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Pro His Ile Ala Ser Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val	
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Asn Phe Pro Glu Pro Pro Tyr Pro Asp Gln Ile Ile Cys Pro Glu Glu	
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gaa ggc gct gag gga gcc att tct ttg tgg agt atc atc tca aaa gtt	640
Glu Gly Ala Glu Gly Ala Ile Ser Leu Trp Ser Ile Ile Ser Lys Val	
175 180 185	
aga att gaa gcc tgc atg tgg ggc att gga aca gcc att gga gag ctg	688
Arg Ile Glu Ala Cys Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu	
190 195 200	
cct cca tat ttc atg gcc agg gca gct cgc ctc tca ggt gct gaa cca	736
Pro Pro Tyr Phe Met Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro	
205 210 215	
gat gat gaa gag tat cag gaa ttt gaa gaa atg ctg gaa cat gca gag	784
Asp Asp Glu Glu Tyr Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu	
220 225 230 235	
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Ala Ala Gln Asp Phe Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu	
240	245
gta cag aaa gtt gga ttt ttt gga att ttg gcc tgt gct tct att cca	880
Val Gln Lys Val Gly Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro	
255	260
aac ccc ctg ttt gac ctg gct gga ata acg tgt ggg cac ttc ctt gta	928
Asn Pro Leu Phe Asp Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val	
270	275
cct ttc tgg acc ttc ttt ggt gca acc ctg att ggg aaa gca atc att	976
Pro Phe Trp Thr Phe Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile	
285	290
aaa atg cat atc cag aaa ata ttt gtt ata gta act ttc agc aag cac	1024
Lys Met His Ile Gln Lys Ile Phe Val Ile Val Thr Phe Ser Lys His	
300	305
atc gtg gag cag atg gtg act ttc att ggt gct gtc ccc ggc ata ggt	1072
Ile Val Glu Gln Met Val Thr Phe Ile Gly Ala Val Pro Gly Ile Gly	
320	325
ccg tct ctg cag aag cct ttt caa gag tac ctg gag gcg cag cgg cag	1120
Pro Ser Leu Gln Lys Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln	
335	340
aag ctt cat cac aga agt gaa gcg ggc aca ccg cag gga gaa aac tgg	1168
Lys Leu His His Arg Ser Glu Ala Gly Thr Pro Gln Gly Glu Asn Trp	
350	355
tta tcc tgg atg ttt gag aag ctg gtg gtt gca atg gtg tgt tac ttt	1216
Leu Ser Trp Met Phe Glu Lys Leu Val Val Ala Met Val Cys Tyr Phe	
365	370
gtc ctg tct att att aac tcc atg gca caa aac tat gcc aaa cga atc	1264

Val Leu Ser Ile Ile Asn Ser Met Ala Gln Asn Tyr Ala Lys Arg Ile

380 385 390 395

cag cag cgc ttg aac tca gag gag aaa act aaa taagcagaga gtttttatct 1317

Gln Gln Arg Leu Asn Ser Glu Glu Lys Thr Lys

400

405

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gaaacagtat aaggaaaatc tgggtggtgt ctcacaaatg agtacgcat tttttattct 1857

gtatatattag aatgaagtcg tgaaaaactt tataaagaca tctttgatca ttccgaaa 1915

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<211> 406

<212> PRT

<213> Mus musculus

<400> 234

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Lys Lys Arg Arg Asp Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg

35 40 45

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Thr Leu Val Val
50 55 60
Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val
65 70 75 80
Ser Phe Leu Leu Leu Leu Ala Ala Leu Val Ala Thr Tyr Tyr Val Glu
85 90 95
Gly Ala His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu
100 105 110
Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly
115 120 125
Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser
130 135 140
Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro
145 150 155 160
Pro Tyr Pro Asp Gln Ile Ile Cys Pro Glu Glu Glu Gly Ala Glu Gly
165 170 175
Ala Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys
180 185 190
Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met
195 200 205
Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr
210 215 220
Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ala Ala Gln Asp Phe
225 230 235 240
Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly
245 250 255
Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp

260 265 270
 Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe
 275 280 285
 Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln
 290 295 300
 Lys Ile Phe Val Ile Val Thr Phe Ser Lys His Ile Val Glu Gln Met
 305 310 315 320
 Val Thr Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
 325 330 335
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Arg
 340 345 350
 Ser Glu Ala Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
 355 360 365
 Glu Lys Leu Val Val Ala Met Val Cys Tyr Phe Val Leu Ser Ile Ile
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<222> (114)..(1331)

<400> 235

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Met	
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gca gag aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag	164
Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys	
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gaa cat cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag	212
Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys	
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aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag	260
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln	
35 40 45	
ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg	308
Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu	
50 55 60 65	
aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct	356
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser	
70 75 80	
ttt tta ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga	404
Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly	
85 90 95	
gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat	452
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr	
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gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca	500

Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr	
115 120 125	
ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt	548
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val	
130 135 140 145	
aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc	596
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro	
150 155 160	
tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc	644
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr	
165 170 175	
att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg	692
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met	
180 185 190	
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Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala	
195 200 205	
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag	788
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln	
210 215 220 225	
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Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala	
230 235 240	
tcc cgg gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt	884
Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe	
245 250 255	
ttt gga att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg	932

Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu
 260 265 270
 gct gga ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt 980
 Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe
 275 280 285
 ggt gca acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa 1028
 Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys
 290 295 300 305
 att ttt gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg 1076
 Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val
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 gct ttc att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca 1124
 Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro
 325 330 335
 ttt cag gag tac ctg gag gct caa cgg cag aag ctt cac cac aaa agc 1172
 Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser
 340 345 350
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 Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu
 355 360 365
 aag ttg gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac 1268
 Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn
 370 375 380 385
 tcc atg gca caa agt tat gcc aaa cga atc cag cag cgg ttg aac tca 1316
 Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser
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 gag gag aaa act aaa taagtagaga aagttttaaa ctgcagaaat tggagtggat 1371

Glu Glu Lys Thr Lys

405

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<212> PRT

<213> Homo sapiens

<400> 236

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 35 40 45
 Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile
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 Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val
 65 70 75 80
 Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu
 85 90 95
 Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu
 100 105 110
 Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly
 115 120 125
 Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser
 130 135 140
 Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro
 145 150 155 160
 Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly
 165 170 175
 Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys
 180 185 190
 Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met
 195 200 205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr
 210 215 220
 Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe
 225 230 235 240
 Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly
 245 250 255
 Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp
 260 265 270
 Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe
 275 280 285
 Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln
 290 295 300
 Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met
 305 310 315 320
 Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
 325 330 335
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys
 340 345 350
 Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
 355 360 365
 Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile
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 Ser Glu Glu Lys Thr Lys
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<211> 2302

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (659).. (1510)

<400> 237

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ggaccccctt gatgtccagc actgggctct gaccatcctg aagacatggt gccccaggg      180
acctttgaca ccctggggtc tgaggggtcc tgactacaag gaggaatgaa taggggggtg      240
ccatgggtctt cgtgtccctt gccaacctct gtcccctctc cttcctgcct ataggtggtt      300
tctacaaaca tcctacttcc cttcaggtaa gaggagaaag actgtctgga gtagaagtct      360
aatgctaata acatgaactt ggtttacaca attagaccag attgctaaga gacatctctg      420
tcatgccgct cttgggaacc cccatgatgt atatagcact gggctctgac caccatgggtg      480
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gatgctgggt gggagtgtag ccctttgtca cctaccagct tgccctgtgt ctttgcagcc      600
tctgcgacag cattgcttct agccctcttg ctattcttac cttgagactg tgagggcc      658
atg gct gag aga gtg ctg gtg ccc acc cag ata ggc cgg ggg gac cgc      706
Met Ala Glu Arg Val Leu Val Pro Thr Gln Ile Gly Arg Gly Asp Arg
1           5           10           15
tac tac aca tac acg gag ttg ttg gct atc tca cgg cgt ttc aag cag      754
Tyr Tyr Thr Tyr Thr Glu Leu Leu Ala Ile Ser Arg Arg Phe Lys Gln
20           25           30
aac ccc aat gag ctc atg gtc acc tgg atc ctg cgg gtg tat gac cag      802
Asn Pro Asn Glu Leu Met Val Thr Trp Ile Leu Arg Val Tyr Asp Gln

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gac ctc acc cat gat gcc atc ttt aac tac cgc tgc aag gcc ctg cgg			898
Asp Leu Thr His Asp Ala Ile Phe Asn Tyr Arg Cys Lys Ala Leu Arg			
65	70	75	80
ggg gct ggc tgc cag act ctc ctg agc tgg ctg ctg cag gcc tgg cgt			946
Gly Ala Gly Cys Gln Thr Leu Leu Ser Trp Leu Leu Gln Ala Trp Arg			
	85	90	95
cag cgt tgg gaa tcc tcc ctg cat ttt gag gcc acc gag tta ccc ttc			994
Gln Arg Trp Glu Ser Ser Leu His Phe Glu Ala Thr Glu Leu Pro Phe			
100	105	110	
agg ccc tgg acc acc atg gag gaa ggc atc cag ttg gtg cgt gag ctg			1042
Arg Pro Trp Thr Thr Met Glu Glu Gly Ile Gln Leu Val Arg Glu Leu			
115	120	125	
ggc atg att gag tgg atc tac ctt gac cca gaa ggg ccc gtg gac ctg			1090
Gly Met Ile Glu Trp Ile Tyr Leu Asp Pro Glu Gly Pro Val Asp Leu			
130	135	140	
gcc cca gag gat gtg gcc ttc act caa ggc ctg cag cgg cgc ctg ctc			1138
Ala Pro Glu Asp Val Ala Phe Thr Gln Gly Leu Gln Arg Arg Leu Leu			
145	150	155	160
aca gca gcc ccc tct gag ctg cgg ctt tca ctg gtc agc ctg ctg gta			1186
Thr Ala Ala Pro Ser Glu Leu Arg Leu Ser Leu Val Ser Leu Leu Val			
	165	170	175
cgt ggc atg aca gtg ttg gag gct gtg atg gag atc cag act att gct			1234
Arg Gly Met Thr Val Leu Glu Ala Val Met Glu Ile Gln Thr Ile Ala			

180	185	190	
gac gtg ggt ctg ctc tgg cgc cag agc cat cca ggc cgc acc aag ctc			1282
Asp Val Gly Leu Leu Trp Arg Gln Ser His Pro Gly Arg Thr Lys Leu			
195	200	205	
atg ttg ggg ccc aac cca act cgt aag gac ctc cta ggc tgg ctg ctc			1330
Met Leu Gly Pro Asn Pro Thr Arg Lys Asp Leu Leu Gly Trp Leu Leu			
210	215	220	
agc cac ggt gta ccc cgg gag caa gta gac aga cag ccc acc aag gta			1378
Ser His Gly Val Pro Arg Glu Gln Val Asp Arg Gln Pro Thr Lys Val			
225	230	235	240
ctc cta gaa ctc tac atc aaa gaa gcc aag cgc agt cgc ggc cac ccc			1426
Leu Leu Glu Leu Tyr Ile Lys Glu Ala Lys Arg Ser Arg Gly His Pro			
245	250	255	
aac tat ggg ctg aac gag gag cag ccc cca cca ccc cct tac tcc gac			1474
Asn Tyr Gly Leu Asn Glu Glu Gln Pro Pro Pro Pro Pro Tyr Ser Asp			
260	265	270	
cag gcc tgt ggg gaa gag caa ccg gtg cgt cat gac taagtcctgg			1520
Gln Ala Cys Gly Glu Glu Gln Pro Val Arg His Asp			
275	280		
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ggctgtctgt aaccaggtg actaggaagc agcttgggga gcgccaagt ggacattccc			1640
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<211> 284

<212> PRT

<213> Mus musculus

<400> 238

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Asn Pro Asn Glu Leu Met Val Thr Trp Ile Leu Arg Val Tyr Asp Gln

35 40 45

Gly Gly Pro Ala Leu Ser Leu Asn Ser Gly Glu Leu Gly Leu Leu Gly

50 55 60

Asp Leu Thr His Asp Ala Ile Phe Asn Tyr Arg Cys Lys Ala Leu Arg

65 70 75 80

Gly Ala Gly Cys Gln Thr Leu Leu Ser Trp Leu Leu Gln Ala Trp Arg

85 90 95

Gln Arg Trp Glu Ser Ser Leu His Phe Glu Ala Thr Glu Leu Pro Phe

100 105 110

Arg Pro Trp Thr Thr Met Glu Glu Gly Ile Gln Leu Val Arg Glu Leu

115 120 125
 Gly Met Ile Glu Trp Ile Tyr Leu Asp Pro Glu Gly Pro Val Asp Leu
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 Ala Pro Glu Asp Val Ala Phe Thr Gln Gly Leu Gln Arg Arg Leu Leu
 145 150 155 160
 Thr Ala Ala Pro Ser Glu Leu Arg Leu Ser Leu Val Ser Leu Leu Val
 165 170 175
 Arg Gly Met Thr Val Leu Glu Ala Val Met Glu Ile Gln Thr Ile Ala
 180 185 190
 Asp Val Gly Leu Leu Trp Arg Gln Ser His Pro Gly Arg Thr Lys Leu
 195 200 205
 Met Leu Gly Pro Asn Pro Thr Arg Lys Asp Leu Leu Gly Trp Leu Leu
 210 215 220
 Ser His Gly Val Pro Arg Glu Gln Val Asp Arg Gln Pro Thr Lys Val
 225 230 235 240
 Leu Leu Glu Leu Tyr Ile Lys Glu Ala Lys Arg Ser Arg Gly His Pro
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<210> 239

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<222> (102).. (710)

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                                     Met Ala Glu Ala Pro
                                     1             5

gtt gac ttg agc aca gga gac aat ctg gag caa aag atc ctg cag gtg      164
Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln Lys Ile Leu Gln Val
                10                15                20

ttg agc gat gac ggc ggc cct gtg aag att ggc cag ctg gtg aag aaa      212
Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly Gln Leu Val Lys Lys
                25                30                35

tgc caa gtg ccc aag aaa acc ctc aat caa gtc ctt tac cgc ctg aag      260
Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val Leu Tyr Arg Leu Lys
                40                45                50

aag gag gac aga gtg tcc tcc cca gag cct gca aca tgg agc ata ggc      308
Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala Thr Trp Ser Ile Gly
                55                60                65

ggg gct gct tct gga gat ggg gct cct gca atc cct gag aac tcc agt      356
Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile Pro Glu Asn Ser Ser
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gcc cag cct agc ctt gat gaa aga ata tta aga ttc ctg gaa gcc aat      404
Ala Gln Pro Ser Leu Asp Glu Arg Ile Leu Arg Phe Leu Glu Ala Asn
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ggg cct cac agg gcc ctg cac atc gcc aag gct ctg gga atg acg aca      452
Gly Pro His Arg Ala Leu His Ile Ala Lys Ala Leu Gly Met Thr Thr

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105	110	115	
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Ala Lys Glu Val Asn Pro Leu Leu Tyr Ser Met Arg Asn Lys His Leu			
120	125	130	
ctg agc tat gac gga cag acg tgg aag atc tac cac tca cgt cag gaa			548
Leu Ser Tyr Asp Gly Gln Thr Trp Lys Ile Tyr His Ser Arg Gln Glu			
135	140	145	
ggc caa gac ata gct cat tct gga gtc aca caa gag tcc cct gcg att			596
Gly Gln Asp Ile Ala His Ser Gly Val Thr Gln Glu Ser Pro Ala Ile			
150	155	160	165
att tgt cag cac aat ccg gtc aac atg atc tgc caa caa gga gcc aac			644
Ile Cys Gln His Asn Pro Val Asn Met Ile Cys Gln Gln Gly Ala Asn			
170	175	180	
agc cac atc tcc att gcc aat tca aac gcc atc cag att ggt cac ggg			692
Ser His Ile Ser Ile Ala Asn Ser Asn Ala Ile Gln Ile Gly His Gly			
185	190	195	
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Asn Val Ile Val Arg Glu			
200			
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 aa 1942

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<211> 203

<212> PRT

<213> Mus musculus

<400> 240

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20 25 30

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35 40 45

Leu Tyr Arg Leu Lys Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala

50 55 60

723/861

caagcagcca ttcttgctg tggattcaga gccccaggcc tgaccacagt gccagaaact	60
gccaccccct gccctaaagg agccccaagg ctgctgtgag c atg gca gaa gct cct	116
Met Ala Glu Ala Pro	
1 5	
gtt gac ttg agc aca gga gac aat ctg gag caa aag atc ctg cag gtg	164
Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln Lys Ile Leu Gln Val	
10 15 20	
ttg agc gat gac ggc ggc cct gtg aag att ggc cag ctg gtg aag aaa	212
Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly Gln Leu Val Lys Lys	
25 30 35	
tgc caa gtg ccc aag aaa acc ctc aat caa gtc ctt tac cgc ctg aag	260
Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val Leu Tyr Arg Leu Lys	
40 45 50	
aag gag gac aga gtg tcc tcc cca gag cct gca aca tgg agc ata ggc	308
Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala Thr Trp Ser Ile Gly	
55 60 65	
ggg gct gct tct gga gat ggg gct cct gca atc cct gag aac tcc agt	356
Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile Pro Glu Asn Ser Ser	
70 75 80 85	
gcc cag cct agc ctt gat gaa aga ata tta aga ttc ctg gaa gcc aat	404
Ala Gln Pro Ser Leu Asp Glu Arg Ile Leu Arg Phe Leu Glu Ala Asn	
90 95 100	
ggg cct cac agg gcc ctg cac atc gcc aag gct ctg gga atg acg aca	452
Gly Pro His Arg Ala Leu His Ile Ala Lys Ala Leu Gly Met Thr Thr	
105 110 115	
gcc aaa gaa gtg aac cca ctc ctg tat tcc atg aga aat aag cac ctt	500
Ala Lys Glu Val Asn Pro Leu Leu Tyr Ser Met Arg Asn Lys His Leu	

120	125	130	
ctg agc tat gac gga cag acg tgg aag atc tac cac tca cgt cag gaa			548
Leu Ser Tyr Asp Gly Gln Thr Trp Lys Ile Tyr His Ser Arg Gln Glu			
135	140	145	
ggc caa gac ata gct cat tct gga gtc aca caa gag tcc cct gcg att			596
Gly Gln Asp Ile Ala His Ser Gly Val Thr Gln Glu Ser Pro Ala Ile			
150	155	160	165
att tgt cag cac aat ccg gtc aac atg atc tgc caa caa gga gcc aac			644
Ile Cys Gln His Asn Pro Val Asn Met Ile Cys Gln Gln Gly Ala Asn			
170	175	180	
agc cac atc tcc att gcc aat tca aac gcc atc cag att ggt cac ggg			692
Ser His Ile Ser Ile Ala Asn Ser Asn Ala Ile Gln Ile Gly His Gly			
185	190	195	
aat gtc ata gta aga gag aaa gcc tgt ggt gag cca ggt ccc agg acc			740
Asn Val Ile Val Arg Glu Lys Ala Cys Gly Glu Pro Gly Pro Arg Thr			
200	205	210	
tct cac cct cta ccc ttg gca tgg gac gcc tct gct cag gac atg ccc			788
Ser His Pro Leu Pro Leu Ala Trp Asp Ala Ser Ala Gln Asp Met Pro			
215	220	225	
cct gtt gcc cac gga gct cag tac atc tac atg gac aag tcc ttg ctc			836
Pro Val Ala His Gly Ala Gln Tyr Ile Tyr Met Asp Lys Ser Leu Leu			
230	235	240	245
caa caa gtg cag ctt ggc cac cac aac gag atg agc ctc gtg ggg gat			884
Gln Gln Val Gln Leu Gly His His Asn Glu Met Ser Leu Val Gly Asp			
250	255	260	
gca ggg aag cac ccc tct tat agc ttt tct gac agc ccc cca gaa gtg			932
Ala Gly Lys His Pro Ser Tyr Ser Phe Ser Asp Ser Pro Pro Glu Val			

265	270	275	
tca acc acc act gct gac cca gga gct tca ttc aac atg caa aca tct			980
Ser Thr Thr Thr Ala Asp Pro Gly Ala Ser Phe Asn Met Gln Thr Ser			
280	285	290	
gag cca ggc cct cac cct gag gga gac aca gtc cag aca gtc cac atc			1028
Glu Pro Gly Pro His Pro Glu Gly Asp Thr Val Gln Thr Val His Ile			
295	300	305	
aaa tcc tgc ttt cta gag gac gcc acc att ggt aac ggc aac aag atg			1076
Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn Gly Asn Lys Met			
310	315	320	325
acc atc cac ctt agg tca aag ggt gaa gtc atg gag tct gga gac agt			1124
Thr Ile His Leu Arg Ser Lys Gly Glu Val Met Glu Ser Gly Asp Ser			
330	335	340	
gaa gag ccg aag aag gaa gac aca ggt aca agc tct gaa gcc act cca			1172
Glu Glu Pro Lys Lys Glu Asp Thr Gly Thr Ser Ser Glu Ala Thr Pro			
345	350	355	
ccc aga agc tgc cag cac acg ccc agt gac tcc atg ctg ccc acc tct			1220
Pro Arg Ser Cys Gln His Thr Pro Ser Asp Ser Met Leu Pro Thr Ser			
360	365	370	
gag ctg aga gct atg gct ctg gga gac agt agc ccc cag acc aca gaa			1268
Glu Leu Arg Ala Met Ala Leu Gly Asp Ser Ser Pro Gln Thr Thr Glu			
375	380	385	
cct gtg ctt aga gag cat gaa gtc cag gac ata gaa agc tct caa gac			1316
Pro Val Leu Arg Glu His Glu Val Gln Asp Ile Glu Ser Ser Gln Asp			
390	395	400	405
aca gga ctg agc aag caa tgaagctgtg ggaccatagg ctgaccctc			1364
Thr Gly Leu Ser Lys Gln			

410

tgccactata agtcaaatac acctttcctg cctcaagatc aatcaatcga tcaaccgcag 1424
 gagccagttc taccactcct ggatgctcac ccaaaggcaa aagtcaacac agagagatct 1484
 ccgcataatcc atgtagattg ggacactggt cacagcagct aagaagtgga accgaccttg 1544
 ctaccagca gtaaaagatg ggtgaattgg agtatgcaca cagccatggg aaatactgag 1604
 gctgtcattg gccagaagag gatgtgacca gaggccacca tgttgaatga atgaaagcca 1664
 tcttagaaaag acaagggcca ctttttctct gctgtggctc ctagacttta gatagattta 1724
 taaaatcata tacacagatg tgacatgaaa gtacatgtaa caccaaccag gggatgagga 1784
 tggtgcatgg ggaggagagg cgggggtcac agcctggggg ggggtcacgg tctgggaggg 1844
 tgtcaccacc taaagagatc acagctgggg ggatcagggc cgggaggggg gacactgctg 1904
 aatgcactgt acttttataa aaaggtgtac ctctgaaa 1942

<210> 242

<211> 411

<212> PRT

<213> Mus musculus

<400> 242

Met Ala Glu Ala Pro Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln
 1 5 10 15
 Lys Ile Leu Gln Val Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly
 20 25 30
 Gln Leu Val Lys Lys Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val
 35 40 45
 Leu Tyr Arg Leu Lys Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala
 50 55 60
 Thr Trp Ser Ile Gly Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile
 65 70 75 80

727/861

Pro Glu Asn Ser Ser Ala Gln Pro Ser Leu Asp Glu Arg Ile Leu Arg
 85 90 95
 Phe Leu Glu Ala Asn Gly Pro His Arg Ala Leu His Ile Ala Lys Ala
 100 105 110
 Leu Gly Met Thr Thr Ala Lys Glu Val Asn Pro Leu Leu Tyr Ser Met
 115 120 125
 Arg Asn Lys His Leu Leu Ser Tyr Asp Gly Gln Thr Trp Lys Ile Tyr
 130 135 140
 His Ser Arg Gln Glu Gly Gln Asp Ile Ala His Ser Gly Val Thr Gln
 145 150 155 160
 Glu Ser Pro Ala Ile Ile Cys Gln His Asn Pro Val Asn Met Ile Cys
 165 170 175
 Gln Gln Gly Ala Asn Ser His Ile Ser Ile Ala Asn Ser Asn Ala Ile
 180 185 190
 Gln Ile Gly His Gly Asn Val Ile Val Arg Glu Lys Ala Cys Gly Glu
 195 200 205
 Pro Gly Pro Arg Thr Ser His Pro Leu Pro Leu Ala Trp Asp Ala Ser
 210 215 220
 Ala Gln Asp Met Pro Pro Val Ala His Gly Ala Gln Tyr Ile Tyr Met
 225 230 235 240
 Asp Lys Ser Leu Leu Gln Gln Val Gln Leu Gly His His Asn Glu Met
 245 250 255
 Ser Leu Val Gly Asp Ala Gly Lys His Pro Ser Tyr Ser Phe Ser Asp
 260 265 270
 Ser Pro Pro Glu Val Ser Thr Thr Thr Ala Asp Pro Gly Ala Ser Phe
 275 280 285
 Asn Met Gln Thr Ser Glu Pro Gly Pro His Pro Glu Gly Asp Thr Val

290 295 300
 Gln Thr Val His Ile Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly
 305 310 315 320
 Asn Gly Asn Lys Met Thr Ile His Leu Arg Ser Lys Gly Glu Val Met
 325 330 335
 Glu Ser Gly Asp Ser Glu Glu Pro Lys Lys Glu Asp Thr Gly Thr Ser
 340 345 350
 Ser Glu Ala Thr Pro Pro Arg Ser Cys Gln His Thr Pro Ser Asp Ser
 355 360 365
 Met Leu Pro Thr Ser Glu Leu Arg Ala Met Ala Leu Gly Asp Ser Ser
 370 375 380
 Pro Gln Thr Thr Glu Pro Val Leu Arg Glu His Glu Val Gln Asp Ile
 385 390 395 400
 Glu Ser Ser Gln Asp Thr Gly Leu Ser Lys Gln
 405 410

<210> 243

<211> 2195

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (179)..(1465)

<400> 243

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 gcaccagget cggccacttc agaagcccca gcctcgacct agcccacct ctcagggccca 120
 cagtgcagaa gcctgcacac ctgccaagtc tctccgactc cttgcagctg ctgtcagc 178

atg gcc cag gct cct gct gac ccg ggc aga gaa ggc cac ctt gaa caa	226
Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln	
1 5 10 15	
aga atc ctg cag gtg ctg aca gag gct ggc tcc ccg gtg aaa ctt gcc	274
Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala	
20 25 30	
cag ctg gtg aag gaa tgc caa gca ccc aag agg gag ctc aac caa gtc	322
Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val	
35 40 45	
ctc tac cga atg aaa aag gag ttg aaa gtc tcc ctc aca tcc cct gcc	370
Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala	
50 55 60	
acc tgg tgc ttg ggc ggg act gat cct gaa ggc gag ggt cct gca gag	418
Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu	
65 70 75 80	
ctg gcc ttg tcc agc cct gcc gag agg ccc cag caa cat gca gct aca	466
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr	
85 90 95	
att cca gag acc cct ggc cct cag ttc agc caa caa cgg gag gaa gac	514
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp	
100 105 110	
atc tac agg ttt ctc aaa gac aat ggt ccc cag agg gcc ctg gtc atc	562
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile	
115 120 125	
gcc caa gca ctg gga atg agg aca gca aaa gat gtg aac cga gac ttg	610
Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu	
130 135 140	

tac agg atg aag agc agg cac ctt ctg gac atg gat gag cag tcc aaa	658
Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys	
145 150 155 160	
gca tgg acg att tac cgc cca gaa gat tct gga aga aga gca aag tca	706
Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser	
165 170 175	
gcc tca att att tac cag cac aat cca atc aac atg atc tgc cag aat	754
Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn	
180 185 190	
gga ccc aac agc tgg att tcc att gca aac tcc gaa gcc atc cag att	802
Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile	
195 200 205	
gga cac ggg aac atc att aca aga cag aca gtc tcc agg gag gac ggt	850
Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly	
210 215 220	
tcc gcc ggt cca cgc cac ctc cct tca atg gca cca ggt gat tcc tca	898
Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser	
225 230 235 240	
act tgg ggg acc cta gtt gat ccc tgg ggg ccc cag gac atc cac atg	946
Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met	
245 250 255	
gag cgg tcc ata ctg aga cgg gtg cag ctg gga cac agc aat gag atg	994
Glu Arg Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met	
260 265 270	
agg ctc cac ggc gtc ccg tcc gag ggc cct gcc cac atc ccc cct ggc	1042
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly	
275 280 285	

agc ccc cca gtc tct gcc act gct gcc ggc cca gaa gct tcg ttt gaa 1090
 Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu
 290 295 300
 gca aga att ccc agt cca gga act cac cct gag ggg gaa gcc gcc cag 1138
 Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln
 305 310 315 320
 aga atc cac atg aaa tcg tgc ttt ctc gag gac gcc acc atc ggc aac 1186
 Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn
 325 330 335
 agc aac aaa atg tct atc agc cca ggg gtg gct ggc cca gga gga gtc 1234
 Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val
 340 345 350
 gca ggg tct gga gag ggg gag cca ggg gag gac gca ggt cgt cgt ccc 1282
 Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro
 355 360 365
 gca gac aca caa tcc aga agt cac ttt cct cga gac att ggt cag ccc 1330
 Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro
 370 375 380
 atc act ccc agc cac tcg aag ctc acc ccc aag ctg gaa act atg act 1378
 Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr
 385 390 395 400
 ctt gga aac agg agt cac aaa gct gca gaa ggc agc cac tat gtg gat 1426
 Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp
 405 410 415
 gaa gcc tca cac gag ggg agc tgg tgg gga ggt ggg att tagtgacag 1475
 Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile
 420 425

cctcacgtgg ggcttggaca caggctgggg gtgggcgcat gctagggaga ctagcctgct 1535
 gctctctgca ttccttagcg tcttgtttga cctgcttgct tccagacata acctgcatga 1595
 atcagttttg ggggaatgga cctggcatgg ggatgggttc aggccaggtc ttttgatggc 1655
 caggagtaga tgacaggag ttgccttggg gaacctttg tgtgccaaga ggaggtgggt 1715
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 cggggcatct gcctggagtt accttccatc atggctacct gctgtggttt gaatgtttga 1835
 gtcccaacaa aattcatatc aaaacataat cccaactggg tgcagtggct cagcctgta 1895
 atcccagcac tttgggaggc cgaggcgggc ggatcaatag gtcaggaaat ccagaccgctc 1955
 ctggctaaca tggtgaaacc ccgtctctac taaaaaaaaa aatacaaaaa attagccggg 2015
 cgttgtggcg ggcacctgga gtcccagcta ctccggaggc tgagggagga gaatggtgtg 2075
 aaccggggag gtggagcttc cagtgagccg agatcgcgcc actgcactcc aggctgggcg 2135
 acagagcgag actccgtctc aaaaaataa atacataaat aaaaaataaa ccaccataa 2195

<210> 244

<211> 429

<212> PRT

<213> Homo sapiens

<400> 244

Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln
 1 5 10 15
 Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala
 20 25 30
 Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val
 35 40 45
 Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala
 50 55 60
 Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu

65	70	75	80
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr			
	85	90	95
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp			
	100	105	110
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile			
	115	120	125
Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu			
	130	135	140
Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys			
145	150	155	160
Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser			
	165	170	175
Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn			
	180	185	190
Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile			
	195	200	205
Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly			
	210	215	220
Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser			
225	230	235	240
Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met			
	245	250	255
Glu Arg Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met			
	260	265	270
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly			
	275	280	285

Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu
290 295 300
Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln
305 310 315 320
Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn
325 330 335
Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val
340 345 350
Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro
355 360 365
Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro
370 375 380
Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr
385 390 395 400
Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp
405 410 415
Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile
420 425

<210> 245

<211> 2195

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (179).. (1465)

<400> 245

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gcaccaggct cggccacttc agaagcccca gcctcgacct agcccaccct ctcagggcca	120
cagtgcagaa gcctgcacac ctgccaagtc tctccgactc cttgcagctg ctgtcagc	178
atg gcc cag gct cct gct gac ccg ggc aga gaa ggc cac ctt gaa caa	226
Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln	
1 5 10 15	
aga atc ctg cag gtg ctg aca gag gct ggc tcc ccg gtg aaa ctt gcc	274
Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala	
20 25 30	
cag ctg gtg aag gaa tgc caa gca ccc aag agg gag ctc aac caa gtc	322
Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val	
35 40 45	
ctc tac cga atg aaa aag gag ttg aaa gtc tcc ctc aca tcc cct gcc	370
Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala	
50 55 60	
acc tgg tgc ttg ggc ggg act gat cct gaa ggc gag ggt cct gca gag	418
Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu	
65 70 75 80	
ctg gcc ttg tcc agc cct gcc gag agg ccc cag caa cat gca gct aca	466
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr	
85 90 95	
att cca gag acc cct ggc cct cag ttc agc caa caa cgg gag gaa gac	514
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp	
100 105 110	
atc tac agg ttt ctc aaa gac aat ggt ccc cag agg gcc ctg gtc atc	562
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile	
115 120 125	

gcc caa gca ctg gga atg agg aca gca aaa gat gtg aac cga gac ttg 610
 Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu
 130 135 140
 tac agg atg aag agc agg cac ctt ctg gac atg gat gag cag tcc aaa 658
 Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys
 145 150 155 160
 gca tgg acg att tac cgc cca gaa gat tct gga aga aga gca aag tca 706
 Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser
 165 170 175
 gcc tca att att tac cag cac aat cca atc aac atg atc tgc cag aat 754
 Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn
 180 185 190
 gga ccc aac agc tgg att tcc att gca aac tcc gaa gcc atc cag att 802
 Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile
 195 200 205
 gga cac ggg aac atc att aca aga cag aca gtc tcc agg gag gac ggt 850
 Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly
 210 215 220
 tcc gcc ggt cca cgc cac ctc cct tca atg gca cca ggt gat tcc tca 898
 Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser
 225 230 235 240
 act tgg ggg acc cta gtt gat ccc tgg ggg ccc cag gac atc cac atg 946
 Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met
 245 250 255
 gag cag tcc ata ctg aga cgg gtg cag ctg gga cac agc aat gag atg 994
 Glu Gln Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met
 260 265 270

agg ctc cac ggc gtc ccg tcc gag ggc cct gcc cac atc ccc cct ggc	1042
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly	
275 280 285	
agc ccc cca gtc tct gcc act gct gcc ggc cca gaa gct tcg ttt gaa	1090
Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu	
290 295 300	
gca aga att ccc agt cca gga act cac cct gag ggg gaa gcc gcc cag	1138
Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln	
305 310 315 320	
aga atc cac atg aaa tcg tgc ttt ctc gag gac gcc acc atc ggc aac	1186
Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn	
325 330 335	
agc aac aaa atg tct atc agc cca ggg gtg gct ggc cca gga gga gtc	1234
Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val	
340 345 350	
gca ggg tct gga gag ggg gag cca ggg gag gac gca ggt cgt cgt ccc	1282
Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro	
355 360 365	
gca gac aca caa tcc aga agt cac ttt cct cga gac att ggt cag ccc	1330
Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro	
370 375 380	
atc act ccc agc cac tcg aag ctc acc ccc aag ctg gaa act atg act	1378
Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr	
385 390 395 400	
ctt gga aac agg agt cac aaa gct gca gaa ggc agc cac tat gtg gat	1426
Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp	
405 410 415	

gaa gcc tca cac gag ggg agc tgg tgg gga ggt ggg att tagtgacag 1475
 Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile

420 425

cctcacgtgg ggcttgaca caggctgggg gtgggcgcat gctagggaga ctagcctgct 1535
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 atcccagcac tttgggaggc cgaggcgggc ggatcaatag gtcaggaaat ccagaccgctc 1955
 ctggctaaca tgggtgaaacc ccgtctctac taaaaaaaaa aatacaaaaa attagccggg 2015
 cgttggtggcg ggcacctgga gtcccagcta ctccggaggc tgaggaggga gaatggtgtg 2075
 aaccggggag gtggagcttc cagtgagccg agatcgcgcc actgcactcc aggctgggcg 2135
 acagagcgag actccgtctc aaaaaataa atacataaat aaaaaataaa ccaccataa 2195

<210> 246

<211> 429

<212> PRT

<213> Homo sapiens

<400> 246

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20 25 30

Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val

35 40 45

Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala
 50 55 60
 Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu
 65 70 75 80
 Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr
 85 90 95
 Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp
 100 105 110
 Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile
 115 120 125
 Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu
 130 135 140
 Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys
 145 150 155 160
 Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser
 165 170 175
 Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn
 180 185 190
 Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile
 195 200 205
 Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly
 210 215 220
 Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser
 225 230 235 240
 Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met
 245 250 255
 Glu Gln Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met

260 265 270
 Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly
 275 280 285
 Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu
 290 295 300
 Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln
 305 310 315 320
 Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn
 325 330 335
 Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val
 340 345 350
 Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro
 355 360 365
 Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro
 370 375 380
 Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr
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 405 410 415
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 420 425

<210> 247

<211> 1926

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14).. (1513)

<400> 247

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Leu Ser Gln Asp Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg
              15              20              25
tca ctg cag acc tct ctg gtc tcc tct cga agg gag cct ccc cca tac      145
Ser Leu Gln Thr Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr
              30              35              40
gga tat agg aaa ggc tgg att cca aga cta tta gag gat ttt gga gat      193
Gly Tyr Arg Lys Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp
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gga ggt gct ttc cca gaa atc cat gtg gcc cag tat cct ctg gat atg      241
Gly Gly Ala Phe Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met
              65              70              75
ggg cga aag aaa aaa atg tcg aat gct ctg gcc att cag gtg gat cct      289
Gly Arg Lys Lys Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro
              80              85              90
gaa ggg aaa att aag tat gat gca att gct cgg cag gga cag tcc aaa      337
Glu Gly Lys Ile Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys
              95              100              105
gac aag gtc att tac agc aaa tac act gac ctg gtt cct aag gag gtt      385
Asp Lys Val Ile Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val
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Lys Glu Ile Thr Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser	
145 150 155	
cag aag gtt gct gca gcc atg cca gtt cgt gca gct gac aag ctg gct	529
Gln Lys Val Ala Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala	
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cct gct cag tat atc cgc tac aca cca tct cag caa gga gta gcg ttc	577
Pro Ala Gln Tyr Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe	
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aat tct gga gct aaa cag agg gtc att cgg atg gta gaa atg cag aaa	625
Asn Ser Gly Ala Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys	
190 195 200	
gac cca atg gag cct cca aga ttc aag att aat aag aaa att ccc cgg	673
Asp Pro Met Glu Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg	
205 210 215 220	
gga cca ccg tct cct cct gca cct gta atg cac tct cct agt cgg aag	721
Gly Pro Pro Ser Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys	
225 230 235	
atg act gta aag gaa caa caa gag tgg aag atc ccg cct tgt att tcc	769
Met Thr Val Lys Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser	
240 245 250	
aac tgg aag aac gct aag ggg tat acg atc cca tta gat aaa cgg ctg	817
Asn Trp Lys Asn Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu	
255 260 265	

gct gct gat gga aga gga ctt cag act gtc cac ata aat gaa aat ttt	865
Ala Ala Asp Gly Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe	
270 275 280	
gcc aaa ctg gct gaa gcg ctc tac att gct gat cgg aag gct cgt gaa	913
Ala Lys Leu Ala Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu	
285 290 295 300	
gcg gtg gaa atg cga gcc cag gta gag aga aag atg gct caa aaa gaa	961
Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu	
305 310 315	
aag gag aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa gcc aga	1009
Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg	
320 325 330	
gaa agg aga gct gga atc aaa acc cac gtg gag aaa gag gat gga gag	1057
Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu	
335 340 345	
gcc cgt gag aga gat gaa atc cgt cat gac agg cga aaa gag agg cag	1105
Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln	
350 355 360	
cat gac cgg aac ctt tcc agg gca gct cct gat aag agg tca aaa cta	1153
His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu	
365 370 375 380	
cag aga aat gaa aat cga gac atc agt gaa gtc att gct ctt ggt gtg	1201
Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val	
385 390 395	
ccc aat cct cga act tcc aat gaa gtt cag tat gac caa agg ctc ttc	1249
Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe	
400 405 410	

aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa gat gaa 1297
 Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu
 415 420 425
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 Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala
 430 435 440
 cag agc atc tac agg ccc agt aaa aat ctg gac aag gac atg tat ggt 1393
 Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly
 445 450 455 460
 gat gac ctg gaa gcc agg ata aag acc aac aga ttt gtt cct gat aag 1441
 Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys
 465 470 475
 gag ttt tct gga tca gac cgc aaa cag aga ggc cga gaa gga cca gtg 1489
 Glu Phe Ser Gly Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val
 480 485 490
 cag ttt gag gaa tca tca gag aga tgaccaggag ggagataaag actggactgt 1543
 Gln Phe Glu Glu Ser Ser Glu Arg
 495 500
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 cctcacctca aatggtgagt gggctaagt tcacacactg gagctctgtc aactgcattt 1843
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<210> 248

<211> 500

<212> PRT

<213> Mus musculus

<400> 248

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 35 40 45
 Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe
 50 55 60
 Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys
 65 70 75 80
 Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro Glu Gly Lys Ile
 85 90 95
 Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile
 100 105 110
 Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp
 115 120 125
 Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr
 130 135 140
 Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala
 145 150 155 160
 Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr
 165 170 175
 Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala

180	185	190
Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu		
195	200	205
Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser		
210	215	220
Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys		
225	230	235
Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn		
245	250	255
Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly		
260	265	270
Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala		
275	280	285
Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met		
290	295	300
Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His		
305	310	315
Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala		
325	330	335
Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg		
340	345	350
Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn		
355	360	365
Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu		
370	375	380
Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg		
385	390	395
		400

Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys
 405 410 415
 Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val
 420 425 430
 Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr
 435 440 445
 Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu
 450 455 460
 Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly
 465 470 475 480
 Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu
 485 490 495
 Ser Ser Glu Arg
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<210> 249

<211> 1844

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14)..(1621)

<400> 249

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Leu Ser Gln Asp Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg
 15 20 25
 tca ctg cag acc tct ctg gtc tcc tct cga agg gag cct ccc cca tac 145
 Ser Leu Gln Thr Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr
 30 35 40
 gga tat agg aaa ggc tgg att cca aga cta tta gag gat ttt gga gat 193
 Gly Tyr Arg Lys Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp
 45 50 55 60
 gga ggt gct ttc cca gaa atc cat gtg gcc cag tat cct ctg gat atg 241
 Gly Gly Ala Phe Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met
 65 70 75
 ggg cga aag aaa aaa atg tcg aat gct ctg gcc att cag gtg gat cct 289
 Gly Arg Lys Lys Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro
 80 85 90
 gaa ggg aaa att aag tat gat gca att gct cgg cag gga cag tcc aaa 337
 Glu Gly Lys Ile Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys
 95 100 105
 gac aag gtc att tac agc aaa tac act gac ctg gtt cct aag gag gtt 385
 Asp Lys Val Ile Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val
 110 115 120
 atg aat gca gat gac cca gac ctg caa cgg ccc gat gaa gag gca att 433
 Met Asn Ala Asp Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile
 125 130 135 140
 aaa gag ata aca gaa aag act aga gtt gcc ttg gag aaa tct gtg tcg 481
 Lys Glu Ile Thr Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser
 145 150 155
 cag aag gtt gct gca gcc atg cca gtt cgt gca gct gac aag ctg gct 529

Gln Lys Val Ala Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala
 160 165 170
 cct gct cag tat atc cgc tac aca cca tct cag caa gga gta gcg ttc 577
 Pro Ala Gln Tyr Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe
 175 180 185
 aat tct gga gct aaa cag agg gtc att cgg atg gta gaa atg cag aaa 625
 Asn Ser Gly Ala Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys
 190 195 200
 gac cca atg gag cct cca aga ttc aag att aat aag aaa att ccc cgg 673
 Asp Pro Met Glu Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg
 205 210 215 220
 gga cca ccg tct cct cct gca cct gta atg cac tct cct agt cgg aag 721
 Gly Pro Pro Ser Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys
 225 230 235
 atg act gta aag gaa caa caa gag tgg aag atc ccg cct tgt att tcc 769
 Met Thr Val Lys Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser
 240 245 250
 aac tgg aag aac gct aag ggg tat acg atc cca tta gat aaa cgg ctg 817
 Asn Trp Lys Asn Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu
 255 260 265
 gct gct gat gga aga gga ctt cag act gtc cac ata aat gaa aat ttt 865
 Ala Ala Asp Gly Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe
 270 275 280
 gcc aaa ctg gct gaa gcg ctc tac att gct gat cgg aag gct cgt gaa 913
 Ala Lys Leu Ala Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu
 285 290 295 300
 gcg gtg gaa atg cga gcc cag gta gag aga aag atg gct caa aaa gaa 961

Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu	
305 310 315	
aag gag aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa gcc aga	1009
Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg	
320 325 330	
gaa agg aga gct gga atc aaa acc cac gtg gag aaa gag gat gga gag	1057
Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu	
335 340 345	
gcc cgt gag aga gat gaa atc cgt cat gac agg cga aaa gag agg cag	1105
Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln	
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cat gac cgg aac ctt tcc agg gca gct cct gat aag agg tca aaa cta	1153
His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu	
365 370 375 380	
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Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val	
385 390 395	
ccc aat cct cga act tcc aat gaa gtt cag tat gac caa agg ctc ttc	1249
Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe	
400 405 410	
aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa gat gaa	1297
Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu	
415 420 425	
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Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala	
430 435 440	
cag agc atc tac agg ccc agt aaa aat ctg gac aag gac atg tat ggt	1393

Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly	
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Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys	
465	470
gag ttt tct gga tca gac cgc aaa cag aga ggc cga gaa gga cca gtg	1489
Glu Phe Ser Gly Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val	
480	485
cag ttt gag gag gat cct ttt ggt ttg gac aag ttt ttg gaa gaa gcc	1537
Gln Phe Glu Glu Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala	
495	500
aaa cag cac ggt ggt tct aaa aga ccc tct gat agc agt cgc ccc aag	1585
Lys Gln His Gly Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys	
510	515
gaa cat gag cat gaa ggc aag aag cgg agg aaa gag tagagggacc	1631
Glu His Glu His Glu Gly Lys Lys Arg Arg Lys Glu	
525	530
tcttaaaact aaatctgaca tatgcagcag aggactgcct ggtctggcct cattgtgaac	1691
agatgtcccc accccctcca gacacttgag actccaggga atagggcgtc ctagtgggtg	1751
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<210> 250

<211> 536

<212> PRT

<213> Mus musculus

<400> 250

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 35 40 45
 Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe
 50 55 60
 Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys
 65 70 75 80
 Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro Glu Gly Lys Ile
 85 90 95
 Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile
 100 105 110
 Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp
 115 120 125
 Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr
 130 135 140
 Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala
 145 150 155 160
 Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr
 165 170 175
 Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala
 180 185 190
 Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu
 195 200 205
 Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser

210	215	220	
Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys			
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Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn			
	245	250	255
Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly			
	260	265	270
Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala			
	275	280	285
Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met			
	290	295	300
Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His			
305	310	315	320
Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala			
	325	330	335
Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg			
	340	345	350
Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn			
	355	360	365
Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu			
	370	375	380
Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg			
385	390	395	400
Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys			
	405	410	415
Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val			
	420	425	430

Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr
 435 440 445

Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu
 450 455 460

Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly
 465 470 475 480

Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu
 485 490 495

Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala Lys Gln His Gly
 500 505 510

Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys Glu His Glu His
 515 520 525

Glu Gly Lys Lys Arg Arg Lys Glu
 530 535

<210> 251

<211> 2121

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1629)

<400> 251

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 act cag cta tct cag gac cag ctt gag gct gaa gaa aag gca aga tcc 99

Thr	Gln	Leu	Ser	Gln	Asp	Gln	Leu	Glu	Ala	Glu	Glu	Lys	Ala	Arg	Ser		
				15					20						25		
cag	aga	tca	cgg	cag	acc	tca	ctg	gtc	tcc	tcc	cga	aga	gaa	cct	ccc	147	
Gln	Arg	Ser	Arg	Gln	Thr	Ser	Leu	Val	Ser	Ser	Arg	Arg	Glu	Pro	Pro		
				30					35					40			
ccg	tac	gga	tac	cgg	aaa	ggc	tgg	ata	cct	cgg	tta	tta	gag	gat	ttt	195	
Pro	Tyr	Gly	Tyr	Arg	Lys	Gly	Trp	Ile	Pro	Arg	Leu	Leu	Glu	Asp	Phe		
				45					50					55			
gga	gat	gga	ggt	gct	ttt	cca	gag	atc	cat	gtg	gcc	cag	tat	cca	ctg	243	
Gly	Asp	Gly	Gly	Ala	Phe	Pro	Glu	Ile	His	Val	Ala	Gln	Tyr	Pro	Leu		
				60					65					70			
gat	atg	gga	cga	aag	aaa	aaa	atg	tcg	aat	gcg	ctg	gcc	att	cag	gtg	291	
Asp	Met	Gly	Arg	Lys	Lys	Lys	Met	Ser	Asn	Ala	Leu	Ala	Ile	Gln	Val		
				75					80					85			
gat	tct	gaa	gga	aaa	att	aaa	tat	gat	gca	att	gct	cga	caa	gga	cag	339	
Asp	Ser	Glu	Gly	Lys	Ile	Lys	Tyr	Asp	Ala	Ile	Ala	Arg	Gln	Gly	Gln		
				95					100					105			
tca	aaa	gac	aag	gtc	att	tat	agc	aaa	tac	act	gac	ctg	gtt	cca	aag	387	
Ser	Lys	Asp	Lys	Val	Ile	Tyr	Ser	Lys	Tyr	Thr	Asp	Leu	Val	Pro	Lys		
				110					115					120			
gag	gtt	atg	aat	gca	gat	gat	cca	gac	ctg	caa	agg	ccc	gat	gaa	gaa	435	
Glu	Val	Met	Asn	Ala	Asp	Asp	Pro	Asp	Leu	Gln	Arg	Pro	Asp	Glu	Glu		
				125					130					135			
gct	att	aaa	gag	ata	aca	gaa	aag	aca	aga	gta	gcc	tta	gaa	aaa	tct	483	
Ala	Ile	Lys	Glu	Ile	Thr	Glu	Lys	Thr	Arg	Val	Ala	Leu	Glu	Lys	Ser		
				140					145					150			
gta	tca	cag	aag	gtc	gcc	gca	gcc	atg	cca	gtt	cga	gca	gct	gac	aaa	531	

757/861

Arg Glu Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln
 300 305 310
 aaa gaa aag gaa aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa 1011
 Lys Glu Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys
 315 320 325 330
 gcc agg gaa aga aga gct ggg atc aaa act cat gtg gaa aaa gag gat 1059
 Ala Arg Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp
 335 340 345
 ggg gag gca cgt gag agg gat gaa atc cgg cat gac agg cga aaa gag 1107
 Gly Glu Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu
 350 355 360
 aga cag cat gac cgg aat ctt tcc agg gca gct cct gat aag agg tcg 1155
 Arg Gln His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser
 365 370 375
 aaa ctt cag aga aat gaa aat cgg gat atc agt gaa gtt att gct ctc 1203
 Lys Leu Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu
 380 385 390
 ggt gtt cct aat cct cgg act tcc aat gaa gtt cag tat gac caa agg 1251
 Gly Val Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg
 395 400 405 410
 ctc ttc aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa 1299
 Leu Phe Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu
 415 420 425
 gat gaa att tat aat gtt tat gat caa gcc tgg aga ggt ggt aaa gat 1347
 Asp Glu Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp
 430 435 440
 atg gcc cag agt att tat agg ccc agt aaa aat ctg gac aag gac atg 1395

Met Ala Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met
445 450 455
tat ggt gat gac cta gaa gcc aga ata aag acc aac aga ttt gtt ccc 1443
Tyr Gly Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro
460 465 470
gac aag gag ttt tct ggt tca gac cgt aga cag aga ggc cga gaa gga 1491
Asp Lys Glu Phe Ser Gly Ser Asp Arg Arg Gln Arg Gly Arg Glu Gly
475 480 485 490
cca gtt cag ttt gag gaa gat cct ttt ggt ttg gac aag ttt ttg gaa 1539
Pro Val Gln Phe Glu Glu Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu
495 500 505
gaa gcc aaa cag cat ggt ggc tct aaa aga ccc tca gat agc agc cgc 1587
Glu Ala Lys Gln His Gly Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg
510 515 520
ccc aag gaa cac gag cat gaa ggc aag aag agg agg aag gaa 1629
Pro Lys Glu His Glu His Glu Gly Lys Lys Arg Arg Lys Glu
525 530 535
taggcacagg tctctccaaa gtgaatgaac tcttaccat aaccctaatg atgcaagtca 1689
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cactactttt tattactgga gaaatggggg ggatagaaaa ttctactttg aattatttag 1809
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gctgccccac atacaaagtc aagaccactt acttttatgt gacactagta gtttgggggtt 1929
aatgttttgt gtaagaacag ctgcatatga gtaaagttac cccaaccaca gtgaggagga 1989
agatgttcac atactggaac tgtcctgcca aataaatttt gccctattg tgctctgttt 2049
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atttagacaa aa 2121

<210> 252

<211> 536

<212> PRT

<213> Homo sapiens

<400> 252

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           20           25           30
Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr Gly Tyr Arg Lys
           35           40           45
Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe
           50           55           60
Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys
65           70           75           80
Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Ser Glu Gly Lys Ile
           85           90           95
Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile
           100          105          110
Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp
           115          120          125
Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr
           130          135          140
Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala
145          150          155          160
Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr
           165          170          175

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Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala
 180 185 190
 Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu
 195 200 205
 Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser
 210 215 220
 Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys
 225 230 235 240
 Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn
 245 250 255
 Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly
 260 265 270
 Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala
 275 280 285
 Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met
 290 295 300
 Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His
 305 310 315 320
 Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala
 325 330 335
 Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg
 340 345 350
 Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn
 355 360 365
 Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu
 370 375 380
 Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg

385 390 395 400
Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys
 405 410 415
Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val
 420 425 430
Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr
 435 440 445
Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu
 450 455 460
Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly
465 470 475 480
Ser Asp Arg Arg Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu
 485 490 495
Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala Lys Gln His Gly
 500 505 510
Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys Glu His Glu His
 515 520 525
Glu Gly Lys Lys Arg Arg Lys Glu
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<210> 253

<211> 2003

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (23).. (1075)

<400> 253

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                               1           5           10

ctc ccg ctg ttc gac tgc ccg act tgg gca ggt aaa cca cca cct ggc      100
Leu Pro Leu Phe Asp Cys Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly
                               15           20           25

tta cat ctg gat gtg gtg aaa gga gac aag cta att gag aag ctg att      148
Leu His Leu Asp Val Val Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile
                               30           35           40

att gat gag aaa aag tat tac tta ttt ggg agg aac ccc gat ctg tgt      196
Ile Asp Glu Lys Lys Tyr Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys
                               45           50           55

gac ttc act atc gac cac cag tca tgc tct cga gtc cac gca gcg ctg      244
Asp Phe Thr Ile Asp His Gln Ser Cys Ser Arg Val His Ala Ala Leu
                               60           65           70

gtg tac cac aaa cac ctg aag aga gtt ttc ttg ata gac ctc aac agc      292
Val Tyr His Lys His Leu Lys Arg Val Phe Leu Ile Asp Leu Asn Ser
                               75           80           85           90

aca cat ggc act ttc ttg ggt cac att cgg ctg gaa cct cac aag cct      340
Thr His Gly Thr Phe Leu Gly His Ile Arg Leu Glu Pro His Lys Pro
                               95           100           105

caa cag att ccc atc gat tct acg gtc tca ttt ggc gcg tcc acg agg      388
Gln Gln Ile Pro Ile Asp Ser Thr Val Ser Phe Gly Ala Ser Thr Arg
                               110           115           120

gca tac act ctg cga gag aag cct cag aca ttg cca tcg gct gtg aaa      436
Ala Tyr Thr Leu Arg Glu Lys Pro Gln Thr Leu Pro Ser Ala Val Lys

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125	130	135	
gga gat gag aag atg ggc gga gag gat gat gaa ctc aag ggc ttg ttg			484
Gly Asp Glu Lys Met Gly Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu			
140	145	150	
gga ctt ccc gaa gag gag acc gag ctg gat aac ctg aca gag ttc aac			532
Gly Leu Pro Glu Glu Glu Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn			
155	160	165	170
act gcc cac aac aag cgg att tca acc ctc act att gag gag ggg aac			580
Thr Ala His Asn Lys Arg Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn			
	175	180	185
ctg gac atc cag aga cca aag agg aag agg aag aac tca agg gtg acc			628
Leu Asp Ile Gln Arg Pro Lys Arg Lys Arg Lys Asn Ser Arg Val Thr			
190	195	200	
ttc agt gag gat gac gag atc atc aac cca gag gac gtg gat ccg tct			676
Phe Ser Glu Asp Asp Glu Ile Ile Asn Pro Glu Asp Val Asp Pro Ser			
205	210	215	
gtt ggt cgg ttc cgg aac atg gtg cag aca gca gtg gtt cca gtc aag			724
Val Gly Arg Phe Arg Asn Met Val Gln Thr Ala Val Val Pro Val Lys			
220	225	230	
aag aag cgg atg gag ggc tct ggc tct ctg ggc ctg gag gag tcg ggg			772
Lys Lys Arg Met Glu Gly Ser Gly Ser Leu Gly Leu Glu Glu Ser Gly			
235	240	245	250
agc agg cgc atg cag aac ttt gcc ttc agt gga gga cta tat ggg ggc			820
Ser Arg Arg Met Gln Asn Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly			
	255	260	265
ctg ccc ccc aca cac agt gaa acg ggc tcc cag ccg cat ggc att cat			868
Leu Pro Pro Thr His Ser Glu Thr Gly Ser Gln Pro His Gly Ile His			

270	275	280	
ggg aca gcg ctc att ggt ggc ttg ccc atg cca tac ccg aac ctc gcc			916
Gly Thr Ala Leu Ile Gly Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala			
285	290	295	
cct gat gtg gac ttg act cct gtt gtg cca tca gca gtg gcc ata aat			964
Pro Asp Val Asp Leu Thr Pro Val Val Pro Ser Ala Val Ala Ile Asn			
300	305	310	
ccc aca cca aac cct gca gtc tat aac cct gag gct gtg aat gaa ccc			1012
Pro Thr Pro Asn Pro Ala Val Tyr Asn Pro Glu Ala Val Asn Glu Pro			
315	320	325	330
aag aag aag aaa tac gcg aag gag gct tgg ccg ggc aag aag ccc aca			1060
Lys Lys Lys Lys Tyr Ala Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr			
335	340	345	
cct tcc tta ctg att tgatattttg gttatggaga ggggtggggag gggggtggag			1115
Pro Ser Leu Leu Ile			
350			
ggatgacaag gggagctact gaactagga gaaaactttc catgtgtgca gtatcgtctt			1175
tcagaaagtc tcctgaggtc ccaaccatgt aatactgaga ccaggggtgg ggctaaagta			1235
ccagtaagga ctaaagtcag gcagcttgaa gtgtagagag aggcttccca gtcccttctg			1295
agccgactgt cctggcgatg tccctgtgcc acctattagg actgttttat gtaaagtcgc			1355
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tcgggagacc caagtaacag agcggttgca tggataccag gttggttgac actgttcatt			1475
taaaccacag taaacgagtg tcctcttgtg cctgtggttt tgaggtctaa taggccattc			1535
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tgaaaaactca tttagttcga gtgcagcctc ctccctgtgg cctcactgtt ggtgtgtgcc			1715
ctgaggcagt tcctggtgaa caggaagact atactgcaag gaccaggtgt gtgttaggag			1775

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 gagctttgta cagatttgta catttgtgta ataggccttt tctgctttaa gtgtagcttt 1955
 ttacctgtaa cctttattac attgtaaatt aaatgtaact tttgtcaa 2003

<210> 254

<211> 351

<212> PRT

<213> Mus musculus

<400> 254

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 20 25 30
 Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu Lys Lys Tyr
 35 40 45
 Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His
 50 55 60
 Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu
 65 70 75 80
 Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu
 85 90 95
 Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp
 100 105 110
 Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu
 115 120 125
 Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu Lys Met Gly

130	135	140	
Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro Glu Glu Glu			
145	150	155	160
Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His Asn Lys Arg			
	165	170	175
Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile Gln Arg Pro			
	180	185	190
Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu Asp Asp Glu			
	195	200	205
Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg Phe Arg Asn			
	210	215	220
Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg Met Glu Gly			
225	230	235	240
Ser Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg Met Gln Asn			
	245	250	255
Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro Thr His Ser			
	260	265	270
Glu Thr Gly Ser Gln Pro His Gly Ile His Gly Thr Ala Leu Ile Gly			
	275	280	285
Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val Asp Leu Thr			
	290	295	300
Pro Val Val Pro Ser Ala Val Ala Ile Asn Pro Thr Pro Asn Pro Ala			
305	310	315	320
Val Tyr Asn Pro Glu Ala Val Asn Glu Pro Lys Lys Lys Lys Tyr Ala			
	325	330	335
Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr Pro Ser Leu Leu Ile			
	340	345	350

<210> 255

<211> 2148

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12).. (1064)

<400> 255

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      Met Ala Ala Ala Ala Asn Ser Gly Ser Ser Leu Pro Leu
              1              5              10

ttc gac tgc cca acc tgg gca ggt aag ccc cct ccc ggt tta cat ctg      98
Phe Asp Cys Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly Leu His Leu
      15              20              25

gat gta gtc aaa gga gac aaa cta att gag aaa ctg att att gat gag      146
Asp Val Val Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu
      30              35              40              45

aag aag tat tac tta ttt ggg aga aac cct gat ttg tgt gac ttt acc      194
Lys Lys Tyr Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr
              50              55              60

att gac cac cag tct tgc tct cgg gtc cat gct gca ctt gtc tac cac      242
Ile Asp His Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His
              65              70              75

aag cat ctg aag aga gtt ttc ctg ata gat ctc aac agt aca cac ggc      290
Lys His Leu Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly
              80              85              90

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act ttc ttg ggt cac att cgg ttg gaa cct cac aag cct cag caa att	338
Thr Phe Leu Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile	
95 100 105	
ccc atc gat tcc acg gtc tca ttt ggc gca tcc aca agg gca tac act	386
Pro Ile Asp Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr	
110 115 120 125	
ctg cgc gag aag cct cag aca ttg cca tcg gct gtg aaa gga gat gag	434
Leu Arg Glu Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu	
130 135 140	
aag atg ggt gga gag gat gat gaa ctc aag ggc tta ctg ggg ctt cca	482
Lys Met Gly Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro	
145 150 155	
gag gag gaa act gag ctt gat aac ctg aca gag ttc aac act gcc cac	530
Glu Glu Glu Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His	
160 165 170	
aac aag cgg att tct acc ctt acc att gag gag gga aat ctg gac att	578
Asn Lys Arg Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile	
175 180 185	
caa aga cca aag agg aag agg aag aac tca cgg gtg aca ttc agt gag	626
Gln Arg Pro Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu	
190 195 200 205	
gat gat gag atc atc aac cca gag gat gtg gat ccc tca gtt ggt cga	674
Asp Asp Glu Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg	
210 215 220	
ttc agg aac atg gtg caa act gca gtg gtc cca gtc aag aag aag cgt	722
Phe Arg Asn Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg	
225 230 235	

gtg gag ggc cct ggc tcc ctg ggc ctg gag gaa tca ggg agc agg cgc 770
 Val Glu Gly Pro Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg
 240 245 250
 atg cag aac ttt gcc ttc agc gga gga ctc tac ggg ggc ctg ccc ccc 818
 Met Gln Asn Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro
 255 260 265
 aca cac agt gaa gca ggc tcc cag cca cat ggc atc cat ggg aca gca 866
 Thr His Ser Glu Ala Gly Ser Gln Pro His Gly Ile His Gly Thr Ala
 270 275 280 285
 ctc atc ggt ggc ttg ccc atg cca tac cca aac ctt gcc cct gat gtg 914
 Leu Ile Gly Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val
 290 295 300
 gac ttg act cct gtt gtg ccg tca gca gtg aac atg aac cct gca cca 962
 Asp Leu Thr Pro Val Val Pro Ser Ala Val Asn Met Asn Pro Ala Pro
 305 310 315
 aac cct gca gtc tat aac cct gaa gct gta aat gaa ccc aag aag aag 1010
 Asn Pro Ala Val Tyr Asn Pro Glu Ala Val Asn Glu Pro Lys Lys Lys
 320 325 330
 aaa tat gca aaa gag gct tgg cca ggc aag aag ccc aca cct tcc ttg 1058
 Lys Tyr Ala Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr Pro Ser Leu
 335 340 345
 ctg att tgatattttt ggcatggag aagggtggga ttgggtggga atggggtgga 1114
 Leu Ile
 350
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<210> 256

<211> 351

<212> PRT

<213> Homo sapiens

<400> 256

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Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly Leu His Leu Asp Val Val

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Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu Lys Lys Tyr

35

40

45

Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His
 50 55 60
 Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu
 65 70 75 80
 Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu
 85 90 95
 Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp
 100 105 110
 Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu
 115 120 125
 Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu Lys Met Gly
 130 135 140
 Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro Glu Glu Glu
 145 150 155 160
 Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His Asn Lys Arg
 165 170 175
 Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile Gln Arg Pro
 180 185 190
 Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu Asp Asp Glu
 195 200 205
 Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg Phe Arg Asn
 210 215 220
 Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg Val Glu Gly
 225 230 235 240
 Pro Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg Met Gln Asn
 245 250 255
 Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro Thr His Ser

260 265 270
 Glu Ala Gly Ser Gln Pro His Gly Ile His Gly Thr Ala Leu Ile Gly
 275 280 285
 Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val Asp Leu Thr
 290 295 300
 Pro Val Val Pro Ser Ala Val Asn Met Asn Pro Ala Pro Asn Pro Ala
 305 310 315 320
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 325 330 335
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<210> 257

<211> 1088

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (15)..(965)

<400> 257

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 Gly Trp Gly Leu Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr
 15 20 25
 tat acc aga ttt aca ggc gcc cca ctg aag ata cac aag acc agc aat 146

Tyr Thr Arg Phe Thr Gly Ala Pro Leu Lys Ile His Lys Thr Ser Asn	
30 35 40	
cct tgg cag agc cct tca gga act ctg cct gct ctt cga acc agt gat	194
Pro Trp Gln Ser Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser Asp	
45 50 55 60	
ggg aaa gtc att aca gtg cca cac aag atc atc acc cat ctt cgt aaa	242
Gly Lys Val Ile Thr Val Pro His Lys Ile Ile Thr His Leu Arg Lys	
65 70 75	
gag aag tat aat gcc gac tac gat ctg tca gct cgc caa gga gca gat	290
Glu Lys Tyr Asn Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp	
80 85 90	
acc cta gcc ttc atg tct ctg ctg gag gag aaa cta ctg cct gtg tta	338
Thr Leu Ala Phe Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu	
95 100 105	
atc cat act ttt tgg ata gac gcc aag aac tat gtg gaa gtg acc cga	386
Ile His Thr Phe Trp Ile Asp Ala Lys Asn Tyr Val Glu Val Thr Arg	
110 115 120	
aag tgg tat gca gag gct atg ccc ttt ccc ctc aac ttc ttc ctg ccc	434
Lys Trp Tyr Ala Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro	
125 130 135 140	
ggc cgc atg cag cgc cag tac atg gag cgg cta cag ctg ctg tgt ggc	482
Gly Arg Met Gln Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Cys Gly	
145 150 155	
gag cac aaa tca gag aac gag gag gaa cta gaa aaa gag cta tac caa	530
Glu His Lys Ser Glu Asn Glu Glu Glu Leu Glu Lys Glu Leu Tyr Gln	
160 165 170	
gag gct cgg gag tgc cta acc ctt ctc tct cag cgt ctg ggc tct cag	578

Glu Ala Arg Glu Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln	
175	180
aag ttc ttc ttt ggg gat gcc cct gcc tcc ctg gac gcc ttt gtt ttt	626
Lys Phe Phe Phe Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe	
190	195
agc cat ttg gcc ctg ctg ctg cag gcc aag ctg ccc agt ggg aag ctg	674
Ser His Leu Ala Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu	
205	210
cag gcc cac ctt cgg ggg ctg cac aac ctc tgc gcc tac tgc acc cac	722
Gln Ala His Leu Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His	
225	230
atc ctc aac ctc tac ttt ccc cgg gat gga gat gag gtg cca ctt cca	770
Ile Leu Asn Leu Tyr Phe Pro Arg Asp Gly Asp Glu Val Pro Leu Pro	
240	245
cgc cag aca cca gca gcc cct gag acc gag gag gag cca tac cgg cgc	818
Arg Gln Thr Pro Ala Ala Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg	
255	260
cgg acc cag att ctc tct gtg ctg gca ggg ctg gca gcc atg gtg ggc	866
Arg Thr Gln Ile Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly	
270	275
tat gcc ctg ctc agt ggc atc gtt tct atc cag cgg aca agc cct gct	914
Tyr Ala Leu Leu Ser Gly Ile Val Ser Ile Gln Arg Thr Ser Pro Ala	
285	290
cgg gcc cca ggc acc cgg gcc ttg ggc ctg gct gag gag gat gaa gag	962
Arg Ala Pro Gly Thr Arg Ala Leu Gly Leu Ala Glu Glu Asp Glu Glu	
305	310
gac tgatggcggtt cctgttccca ggactgactt ttctactcgt gcattccagc	1015

Asp

tgtccctcgt ctcccatgg ttggagcagc caaaaatggg gcgctgtcct cagaataaac 1075

ctgtttacac taa 1088

<210> 258

<211> 317

<212> PRT

<213> Mus musculus

<400> 258

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu

1 5 10 15

Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Thr Arg Phe

20 25 30

Thr Gly Ala Pro Leu Lys Ile His Lys Thr Ser Asn Pro Trp Gln Ser

35 40 45

Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser Asp Gly Lys Val Ile

50 55 60

Thr Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn

65 70 75 80

Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe

85 90 95

Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Ile His Thr Phe

100 105 110

Trp Ile Asp Ala Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala

115 120 125

Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln

130 135 140

Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Cys Gly Glu His Lys Ser
 145 150 155 160
 Glu Asn Glu Glu Glu Leu Glu Lys Glu Leu Tyr Gln Glu Ala Arg Glu
 165 170 175
 Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe
 180 185 190
 Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser His Leu Ala
 195 200 205
 Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Ala His Leu
 210 215 220
 Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Asn Leu
 225 230 235 240
 Tyr Phe Pro Arg Asp Gly Asp Glu Val Pro Leu Pro Arg Gln Thr Pro
 245 250 255
 Ala Ala Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Thr Gln Ile
 260 265 270
 Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu
 275 280 285
 Ser Gly Ile Val Ser Ile Gln Arg Thr Ser Pro Ala Arg Ala Pro Gly
 290 295 300
 Thr Arg Ala Leu Gly Leu Ala Glu Glu Asp Glu Glu Asp
 305 310 315

<210> 259

<211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (951)

<400> 259

atg gcg gcg ccc atg gag ctg ttc tgc tgg tca ggg ggc tgg ggg ctg 48

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu

1 5 10 15

ccg tca gtg gac ctg gac agc ctg gcc gtg ctg acc tat gcc aga ttt 96

Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Ala Arg Phe

20 25 30

act ggt gct cca ctg aag gta cac aag atc agc aac ccc tgg cag agc 144

Thr Gly Ala Pro Leu Lys Val His Lys Ile Ser Asn Pro Trp Gln Ser

35 40 45

cct tca gga act ctg cct gcc ctt cgg acc agt cat gga gag gtc atc 192

Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser His Gly Glu Val Ile

50 55 60

tca gtt cca cac aag atc atc acc cac ctt cga aaa gag aag tac aat 240

Ser Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn

65 70 75 80

gct gat tat gat ctg tca gct cgg caa ggg gca gac acc ctg gcc ttc 288

Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe

85 90 95

atg tct ctc ctg gag gag aag ttg ctc ccg gtg ctg gta cat act ttt 336

Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Val His Thr Phe

100 105 110

tgg ata gac acc aag aac tac gtg gaa gtg acc cgg aag tgg tat gca 384

Trp Ile Asp Thr Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala

115	120	125	
gag gct atg ccc ttt ccc ctc aac ttc ttc ctg cct ggc cgc atg cag			432
Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln			
130	135	140	
cgg cag tac atg gaa cgg cta cag ctg ctg act ggg gag cac agg cct			480
Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Thr Gly Glu His Arg Pro			
145	150	155	160
gag gac gag gaa gag ctg gag aag gag ctg tac cga gag gct cgg gag			528
Glu Asp Glu Glu Glu Leu Glu Lys Glu Leu Tyr Arg Glu Ala Arg Glu			
165	170	175	
tgt ctg acc ctg ctc tct cag cgc ctg ggc tct caa aag ttc ttc ttt			576
Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe			
180	185	190	
gga gat gcc cct gcc tcc ttg gac gcc ttc gtc ttc agc tac ttg gcc			624
Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser Tyr Leu Ala			
195	200	205	
ctg ctg ctg cag gca aag ctg ccc agt ggg aag ctg cag gtc cac ctg			672
Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Val His Leu			
210	215	220	
cgt ggg ctg cac aac ctc tgt gcc tat tgt acc cac att ctc agt ctc			720
Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Ser Leu			
225	230	235	240
tac ttc ccc tgg gat gga gct gag gta cca ccg caa cgc cag aca cca			768
Tyr Phe Pro Trp Asp Gly Ala Glu Val Pro Pro Gln Arg Gln Thr Pro			
245	250	255	
gca ggc cca gag act gag gag gag cca tac cgg cgc cgg aac cag atc			816
Ala Gly Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Asn Gln Ile			

260	265	270	
cta tct gtg ctg gca gga ctg gca gcc atg gtg ggc tac gcc ttg ctc			864
Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu			
275	280	285	
agc ggc att gtc tcc atc cag cgg gca acg cct gct cgg gcc cca ggc			912
Ser Gly Ile Val Ser Ile Gln Arg Ala Thr Pro Ala Arg Ala Pro Gly			
290	295	300	
acc cgg acc ctg ggc atg gct gag gag gat gaa gag gaa tgatttgtcc			961
Thr Arg Thr Leu Gly Met Ala Glu Glu Asp Glu Glu Glu			
305	310	315	
tcacgtcccc aagactggtt tttctactct catgcattcc agaggccccc gtgcctcctc			1021
gttggttgta cagccggaca cggggtgctg ccaccagaa taaa			1065

<210> 260

<211> 317

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu

1 5 10 15

Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Ala Arg Phe

20 25 30

Thr Gly Ala Pro Leu Lys Val His Lys Ile Ser Asn Pro Trp Gln Ser

35 40 45

Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser His Gly Glu Val Ile

50 55 60

Ser Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn

65	70	75	80
Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe			
	85	90	95
Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Val His Thr Phe			
	100	105	110
Trp Ile Asp Thr Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala			
	115	120	125
Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln			
	130	135	140
Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Thr Gly Glu His Arg Pro			
145	150	155	160
Glu Asp Glu Glu Glu Leu Glu Lys Glu Leu Tyr Arg Glu Ala Arg Glu			
	165	170	175
Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe			
	180	185	190
Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser Tyr Leu Ala			
	195	200	205
Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Val His Leu			
	210	215	220
Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Ser Leu			
225	230	235	240
Tyr Phe Pro Trp Asp Gly Ala Glu Val Pro Pro Gln Arg Gln Thr Pro			
	245	250	255
Ala Gly Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Asn Gln Ile			
	260	265	270
Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu			
	275	280	285

Ser Gly Ile Val Ser Ile Gln Arg Ala Thr Pro Ala Arg Ala Pro Gly
 290 295 300

Thr Arg Thr Leu Gly Met Ala Glu Glu Asp Glu Glu Glu
 305 310 315

<210> 261

<211> 1580

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (29).. (223)

<400> 261

agagcctccg aagaggggac tgcgcacc atg gcc tcc cgt gca gcg ccg gtc 52

Met Ala Ser Arg Ala Ala Pro Val

1 5

aga cag aca tgc tgt tgt ttc aac atc cga gtc gcc acc ata gcc ctg 100

Arg Gln Thr Cys Cys Cys Phe Asn Ile Arg Val Ala Thr Ile Ala Leu

10 15 20

gcc att tac cac ata gtc atg agt gtc ctg ctg ttc att gag cat gtg 148

Ala Ile Tyr His Ile Val Met Ser Val Leu Leu Phe Ile Glu His Val

25 30 35 40

gtg gag gtg gcc cgc ggt aaa gtg tcc tgt agg ttc ttc aag atg ccg 196

Val Glu Val Ala Arg Gly Lys Val Ser Cys Arg Phe Phe Lys Met Pro

45 50 55

agc gat acg acg aaa tgg tgg aat caa tgaagaaagt agcagggatg 243

Ser Asp Thr Thr Lys Trp Trp Asn Gln

60

65

gacgtggagc tgacagttga agaacgaaac cttttatctg ttgcatataa aaatgtgatt 303
 ggagccagaa gagcatcctg gagaataatc agcagcattg aacagaagga agaaaacaag 363
 ggaggagagg acaaattaaa gatgattcgg gagtaccggc aaatggttga aactgagctc 423
 aagttaatct gttgtgacat tctggatgta ctggacaaac acctcattcc agcagctaac 483
 actggttggc aaaagcagct tttgatgacg cgattgcaga actggacacg ctgagtgaag 543
 aaagttataa ggactctacg ctcatcatgc agctgctacg tgataacctg acgctgtgga 603
 cctcagacat gcagggcgat ggtgaagagc agaataaaga agcgctgcag gatgtggaag 663
 atgagaatca gtgagacgta ataaaagcca acaagagaaa ccatctctga ctacccttc 723
 cccccctccc cttggaagtt ccccatgtgc actgagaacc accaaatttg actttcacat 783
 ttggtctcag aatttaggtt cctgccctgt tgttttcttt ctttttcttt ttttttctc 843
 ccctcccctt ttttaaaaca aacaaacaaa caaacagttt tcagaagttc ttaaggcaag 903
 agtgaatttc tgtggatttt actggtccca gctttaggtt ctttacgaca ctaacaggac 963
 tgcatagagg ctttttcagc attactgtat tgtctccggc cacactggca agatcatcat 1023
 tagaaatgga aatgacattt gaaagccatt agacttctag gtgatgcac taagaaagat 1083
 taatcacaca atagaggcat atgcgctgtc atttttcctt ttttaattg ttaaattgaa 1143
 tttatacca atgtttaaac ttaaattggg tgttagcttg aggtgttttg ggggagtttg 1203
 ttgtaatggt tttgctgtaa actgtgtttg gaactctgct gaagtgttgc tgaaaagcat 1263
 ggtgctggta acagttcaac aatccgtggc tgctcattct tgccgactcc tccccctctg 1323
 aagcaggtta gcattgaagg tggatatgaa gcctgcatgc gtgttcaact ctgttctcc 1383
 tccctcctcc tcggcctccc tcctccctc cttcgctcgc tcaacctctt ttgttcagta 1443
 cgtgtaactt gaagctaatt tgtactactg gatctctgac tggagccgca ggtacagatc 1503
 tgtattgttc ttactgaaac acagcatgga attaacatta aacttaaata aaacaaacct 1563
 aaattaaaaa tgccaaa 1580

<210> 262

<211> 65

<212> PRT

<213> Mus musculus

<400> 262

Met Ala Ser Arg Ala Ala Pro Val Arg Gln Thr Cys Cys Cys Phe Asn

1 5 10 15

Ile Arg Val Ala Thr Ile Ala Leu Ala Ile Tyr His Ile Val Met Ser

20 25 30

Val Leu Leu Phe Ile Glu His Val Val Glu Val Ala Arg Gly Lys Val

35 40 45

Ser Cys Arg Phe Phe Lys Met Pro Ser Asp Thr Thr Lys Trp Trp Asn

50 55 60

Gln

65

<210> 263

<211> 1373

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (4)..(327)

<400> 263

gaa atg gtg gaa tca atg aag aaa gta gca ggg atg gac gtg gag ctg 48

Met Val Glu Ser Met Lys Lys Val Ala Gly Met Asp Val Glu Leu

1 5 10 15

aca gtt gaa gaa cga aac ctt tta tct gtt gca tat aaa aat gtg att 96

Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile

20	25	30	
gga gcc aga aga gca tcc tgg aga ata atc agc agc att gaa cag aag			144
Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys			
35	40	45	
gaa gaa aac aag gga gga gag gac aaa tta aag atg att cgg gag tac			192
Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys Met Ile Arg Glu Tyr			
50	55	60	
cgg caa atg gtt gaa act gag ctc aag tta atc tgt tgt gac att ctg			240
Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile Cys Cys Asp Ile Leu			
65	70	75	
gat gta ctg gac aaa cac ctc att cca gca gct aac act ggt tgg caa			288
Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala Asn Thr Gly Trp Gln			
80	85	90	95
aag cag ctt ttg atg acg caa ttg cag aac tgg aca cgc tgagtgaaga			337
Lys Gln Leu Leu Met Thr Gln Leu Gln Asn Trp Thr Arg			
100	105		
aagttataag gactctacgc tcatcatgca gctgctacgt gataacctga cgctgtggac			397
ctcagacatg cagggcgatg gtgaagagca gaataaagaa gcgctgcagg atgtggaaga			457
tgagaatcag tgagacgtaa taaaagccaa caagagaaac catctctgac tacccttcc			517
ccccctcccc ttggaagttc ccattgtca ctgagaacca ccaaatttga ctttcacatt			577
tggtctcaga atttaggttc ctgccctgtt gttttctttc tttttctttt tttttctcc			637
cctcccccttt tttaaaacaa acaaacaac aaacagtttt cagaagttct taaggcaaga			697
gtgaatttct gtggatttta ctggtcccag ctttaggttc tttacgacac taacaggact			757
gcatagaggc tttttcagca ttactgtatt gtctccggcc aactggcaa gatcatcatt			817
agaaatggaa atgacatttg aaagccatta gacttctagg tgatgcatct aagaaagatt			877
aatcacacaa tagaggcata tgcgctgtca tttttctttt ttttaattgt taaattgaat			937
tttataccaa tgtttaaact taaattgggt gttagcttga ggtgttttgg gggagtttgt			997

tgtaatgggtt ttgctgtaaa ctgtgttttg aactctgctg aagtgttgct gaaaagcatg 1057
 gtgctggtaa cagttcaaca atccgtggct gtcattctt gccgactcct cccctctga 1117
 agcaggtag cattgaaggt ggtatggaag cctgcatgcg tgttcaactc tgttcctcct 1177
 cctcctcct cggcctcct cctccctcc ttcgctcgt caacctctt tgttcagtag 1237
 gtgtaacttg aagctaattt gtactactgg atatctgact ggagccgcag gtacagatct 1297
 gtattgttct tactgaaaca cagcatggaa ttaacattaa acttaaataa aacaaaccta 1357
 aattaataat gccaaa 1373

<210> 264

<211> 108

<212> PRT

<213> Mus musculus

<400> 264

Met Val Glu Ser Met Lys Lys Val Ala Gly Met Asp Val Glu Leu Thr
 1 5 10 15
 Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
 20 25 30
 Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys Glu
 35 40 45
 Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys Met Ile Arg Glu Tyr Arg
 50 55 60
 Gln Met Val Glu Thr Glu Leu Lys Leu Ile Cys Cys Asp Ile Leu Asp
 65 70 75 80
 Val Leu Asp Lys His Leu Ile Pro Ala Ala Asn Thr Gly Trp Gln Lys
 85 90 95
 Gln Leu Leu Met Thr Gln Leu Gln Asn Trp Thr Arg
 100 105

<210> 265

<211> 1704

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)..(825)

<400> 265

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atg gat gat cga gag gat ctg gtg tac cag gcg aag ctg gcc gag cag      108
Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln
1           5           10           15
gct gag cga tac gac gaa atg gtg gag tca atg aag aaa gta gca ggg      156
Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
           20           25           30
atg gat gtg gag ctg aca gtt gaa gaa aga aac ctc cta tct gtt gca      204
Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
           35           40           45
tat aag aat gtg att gga gct aga aga gcc tcc tgg aga ata atc agc      252
Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
           50           55           60
agc att gaa cag aaa gaa gaa aac aag gga gga gaa gac aag cta aaa      300
Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
           65           70           75           80
atg att cgg gaa tat cgg caa atg gtt gag act gag cta aag tta atc      348
Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile

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85	90	95	
tgt tgt gac att ctg gat gta ctg gac aaa cac ctc att cca gca gct			396
Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala			
100	105	110	
aac act ggc gag tcc aag gtt ttc tat tat aaa atg aaa ggg gac tac			444
Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr			
115	120	125	
cac agg tat ctg gca gaa ttt gcc aca gga aac gac agg aag gag gct			492
His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala			
130	135	140	
gcg gag aac agc cta gtg gct tat aaa gct gct agt gat att gca atg			540
Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met			
145	150	155	160
aca gaa ctt cca cca acg cat cct att cgc tta ggt ctt gct ctc aat			588
Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn			
165	170	175	
ttt tcc gta ttc tac tac gaa att ctt aat tcc cct gac cgt gcc tgc			636
Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys			
180	185	190	
agg ttg gca aaa gca gct ttt gat gat gca att gca gaa ctg gat acg			684
Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr			
195	200	205	
ctg agt gaa gaa agc tat aag gac tct aca ctt atc atg cag ttg tta			732
Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu			
210	215	220	
cgt gat aat ctg aca cta tgg act tca gac atg cag ggt gac ggt gaa			780
Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu			

225	230	235	240	
gag cag aat aaa gaa gcg ctg cag gac gtg gaa gac gaa aat cag				825
Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln				
	245	250	255	
tgagacataa gccaacaaga gaaaccatct ctgaccaccc cctcctcccc atcccaccct				885
ttggaaactc ccatttgtca ctgagaacca ccaaactctga cttttacatt tgggtctcaga				945
atttaggttc ctgccctgtt ggtttttttt tttttttttt ttaaacagtt ttcaaaagtt				1005
cttaaaggca agagtgaatt tctgtggatt ttactgggtcc cagcttttag gttctttaag				1065
acactaacag gactacatag aggctttttc agcattactg tgtcgtctcc gtgccagatg				1125
tggcaagatc accattagca aatggaaatt acatttgaaa gccattagac ttataggtga				1185
tgcaagcatc taagagagag gttaatcaca ctatagaggc aataagtggc atcagttttc				1245
atTTTTtctaa ttgtttaaac tgtgttttat accagtgttt gcaagtaatt ggggtgttagc				1305
ttgagatggc taaaggtggc ttggggaggg acttcgttgt aatggttttg ctgttgctga				1365
aaagcatggc gctggtaaca gttcaacaat ccgtggctgc tcattcttgc ctactttact				1425
ctccactga agcaggttag ctgttgaagg tggatatgaa aagcctgcat gcctgttcaa				1485
ttcttttggt tcttctcctt cccctcctcc ctacctcctt cccctcactc ctccctcct				1545
tcgctcgtc aacctctttt gttcagtatg tgtaacttga agctaatttg tactactgga				1605
tatctgactg gagccacaga tacagaatct gtattgttct tactgaaaca cagcatggaa				1665
ttaacattaa acttaaataa aacaaaccta aattaaana				1704

<210> 266

<211> 255

<212> PRT

<213> Homo sapiens

<400> 266

Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln

1

5

10

15

Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
 20 25 30
 Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
 35 40 45
 Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
 50 55 60
 Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
 65 70 75 80
 Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile
 85 90 95
 Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala
 100 105 110
 Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr
 115 120 125
 His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala
 130 135 140
 Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met
 145 150 155 160
 Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn
 165 170 175
 Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys
 180 185 190
 Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr
 195 200 205
 Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu
 210 215 220
 Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu

225	230	235	240
Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln			
	245	250	255
<p><210> 267</p> <p><211> 2162</p> <p><212> DNA</p> <p><213> Homo sapiens</p> <p><221> CDS</p> <p><222> (104).. (1546)</p> <p><400> 267</p>			
gggctgcgct gtccagctgt ggctatggcc ccagccccga gatgaggagg gagagaacta			60
ggggccccgca ggcctgggaa tttccgtccc ccaccaagtc cgg atg ctc act cca			115
Met Leu Thr Pro			
1			
aag tct cag cag gcc cct gag gga ggg agc tgt cag cca ggg aaa acc			163
Lys Ser Gln Gln Ala Pro Glu Gly Gly Ser Cys Gln Pro Gly Lys Thr			
5	10	15	20
gag aac acc atc acc atg aca acc agt cac cag cct cag gac aga tac			211
Glu Asn Thr Ile Thr Met Thr Thr Ser His Gln Pro Gln Asp Arg Tyr			
	25	30	35
aaa gct gtc tgg ctt atc ttc ttc atg ctg ggt ctg gga acg ctg ctc			259
Lys Ala Val Trp Leu Ile Phe Phe Met Leu Gly Leu Gly Thr Leu Leu			
40	45	50	
ccg tgg aat ttt ttc atg acg gcc act cag tat ttc aca aac cgc ctg			307
Pro Trp Asn Phe Phe Met Thr Ala Thr Gln Tyr Phe Thr Asn Arg Leu			
55	60	65	

gac atg tcc cag aat gtg tcc ttg gtc act gct gaa ctg agc aag gac 355
 Asp Met Ser Gln Asn Val Ser Leu Val Thr Ala Glu Leu Ser Lys Asp
 70 75 80
 gcc cag gcg tca gcc gcc cct gca gca ccc ttg cct gag cgg aac tct 403
 Ala Gln Ala Ser Ala Ala Pro Ala Ala Pro Leu Pro Glu Arg Asn Ser
 85 90 95 100
 ctc agt gcc atc ttc aac aat gtc atg acc cta tgt gcc atg ctg ccc 451
 Leu Ser Ala Ile Phe Asn Asn Val Met Thr Leu Cys Ala Met Leu Pro
 105 110 115
 ctg ctg tta ttc acc tac ctc aac tcc ttc ctg cat cag agg atc ccc 499
 Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His Gln Arg Ile Pro
 120 125 130
 cag tcc gta cgg atc ctg ggc agc ctg gtg gcc atc ctg ctg gtg ttt 547
 Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile Leu Leu Val Phe
 135 140 145
 ctg atc act gcc atc ctg gtg aag gtg cag ctg gat gct ctg ccc ttc 595
 Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp Ala Leu Pro Phe
 150 155 160
 ttt gtc atc acc atg atc aag atc gtg ctc att aat tca ttt ggt gcc 643
 Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn Ser Phe Gly Ala
 165 170 175 180
 atc ctg cag ggc agc ctg ttt ggt ctg gct ggc ctt ctg cct gcc agc 691
 Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu Leu Pro Ala Ser
 185 190 195
 tac acg gcc ccc atc atg agt ggc cag ggc cta gca ggc ttc ttt gcc 739
 Tyr Thr Ala Pro Ile Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala
 200 205 210

tcc gtg gcc atg atc tgc gct att gcc agt ggc tcg gag cta tca gaa	787
Ser Val Ala Met Ile Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu	
215 220 225	
agt gcc ttc ggc tac ttt atc aca gcc tgt gct gtt atc att ttg acc	835
Ser Ala Phe Gly Tyr Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr	
230 235 240	
atc atc tgt tac ctg ggc ctg ccc cgc ctg gaa ttc tac cgc tac tac	883
Ile Ile Cys Tyr Leu Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr	
245 250 255 260	
cag cag ctc aag ctt gaa gga ccc ggg gag cag gag acc aag ttg gac	931
Gln Gln Leu Lys Leu Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp	
265 270 275	
ctc att agc aaa gga gag gag cca aga gca ggc aaa gag gaa tct gga	979
Leu Ile Ser Lys Gly Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly	
280 285 290	
gtt tca gtc tcc aac tct cag ccc acc aat gaa agc cac tct atc aaa	1027
Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser His Ser Ile Lys	
295 300 305	
gcc atc ctg aaa aat atc tca gtc ctg gct ttc tct gtc tgc ttc atc	1075
Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser Val Cys Phe Ile	
310 315 320	
ttc act atc acc att ggg atg ttt cca gcc gtg act gtt gag gtc aag	1123
Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu Val Lys	
325 330 335 340	
tcc agc atc gca ggc agc agc acc tgg gaa cgt tac ttc att cct gtg	1171
Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val	
345 350 355	

tcc tgt ttc ttg act ttc aat atc ttt gac tgg ttg ggc cgg agc ctc 1219
 Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu
 360 365 370
 aca gct gta ttc atg tgg cct ggg aag gac agc cgc tgg ctg cca agc 1267
 Thr Ala Val Phe Met Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser
 375 380 385
 ctg gtg ctg gcc cgg ctg gtg ttt gtg cca ctg ctg ctg ctg tgc aac 1315
 Leu Val Leu Ala Arg Leu Val Phe Val Pro Leu Leu Leu Leu Cys Asn
 390 395 400
 att aag ccc cgc cgc tac ctg act gtg gtc ttc gag cac gat gcc tgg 1363
 Ile Lys Pro Arg Arg Tyr Leu Thr Val Val Phe Glu His Asp Ala Trp
 405 410 415 420
 ttc atc ttc ttc atg gct gcc ttt gcc ttc tcc aac ggc tac ctc gcc 1411
 Phe Ile Phe Phe Met Ala Ala Phe Ala Phe Ser Asn Gly Tyr Leu Ala
 425 430 435
 agc ctc tgc atg tgc ttc ggg ccc aag aaa gtg aag cca gct gag gca 1459
 Ser Leu Cys Met Cys Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala
 440 445 450
 gag acc gca gga gcc atc atg gcc ttc ttc ctg tgt ctg ggt ctg gca 1507
 Glu Thr Ala Gly Ala Ile Met Ala Phe Phe Leu Cys Leu Gly Leu Ala
 455 460 465
 ctg ggg gct gtt ttc tcc ttc ctg ttc cgg gca att gtg tgacaaagga 1556
 Leu Gly Ala Val Phe Ser Phe Leu Phe Arg Ala Ile Val
 470 475 480
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 gccagttttt taccatcat gcaccctgta cagttgccac gttactgcct tttttaaaaa 2096
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<210> 268

<211> 481

<212> PRT

<213> Homo sapiens

<400> 268

Met Leu Thr Pro Lys Ser Gln Gln Ala Pro Glu Gly Gly Ser Cys Gln

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Pro Gly Lys Thr Glu Asn Thr Ile Thr Met Thr Thr Ser His Gln Pro

20 25 30

Gln Asp Arg Tyr Lys Ala Val Trp Leu Ile Phe Phe Met Leu Gly Leu

35 40 45

Gly Thr Leu Leu Pro Trp Asn Phe Phe Met Thr Ala Thr Gln Tyr Phe

50 55 60

Thr Asn Arg Leu Asp Met Ser Gln Asn Val Ser Leu Val Thr Ala Glu

65 70 75 80

Leu Ser Lys Asp Ala Gln Ala Ser Ala Ala Pro Ala Ala Pro Leu Pro

85 90 95

Glu Arg Asn Ser Leu Ser Ala Ile Phe Asn Asn Val Met Thr Leu Cys

100	105	110
Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His		
115	120	125
Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile		
130	135	140
Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp		
145	150	155
Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn		
165	170	175
Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu		
180	185	190
Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly Gln Gly Leu Ala		
195	200	205
Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile Ala Ser Gly Ser		
210	215	220
Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr Ala Cys Ala Val		
225	230	235
Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro Arg Leu Glu Phe		
245	250	255
Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro Gly Glu Gln Glu		
260	265	270
Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro Arg Ala Gly Lys		
275	280	285
Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser		
290	295	300
His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser		
305	310	315
		320

Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr
 325 330 335
 Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr
 340 345 350
 Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu
 355 360 365
 Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly Lys Asp Ser Arg
 370 375 380
 Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe Val Pro Leu Leu
 385 390 395 400
 Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr Val Val Phe Glu
 405 410 415
 His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe Ala Phe Ser Asn
 420 425 430
 Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro Lys Lys Val Lys
 435 440 445
 Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala Phe Phe Leu Cys
 450 455 460
 Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu Phe Arg Ala Ile
 465 470 475 480
 Val

<210> 269

<211> 1373

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (105).. (656)

<400> 269

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tccgcggggcg agctcgagca gccaaaccccg ggcgcgctcgg ggcc atg gac ggc ctg      116
                                     Met Asp Gly Leu
                                     1
agg cag cgc gtg gag cac ttc ctg gag caa agg aac ctg gtc acc gaa      164
Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu
5              10              15              20
gtg ctg ggg gcg ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg      212
Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu
                25              30              35
gct gca gga gcc gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac      260
Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr
                40              45              50
gga gcg tct ctg ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat      308
Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr
                55              60              65
gcc tca atc aaa gct atc gag agc cca agc aag gac gac gac act gtg      356
Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val
                70              75              80
tgg ctc acc tac tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc      404
Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe
85              90              95              100
ttc agc gat cta ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag      452
Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys

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105	110	115	
tgc gcc ttc ctg ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct			500
Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala			
120	125	130	
ctc atg ctg tat cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac			548
Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His			
135	140	145	
ggg gcc gta gac aga atc atg aac gac ctc agc ggg cga gcc ctg gac			596
Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp			
150	155	160	
gcg gcg gcc gga ata acc agg aac gtc aag cca agc cag acc ccg cag			644
Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln			
165	170	175	180
ccg aag gac aag tgaagcagcc ccctgagcct cacaaggacc tcctggetgg			696
Pro Lys Asp Lys			
tgaggagggg gccgcgccag gctcccaggc ctccacagag tcttcagegc atcccccaac			756
agcagccccct gccagtcctt cgggtccagg caaggccctg ggggtctcct taaatgccac			816
ctcgggcaag tcccagtccc agtcctcggc cccccccagc tctggatccc agggccagct			876
gccctctggc tctggctgtg gctcccgctt gtccggcagg gccaggggc agcgtcgggc			936
acagggcagc tcccactggt ctcggaaca caccagccg cctggtactt cctccagccc			996
ctcccagtca gccctcccgt cctcggggcc cctgcagcca cccaacgtca cctccagccc			1056
ggtctcaccc atggtccagt ctcccagcag cagcaacatc cccacgcagc cccccagcaa			1116
gtcctctggc aagccggagg acgcagcccc caagaccagc ggacagcgcc agaaggaatc			1176
gtcgaacacag cctgccagca gcgcctcagt gcccgagctg gtcccctgcc attccgggac			1236
ctctctggag tacacttcgg agtccaccac cgagatcacc tgcagctggc cacaccacag			1296
gccccgtgc ctgcagcact actggtgcct gaaacacctg gcctgctagg aggctccaat			1356
aaagctaacc cggacca			1373

<210> 270

<211> 184

<212> PRT

<213> Homo sapiens

<400> 270

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn

1 5 10 15

Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu

20 25 30

Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu

35 40 45

Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val

50 55 60

Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp

65 70 75 80

Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly

85 90 95

Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr

100 105 110

Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro

115 120 125

Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

130 135 140

Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly

145 150 155 160

Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser

	165	170	175	
Gln Thr Pro Gln Pro Lys Asp Lys				
	180			
<210>	271			
<211>	885			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(15).. (785)			
<400>	271			
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Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile				
	1	5	10	
gcc ttc ggg cct gcg ctc gcc ctt tat gtc ttc acc atc gcc acc gag				98
Ala Phe Gly Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Thr Glu				
	15	20	25	
ccg ttg cgt atc atc ttc ctc atc gcc gga gct ttc ttc tgg ttg gtg				146
Pro Leu Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val				
	30	35	40	
tct cta ctg att tcg tcc ctt gtt tgg ttc atg gca aga gtc att att				194
Ser Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile				
	45	50	55	60
gac aac aaa gat gga cca aca cag aaa tat ctg ctg atc ttt gga gcg				242
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly Ala				
	65	70	75	

ttt gtc tct gtc tat atc caa gaa atg ttc cga ttt gca tat tat aaa	290
Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr Tyr Lys	
80 85 90	
ctc tta aaa aaa gcc agt gaa ggt ttg aag agt ata aac cca ggt gag	338
Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Gly Glu	
95 100 105	
aca gca ccc tct atg cga ctg ctg gcc tat gtt tct ggc ttg ggc ttt	386
Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe	
110 115 120	
gga atc atg agt gga gta ttt tcc ttt gtg aat acc cta tct gac tcc	434
Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asp Ser	
125 130 135 140	
ttg ggg cca ggc aca gtg ggc att cat gga gat tct cct caa ttc ttc	482
Leu Gly Pro Gly Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe	
145 150 155	
ctt tat tca gct ttc atg acg ctg gtc att atc ttg ctg cat gta ttc	530
Leu Tyr Ser Ala Phe Met Thr Leu Val Ile Ile Leu Leu His Val Phe	
160 165 170	
tgg ggc att gta ttt ttt gat ggc tgt gag aag aaa aag tgg ggc atc	578
Trp Gly Ile Val Phe Phe Asp Gly Cys Glu Lys Lys Lys Trp Gly Ile	
175 180 185	
ctc ctt atc gtt ctc ctg acc cac ctg ctg gtg tca gcc cag acc ttc	626
Leu Leu Ile Val Leu Leu Thr His Leu Leu Val Ser Ala Gln Thr Phe	
190 195 200	
ata agt tct tat tat gga ata aac ctg gcg tca gca ttt ata atc ctg	674
Ile Ser Ser Tyr Tyr Gly Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu	
205 210 215 220	

gtg ctc atg ggc acc tgg gca ttc tta gct gcg gga ggc agc tgc cga 722
 Val Leu Met Gly Thr Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg
 225 230 235
 agc ctg aaa ctc tgc ctg ctc tgc caa gac aag aac ttt ctt ctt tac 770
 Ser Leu Lys Leu Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr
 240 245 250
 aac cag cgc tcc aga taacctcagg gaaccagcac ttcccaaacc gcagactaca 825
 Asn Gln Arg Ser Arg
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<210> 272

<211> 257

<212> PRT

<213> Homo sapiens

<400> 272

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 20 25 30
 Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Ile
 35 40 45
 Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile Asp Asn Lys Asp
 50 55 60
 Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly Ala Phe Val Ser Val
 65 70 75 80
 Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys

85	90	95
Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Gly Glu Thr Ala Pro Ser		
100	105	110
Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe Gly Ile Met Ser		
115	120	125
Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asp Ser Leu Gly Pro Gly		
130	135	140
Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala		
145	150	155
Phe Met Thr Leu Val Ile Ile Leu Leu His Val Phe Trp Gly Ile Val		
165	170	175
Phe Phe Asp Gly Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val		
180	185	190
Leu Leu Thr His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr		
195	200	205
Tyr Gly Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly		
210	215	220
Thr Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu		
225	230	235
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg Ser		
245	250	255
Arg		

<210> 273

<211> 2670

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(1664)

<400> 273

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            1              5              10

cct agg ctg gcc gcg ggc ctc cgg ctg ctc cca atg ctg ggt ttg ctg      98
Pro Arg Leu Ala Ala Gly Leu Arg Leu Leu Pro Met Leu Gly Leu Leu
15              20              25              30

cag ttg ctg gcc gag cct ggc ctg ggc cgc gtc cat cac ctg gca ctc      146
Gln Leu Leu Ala Glu Pro Gly Leu Gly Arg Val His His Leu Ala Leu
            35              40              45

aag gat gat gtg agg cat aaa gtt cat ctg aac acc ttt ggc ttc ttc      194
Lys Asp Asp Val Arg His Lys Val His Leu Asn Thr Phe Gly Phe Phe
            50              55              60

aag gat ggg tac atg gtg gtg aat gtc agt agc ctc tca ctg aat gag      242
Lys Asp Gly Tyr Met Val Val Asn Val Ser Ser Leu Ser Leu Asn Glu
            65              70              75

cct gaa gac aag gat gtg act att gga ttt agc cta gac cgt aca aag      290
Pro Glu Asp Lys Asp Val Thr Ile Gly Phe Ser Leu Asp Arg Thr Lys
            80              85              90

aat gat ggc ttt tct tct tac ctg gat gaa gat gtg aat tac tgt att      338
Asn Asp Gly Phe Ser Ser Tyr Leu Asp Glu Asp Val Asn Tyr Cys Ile
95              100              105              110

tta aag aaa cag tct gtc tct gtc acc ctt tta atc cta gac atc tcc      386
Leu Lys Lys Gln Ser Val Ser Val Thr Leu Leu Ile Leu Asp Ile Ser

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115	120	125	
aga agt gag gta aga gta aag tct cca cca gaa gct ggt acc cag tta			434
Arg Ser Glu Val Arg Val Lys Ser Pro Pro Glu Ala Gly Thr Gln Leu			
130	135	140	
cca aag atc atc ttc agc agg gat gag aaa gtc ctt ggt cag agc cag			482
Pro Lys Ile Ile Phe Ser Arg Asp Glu Lys Val Leu Gly Gln Ser Gln			
145	150	155	
gag cct aat gtt aac cct gct tca gca ggc aac cag acc cag aag aca			530
Glu Pro Asn Val Asn Pro Ala Ser Ala Gly Asn Gln Thr Gln Lys Thr			
160	165	170	
caa gat ggt gga aag tct aaa aga agt aca gtg gat tca aag gcc atg			578
Gln Asp Gly Gly Lys Ser Lys Arg Ser Thr Val Asp Ser Lys Ala Met			
175	180	185	190
gga gag aaa tcc ttt tct gtt cat aat aat ggt ggg gca gtg tca ttt			626
Gly Glu Lys Ser Phe Ser Val His Asn Asn Gly Gly Ala Val Ser Phe			
195	200	205	
cag ttt ttc ttt aac atc agc act gat gac caa gaa ggc ctt tac agt			674
Gln Phe Phe Phe Asn Ile Ser Thr Asp Asp Gln Glu Gly Leu Tyr Ser			
210	215	220	
ctt tat ttt cat aaa tgc ctt gga aaa gaa ttg cca agt gac aag ttt			722
Leu Tyr Phe His Lys Cys Leu Gly Lys Glu Leu Pro Ser Asp Lys Phe			
225	230	235	
aca ttc agc ctt gat att gag atc aca gag aag aat cct gac agc tac			770
Thr Phe Ser Leu Asp Ile Glu Ile Thr Glu Lys Asn Pro Asp Ser Tyr			
240	245	250	
ctc tca gca gga gaa att cct ctc ccc aaa tta tac atc tca atg gcc			818
Leu Ser Ala Gly Glu Ile Pro Leu Pro Lys Leu Tyr Ile Ser Met Ala			

255	260	265	270	
ttt ttc ttc ttt ctt tct ggg acc atc tgg att cat atc ctt cga aaa				866
Phe Phe Phe Phe Leu Ser Gly Thr Ile Trp Ile His Ile Leu Arg Lys				
	275	280	285	
cga cgg aat gat gta ttt aaa atc cac tgg ctg atg gcg gcc ctt cct				914
Arg Arg Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Pro				
	290	295	300	
ttc acc aag tct ctt tcc ttg gtg ttc cat gca att gac tac cac tac				962
Phe Thr Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His Tyr				
	305	310	315	
atc tcc tcc cag ggc ttc cct atc gaa ggc tgg gct gtt gtg tac tac				1010
Ile Ser Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr Tyr				
	320	325	330	
ata act cac ctt ttg aaa ggg gcg cta ctc ttc atc acc att gca ctc				1058
Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu				
335	340	345	350	
att ggc act ggc tgg gct ttc att aag cac atc ctt tct gat aaa gac				1106
Ile Gly Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys Asp				
	355	360	365	
aaa aag atc ttc atg att gtc att cca ctc cag gtc ctg gca aat gta				1154
Lys Lys Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val				
	370	375	380	
gcc tac atc atc ata gag tcc acc gag gag ggc acg act gaa tat ggc				1202
Ala Tyr Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr Gly				
	385	390	395	
ttg tgg aag gac tct cta ttt ctg gtc gac ctg ttg tgt tgt ggt gcc				1250
Leu Trp Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly Ala				

400	405	410	
atc ctc ttc cca gtg gtg tgg tca atc aga cat tta caa gaa gca tca			1298
Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala Ser			
415	420	425	430
gca aca gat gga aaa gct gct att aac tta gca aag ctg aaa ctt ttc			1346
Ala Thr Asp Gly Lys Ala Ala Ile Asn Leu Ala Lys Leu Lys Leu Phe			
	435	440	445
aga cat tat tac gtc ttg att gtg tgt tac ata tac ttc act agg atc			1394
Arg His Tyr Tyr Val Leu Ile Val Cys Tyr Ile Tyr Phe Thr Arg Ile			
	450	455	460
att gca ttt ctc ctc aaa ctc gct gtt cca ttc cag tgg aag tgg ctc			1442
Ile Ala Phe Leu Leu Lys Leu Ala Val Pro Phe Gln Trp Lys Trp Leu			
	465	470	475
tac cag ctc ctg gat gaa acg gcc aca ctg gtc ttc ttt gtt cta acg			1490
Tyr Gln Leu Leu Asp Glu Thr Ala Thr Leu Val Phe Phe Val Leu Thr			
	480	485	490
ggg tat aaa ttc cgt ccg gct tca gat aac ccc tac cta caa ctt tct			1538
Gly Tyr Lys Phe Arg Pro Ala Ser Asp Asn Pro Tyr Leu Gln Leu Ser			
495	500	505	510
cag gaa gaa gaa gac ttg gaa atg gag tcc gtt gtg aca aca tct ggg			1586
Gln Glu Glu Glu Asp Leu Glu Met Glu Ser Val Val Thr Thr Ser Gly			
	515	520	525
gtg atg gaa agt atg aag aaa gtc aag aag gtg acc aac ggc tcc gtg			1634
Val Met Glu Ser Met Lys Lys Val Lys Lys Val Thr Asn Gly Ser Val			
	530	535	540
gag ccc cag ggc gag tgg gaa ggc gcc gtg tgacagagcc gaccctgagg			1684
Glu Pro Gln Gly Glu Trp Glu Gly Ala Val			

545

550

atggcactgt ccaaggaaac tgtaactta ttcatagtcc tattggacag caggagcagc 1744
 tcctacagtg aactattggc accaccgaca gtgacaccag ggcacatggc tggagcacag 1804
 tgccgcggaa acctgatttt gtactctctt ttatggaaac gatctgtggc tgttttagagg 1864
 cagctggatc ctctttcagg cgggaatggg agggcgggca cagggaggag gagaggaaga 1924
 gaaaaggaag aattcathtt taatttaggt ttcttttttt cttcttcatt tcggagctct 1984
 aaggtgtatg cagttgtgac cccatgtgtg gggaagtgtg gcaaggacgg ctggtggagg 2044
 gggaaggagg gtgcgaggtg tctgtctgat gctttaggaa atgtctactg aggaccctgg 2104
 gacttaagaa gaagggcggg gagagtgcc a ttgcctgttt gggagacaaa aatgaacgaa 2164
 aacaggtgac tttggaaagc aaagtcaaaa cccagtttag gatgtagcac ctgccccagg 2224
 attcctgccc tcggctttgc cccagaccct tattccagat gctgagagtg accaggacag 2284
 cagctcctga ggcccagtgg tcttctttcc aacaggaaaa gaaggctgtg atgtcgctgt 2344
 caggatcatg ccctgtggca cagcacaggt ggtgggaggt ggttttctga ctgagatgtt 2404
 gcctgatgga tggaagaaa tgtattttta agttcaaaaa gcattatcct gtggcggtgc 2464
 ctggacatcc actccctgac agcccagagc agcactgtct ggcttccctt catgcttgtg 2524
 gctttgttgt gtttgatcag aattttgggg gaaatggaaa gttttcctca aggagcagct 2584
 gggggcagaa taggtagtat ttaagcaa atcttaagtcc aagcaaatca tccccattaa 2644
 aaagcttttc ctgtaggcta gtagga 2670

<210> 274

<211> 552

<212> PRT

<213> Homo sapiens

<400> 274

Met Ala Ala Leu Ala Pro Val Gly Ser Pro Ala Ser Arg Gly Pro Arg

1

5

10

15

Leu Ala Ala Gly Leu Arg Leu Leu Pro Met Leu Gly Leu Leu Gln Leu

	20		25		30										
Leu	Ala	Glu	Pro	Gly	Leu	Gly	Arg	Val	His	His	Leu	Ala	Leu	Lys	Asp
	35					40						45			
Asp	Val	Arg	His	Lys	Val	His	Leu	Asn	Thr	Phe	Gly	Phe	Phe	Lys	Asp
	50					55						60			
Gly	Tyr	Met	Val	Val	Asn	Val	Ser	Ser	Leu	Ser	Leu	Asn	Glu	Pro	Glu
65					70					75				80	
Asp	Lys	Asp	Val	Thr	Ile	Gly	Phe	Ser	Leu	Asp	Arg	Thr	Lys	Asn	Asp
			85						90				95		
Gly	Phe	Ser	Ser	Tyr	Leu	Asp	Glu	Asp	Val	Asn	Tyr	Cys	Ile	Leu	Lys
			100						105				110		
Lys	Gln	Ser	Val	Ser	Val	Thr	Leu	Leu	Ile	Leu	Asp	Ile	Ser	Arg	Ser
		115						120				125			
Glu	Val	Arg	Val	Lys	Ser	Pro	Pro	Glu	Ala	Gly	Thr	Gln	Leu	Pro	Lys
		130					135					140			
Ile	Ile	Phe	Ser	Arg	Asp	Glu	Lys	Val	Leu	Gly	Gln	Ser	Gln	Glu	Pro
145				150						155				160	
Asn	Val	Asn	Pro	Ala	Ser	Ala	Gly	Asn	Gln	Thr	Gln	Lys	Thr	Gln	Asp
				165						170				175	
Gly	Gly	Lys	Ser	Lys	Arg	Ser	Thr	Val	Asp	Ser	Lys	Ala	Met	Gly	Glu
			180						185				190		
Lys	Ser	Phe	Ser	Val	His	Asn	Asn	Gly	Gly	Ala	Val	Ser	Phe	Gln	Phe
		195						200					205		
Phe	Phe	Asn	Ile	Ser	Thr	Asp	Asp	Gln	Glu	Gly	Leu	Tyr	Ser	Leu	Tyr
		210					215					220			
Phe	His	Lys	Cys	Leu	Gly	Lys	Glu	Leu	Pro	Ser	Asp	Lys	Phe	Thr	Phe
225					230						235			240	

Ser Leu Asp Ile Glu Ile Thr Glu Lys Asn Pro Asp Ser Tyr Leu Ser
245 250 255

Ala Gly Glu Ile Pro Leu Pro Lys Leu Tyr Ile Ser Met Ala Phe Phe
260 265 270

Phe Phe Leu Ser Gly Thr Ile Trp Ile His Ile Leu Arg Lys Arg Arg
275 280 285

Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Pro Phe Thr
290 295 300

Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His Tyr Ile Ser
305 310 315 320

Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr Tyr Ile Thr
325 330 335

His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile Gly
340 345 350

Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys Asp Lys Lys
355 360 365

Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val Ala Tyr
370 375 380

Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr Gly Leu Trp
385 390 395 400

Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly Ala Ile Leu
405 410 415

Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala Ser Ala Thr
420 425 430

Asp Gly Lys Ala Ala Ile Asn Leu Ala Lys Leu Lys Leu Phe Arg His
435 440 445

Tyr Tyr Val Leu Ile Val Cys Tyr Ile Tyr Phe Thr Arg Ile Ile Ala

450 455 460
 Phe Leu Leu Lys Leu Ala Val Pro Phe Gln Trp Lys Trp Leu Tyr Gln
 465 470 475 480
 Leu Leu Asp Glu Thr Ala Thr Leu Val Phe Phe Val Leu Thr Gly Tyr
 485 490 495
 Lys Phe Arg Pro Ala Ser Asp Asn Pro Tyr Leu Gln Leu Ser Gln Glu
 500 505 510
 Glu Glu Asp Leu Glu Met Glu Ser Val Val Thr Thr Ser Gly Val Met
 515 520 525
 Glu Ser Met Lys Lys Val Lys Lys Val Thr Asn Gly Ser Val Glu Pro
 530 535 540
 Gln Gly Glu Trp Glu Gly Ala Val
 545 550

<210> 275

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)..(1593)

<400> 275

gtcctgtgag gtccagtggc cgcccaggcg cgaccagatc tgggtgcgcg gagagcgcg 60
 atg gcg gct gtg gga ccg cgg acc ggc ccc gga acc ggc gcc gag gct 108
 Met Ala Ala Val Gly Pro Arg Thr Gly Pro Gly Thr Gly Ala Glu Ala
 1 5 10 15
 cta gcg ctg gcg gca gag ctg cag ggc gag gcg acg tgc tcc atc tgc 156

His Ala Val Leu Pro Leu Asp Glu Ala Val Gln Glu Ala Lys Glu Leu

165

170

175

ttg gag tcc agg ctg agg gtc ttg aag aag gaa ctg gag gac tgt gag 636

Leu Glu Ser Arg Leu Arg Val Leu Lys Lys Glu Leu Glu Asp Cys Glu

180

185

190

gtg ttc cgg tcc acg gaa aag aag gag agc aag gag ctg ctg aaa cag 684

Val Phe Arg Ser Thr Glu Lys Lys Glu Ser Lys Glu Leu Leu Lys Gln

195

200

205

atg gca gcg gag cag gag aag gtg ggg gca gag ttc cag gca ctg agg 732

Met Ala Ala Glu Gln Glu Lys Val Gly Ala Glu Phe Gln Ala Leu Arg

210

215

220

gct ttc ctg gtg gag cag gag ggt cgg ctg cta ggc cgc ctg gag gaa 780

Ala Phe Leu Val Glu Gln Glu Gly Arg Leu Leu Gly Arg Leu Glu Glu

225

230

235

240

ctg tcc cgg gag gtg gca cag aag cag aat gag aac ctg gcc cag ctc 828

Leu Ser Arg Glu Val Ala Gln Lys Gln Asn Glu Asn Leu Ala Gln Leu

245

250

255

ggg gtt gag atc acc cag ctg tcc aag ctc agc agc cag atc cag gag 876

Gly Val Glu Ile Thr Gln Leu Ser Lys Leu Ser Ser Gln Ile Gln Glu

260

265

270

aca gct caa aag cct gac ctt gac ttt ctc cag gaa ttc aaa agc acg 924

Thr Ala Gln Lys Pro Asp Leu Asp Phe Leu Gln Glu Phe Lys Ser Thr

275

280

285

ctg agc agg tgt agc aat gtg cct ggc ccc aag cca acc aca gtc tct 972

Leu Ser Arg Cys Ser Asn Val Pro Gly Pro Lys Pro Thr Thr Val Ser

290

295

300

tct gag atg aag aat aaa gtc tgg aat gtt tct ctc aag acc ttt gtc 1020

Ser Glu Met Lys Asn Lys Val Trp Asn Val Ser Leu Lys Thr Phe Val
 305 310 315 320
 tta aaa ggg atg ctg aag aag ttc aaa gag gac ctt cgg gga gag ctg 1068
 Leu Lys Gly Met Leu Lys Lys Phe Lys Glu Asp Leu Arg Gly Glu Leu
 325 330 335
 gag aaa gag gag aaa gtg gag ctc acc ttg gat ccc gac acg gcc aac 1116
 Glu Lys Glu Glu Lys Val Glu Leu Thr Leu Asp Pro Asp Thr Ala Asn
 340 345 350
 ccg cgc ctc atc ctc tct ctg gat ctt aag ggc gtg cgc ctc ggc gag 1164
 Pro Arg Leu Ile Leu Ser Leu Asp Leu Lys Gly Val Arg Leu Gly Glu
 355 360 365
 cgg gcc cag gac ctg ccc aac cac ccc tgc cgc ttc gac acc aac acc 1212
 Arg Ala Gln Asp Leu Pro Asn His Pro Cys Arg Phe Asp Thr Asn Thr
 370 375 380
 cgc gtc ctg gcg tcc tgc ggc ttc tcc tcg ggc cgg cat cac tgg gag 1260
 Arg Val Leu Ala Ser Cys Gly Phe Ser Ser Gly Arg His His Trp Glu
 385 390 395 400
 gtg gag gtg ggc tct aag gac ggc tgg gcc ttt ggc gtg gcc cgc gag 1308
 Val Glu Val Gly Ser Lys Asp Gly Trp Ala Phe Gly Val Ala Arg Glu
 405 410 415
 agc gtg cgc cga aag ggc ctg acg ccc ttc act ccc gag gag ggc gtc 1356
 Ser Val Arg Arg Lys Gly Leu Thr Pro Phe Thr Pro Glu Glu Gly Val
 420 425 430
 tgg gcc ctg cag ctc aac ggc ggc cag tac tgg gcc gtg acc agc ccc 1404
 Trp Ala Leu Gln Leu Asn Gly Gly Gln Tyr Trp Ala Val Thr Ser Pro
 435 440 445
 gag cgg tcg ccc ctc agc tgc ggg cac ctg tcg cgc gtg cgg gtg gcc 1452

Glu Arg Ser Pro Leu Ser Cys Gly His Leu Ser Arg Val Arg Val Ala
 450 455 460
 ctg gac ctg gag gtg gga gcc gtg tcc ttc tac gct gtg gag gac atg 1500
 Leu Asp Leu Glu Val Gly Ala Val Ser Phe Tyr Ala Val Glu Asp Met
 465 470 475 480
 cgc cac ctc tac acc ttc cgc gtc aac ttc cag gag cgc gtg ttc ccg 1548
 Arg His Leu Tyr Thr Phe Arg Val Asn Phe Gln Glu Arg Val Phe Pro
 485 490 495
 ctt ttc tct gtt tgc tcc acg ggc acc tac ttg cga atc tgg cct 1593
 Leu Phe Ser Val Cys Ser Thr Gly Thr Tyr Leu Arg Ile Trp Pro
 500 505 510
 tgaggggcac tgctggggag ctctgtctc tgggctgccg gtgggagggg atgtcgcctc 1653
 ccagagatg cctgggtccgt cttgggtctg ccctccgtgc tctgacccc tgctgcccac 1713
 gagagcctgc tacagacaca accccgaggc aggagagtga ctgtggccaa ccgagcaggg 1773
 gaacaggggc tttggactcc tgagggtgtt cccttcctga ggtcacatgt ggatttggcc 1833
 agagccttca ggaggtggag gccggtgagg tcaggagccc agctctccag ggggcttctg 1893
 ccctgactgg gaagggtgcc tggctcccta aaacaatgtc aaagccagtc ctgctgttct 1953
 ctgttgccag ggggcaggtc tgggcctggg ccaaccacgt ttgttatcat ggctgctgcc 2013
 ttctggacag ctgccagctc tgccttgaga ggttgtggga cctctggatc cagctgacct 2073
 gacaggtcat ctactcaggg aggagccctg tgctcccagc tcagaggaca gtctgggcca 2133
 gaactggaag gagaca 2149

<210> 276

<211> 511

<212> PRT

<213> Homo sapiens

<400> 276

Met Ala Ala Val Gly Pro Arg Thr Gly Pro Gly Thr Gly Ala Glu Ala
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 Leu Ala Leu Ala Ala Glu Leu Gln Gly Glu Ala Thr Cys Ser Ile Cys
 20 25 30
 Leu Glu Leu Phe Arg Glu Pro Val Ser Val Glu Cys Gly His Ser Phe
 35 40 45
 Cys Arg Ala Cys Ile Gly Arg Cys Trp Glu Arg Pro Gly Ala Gly Ser
 50 55 60
 Val Gly Ala Ala Thr Arg Ala Pro Pro Phe Pro Leu Pro Cys Pro Gln
 65 70 75 80
 Cys Arg Glu Pro Ala Arg Pro Ser Gln Leu Arg Pro Asn Arg Gln Leu
 85 90 95
 Ala Ala Val Ala Thr Leu Leu Arg Arg Phe Ser Leu Pro Ala Ala Ala
 100 105 110
 Pro Gly Glu His Gly Ser Gln Ala Ala Ala Arg Ala Ala Ala Ala
 115 120 125
 Arg Cys Gly Gln His Gly Glu Pro Phe Lys Leu Tyr Cys Gln Asp Asp
 130 135 140
 Gly Arg Ala Ile Cys Val Val Cys Asp Arg Ala Arg Glu His Arg Glu
 145 150 155 160
 His Ala Val Leu Pro Leu Asp Glu Ala Val Gln Glu Ala Lys Glu Leu
 165 170 175
 Leu Glu Ser Arg Leu Arg Val Leu Lys Lys Glu Leu Glu Asp Cys Glu
 180 185 190
 Val Phe Arg Ser Thr Glu Lys Lys Glu Ser Lys Glu Leu Leu Lys Gln
 195 200 205
 Met Ala Ala Glu Gln Glu Lys Val Gly Ala Glu Phe Gln Ala Leu Arg

210	215	220
Ala Phe Leu Val Glu Gln Glu Gly Arg Leu Leu Gly Arg Leu Glu Glu		
225	230	235
Leu Ser Arg Glu Val Ala Gln Lys Gln Asn Glu Asn Leu Ala Gln Leu		240
	245	250
Gly Val Glu Ile Thr Gln Leu Ser Lys Leu Ser Ser Gln Ile Gln Glu		255
260	265	270
Thr Ala Gln Lys Pro Asp Leu Asp Phe Leu Gln Glu Phe Lys Ser Thr		
275	280	285
Leu Ser Arg Cys Ser Asn Val Pro Gly Pro Lys Pro Thr Thr Val Ser		
290	295	300
Ser Glu Met Lys Asn Lys Val Trp Asn Val Ser Leu Lys Thr Phe Val		
305	310	315
Leu Lys Gly Met Leu Lys Lys Phe Lys Glu Asp Leu Arg Gly Glu Leu		320
	325	330
Glu Lys Glu Glu Lys Val Glu Leu Thr Leu Asp Pro Asp Thr Ala Asn		335
340	345	350
Pro Arg Leu Ile Leu Ser Leu Asp Leu Lys Gly Val Arg Leu Gly Glu		
355	360	365
Arg Ala Gln Asp Leu Pro Asn His Pro Cys Arg Phe Asp Thr Asn Thr		
370	375	380
Arg Val Leu Ala Ser Cys Gly Phe Ser Ser Gly Arg His His Trp Glu		
385	390	395
Val Glu Val Gly Ser Lys Asp Gly Trp Ala Phe Gly Val Ala Arg Glu		400
	405	410
Ser Val Arg Arg Lys Gly Leu Thr Pro Phe Thr Pro Glu Glu Gly Val		415
420	425	430

Trp Ala Leu Gln Leu Asn Gly Gly Gln Tyr Trp Ala Val Thr Ser Pro

435

440

445

Glu Arg Ser Pro Leu Ser Cys Gly His Leu Ser Arg Val Arg Val Ala

450

455

460

Leu Asp Leu Glu Val Gly Ala Val Ser Phe Tyr Ala Val Glu Asp Met

465

470

475

480

Arg His Leu Tyr Thr Phe Arg Val Asn Phe Gln Glu Arg Val Phe Pro

485

490

495

Leu Phe Ser Val Cys Ser Thr Gly Thr Tyr Leu Arg Ile Trp Pro

500

505

510

<210> 277

<211> 3113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (193).. (1656)

<400> 277

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gtcaaacgag gatacagtgt ctggaactat tggttctaag atataagtgg aatgagcctg 120

gatcaggaga agtatgctga gctagagttg aaggaagctt ctctttctaa caagagaaag 180

cagagttaaa tt atg gca gag aca agt ctg tta gag gct ggg gcc tct gca 231

Met Ala Glu Thr Ser Leu Leu Glu Ala Gly Ala Ser Ala

1

5

10

gcc tct aca gct gcg gct ttg gag aac tta cag gtg gag gcg agc tgc 279

Ala Ser Thr Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser Cys

15	20	25	
tct gtg tgc ctg gag tat ctg aag gaa cct gtc atc att gag tgt ggg			327
Ser Val Cys Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys Gly			
30	35	40	45
cac aac ttc tgc aaa gct tgc atc acc cgc tgg tgg gag gac cta gag			375
His Asn Phe Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu Glu			
50	55	60	
agg gac ttc cct tgt cct gtc tgt cga aag aca tcc cgc tac cgc agt			423
Arg Asp Phe Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg Ser			
65	70	75	
ctc cga cct aat cgg caa cta ggc agt atg gtg gaa att gcc aag cag			471
Leu Arg Pro Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys Gln			
80	85	90	
ctc cag gcc gtc aag cgg aag atc cgg gat gag agc ctc tgc ccc caa			519
Leu Gln Ala Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro Gln			
95	100	105	
cac cat gag gcc ctc agc ctt ttc tgt tat gag gac cag gag gct gta			567
His His Glu Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala Val			
110	115	120	125
tgc ttg ata tgt gca att tcc cac acc cac cgg gcc cac acc gtt gtg			615
Cys Leu Ile Cys Ala Ile Ser His Thr His Arg Ala His Thr Val Val			
130	135	140	
cca ctg gac gac gct aca cag gag tac aag gaa aaa ctg cag aag tgt			663
Pro Leu Asp Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys Cys			
145	150	155	
ctg gag ccc ctg gaa cag aag ctg cag gag atc act cgc tgc aag tcc			711
Leu Glu Pro Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys Ser			

160	165	170	
tct gag gag aag aag cct ggt gag ctc aag aga cta gtg gaa agt cgc			759
Ser Glu Glu Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser Arg			
175	180	185	
cga cag cag atc ttg agg gag ttt gaa gag ctt cat agg cgg ctg gat			807
Arg Gln Gln Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu Asp			
190	195	200	205
gaa gag cag cag gtg ttg ctt tca cga ctg gaa gaa gag gaa cag gac			855
Glu Glu Gln Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln Asp			
210	215	220	
att ctg cag cga ctc cga gaa aat gct gct cac ctt ggg gac aag cgc			903
Ile Leu Gln Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys Arg			
225	230	235	
cgg gac ctg gcc cac ttg gct gcc gag gtg gag ggc aag tgc tta cag			951
Arg Asp Leu Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu Gln			
240	245	250	
tca ggc ttc gag atg ctt aag gat gtc aaa agt acc ctg gaa aaa tgt			999
Ser Gly Phe Glu Met Leu Lys Asp Val Lys Ser Thr Leu Glu Lys Cys			
255	260	265	
gaa aag gtg aag acc atg gag gtg act tca gta tcc ata gag ctg gaa			1047
Glu Lys Val Lys Thr Met Glu Val Thr Ser Val Ser Ile Glu Leu Glu			
270	275	280	285
aag aac ttc agc aat ttt ccc cga cag tac ttt gcc cta agg aaa atc			1095
Lys Asn Phe Ser Asn Phe Pro Arg Gln Tyr Phe Ala Leu Arg Lys Ile			
290	295	300	
ctt aaa cag cta att gcg gat gtg acc ctg gac cct gag aca gct cat			1143
Leu Lys Gln Leu Ile Ala Asp Val Thr Leu Asp Pro Glu Thr Ala His			

305	310	315	
cct aac cta gtc ctg tca gag gat cgt aag agc gtc aag ttc gtg gag			1191
Pro Asn Leu Val Leu Ser Glu Asp Arg Lys Ser Val Lys Phe Val Glu			
320	325	330	
aca aga ctc cgg gat ctc cct gac aca cca agg cgt ttc acc ttc tac			1239
Thr Arg Leu Arg Asp Leu Pro Asp Thr Pro Arg Arg Phe Thr Phe Tyr			
335	340	345	
cct tgc gtc ctg gct act gag ggt ttc acc tca ggt cga cac tac tgg			1287
Pro Cys Val Leu Ala Thr Glu Gly Phe Thr Ser Gly Arg His Tyr Trp			
350	355	360	365
gag gtg gag gtg ggc gac aag acc cac tgg gca gtg ggt gta tgc cgg			1335
Glu Val Glu Val Gly Asp Lys Thr His Trp Ala Val Gly Val Cys Arg			
370	375	380	
gac tcc gtg agc cga aag ggc gag ttg act cca ctc cct gag act ggc			1383
Asp Ser Val Ser Arg Lys Gly Glu Leu Thr Pro Leu Pro Glu Thr Gly			
385	390	395	
tac tgg cgg gtg cgg cta tgg aat ggg gac aaa tat gca gcc acc acc			1431
Tyr Trp Arg Val Arg Leu Trp Asn Gly Asp Lys Tyr Ala Ala Thr Thr			
400	405	410	
aca cct ttt acc cct ttg cac atc aag gtg aaa ccc aag cgg gta ggc			1479
Thr Pro Phe Thr Pro Leu His Ile Lys Val Lys Pro Lys Arg Val Gly			
415	420	425	
ata ttc cta gac tat gag gcc ggc aca ctg tct ttc tac aat gtc aca			1527
Ile Phe Leu Asp Tyr Glu Ala Gly Thr Leu Ser Phe Tyr Asn Val Thr			
430	435	440	445
gac cgc tct cat atc tac acc ttc act gat act ttt act gag aaa ctt			1575
Asp Arg Ser His Ile Tyr Thr Phe Thr Asp Thr Phe Thr Glu Lys Leu			

450	455	460	
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Trp Pro Leu Phe Tyr Pro Gly Ile Arg Ala Gly Arg Lys Asn Ala Ala			
465	470	475	
cca ctt acc atc agg ccc cca aca gat tgg gag tgacaggttg ggatgtggga			1676
Pro Leu Thr Ile Arg Pro Pro Thr Asp Trp Glu			
480	485		
atgactgggg tgaggcaggg tcaagtgcta cgggcctcct tcccgtgtcc tgctggaacg			1736
tcttcgtgtc cacctgggtc cagtcctgaa tcatcttgga gaaacacctt ggtttctagg			1796
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gagaatgtaa atgattttca tgtaggcca aaataaacia cttatagggt atatatgttg			2876

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<211> 488

<212> PRT

<213> Homo sapiens

<400> 278

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 35 40 45
 Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu Glu Arg Asp Phe
 50 55 60
 Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg Ser Leu Arg Pro
 65 70 75 80
 Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys Gln Leu Gln Ala
 85 90 95
 Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro Gln His His Glu
 100 105 110
 Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala Val Cys Leu Ile
 115 120 125
 Cys Ala Ile Ser His Thr His Arg Ala His Thr Val Val Pro Leu Asp

130	135	140	
Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys Cys Leu Glu Pro			
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Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys Ser Ser Glu Glu			
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Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser Arg Arg Gln Gln			
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Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu Asp Glu Glu Gln			
195	200	205	
Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln Asp Ile Leu Gln			
210	215	220	
Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys Arg Arg Asp Leu			
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Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu Gln Ser Gly Phe			
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Glu Met Leu Lys Asp Val Lys Ser Thr Leu Glu Lys Cys Glu Lys Val			
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Lys Thr Met Glu Val Thr Ser Val Ser Ile Glu Leu Glu Lys Asn Phe			
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Ser Asn Phe Pro Arg Gln Tyr Phe Ala Leu Arg Lys Ile Leu Lys Gln			
290	295	300	
Leu Ile Ala Asp Val Thr Leu Asp Pro Glu Thr Ala His Pro Asn Leu			
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Val Leu Ser Glu Asp Arg Lys Ser Val Lys Phe Val Glu Thr Arg Leu			
325	330	335	
Arg Asp Leu Pro Asp Thr Pro Arg Arg Phe Thr Phe Tyr Pro Cys Val			
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 Val Gly Asp Lys Thr His Trp Ala Val Gly Val Cys Arg Asp Ser Val
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 385 390 395 400
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 Asp Tyr Glu Ala Gly Thr Leu Ser Phe Tyr Asn Val Thr Asp Arg Ser
 435 440 445
 His Ile Tyr Thr Phe Thr Asp Thr Phe Thr Glu Lys Leu Trp Pro Leu
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 Ile Arg Pro Pro Thr Asp Trp Glu
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<210> 279

<211> 2967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (359).. (1897)

<400> 279

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His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu	
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Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His	
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Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln	
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Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys	
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gag aag cac cgc gag ccc ctg aag ctg tac tgc gag gag gac cag atg	694
Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met	
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Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser	
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Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln	
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Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg	
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180 185 190	
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Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp	
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Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys	
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Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser	
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Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp	
260 265 270	
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Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr	
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gag agt cta aag cag ttc aca gaa aaa atg cag tca gat atg gag aaa	1270
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys	
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Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu	
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 Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu Arg Thr Pro
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 435 440 445
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 Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe Ser His Ala
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 Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser Tyr Ser Gly
 465 470 475 480
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 Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser Gly Ile Asp
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<211> 513

<212> PRT

<213> Homo sapiens

<400> 280

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Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly

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30

His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu

35

40

45

Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His

50

55

60

Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln
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 Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys
 85 90 95
 Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met
 100 105 110
 Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser
 115 120 125
 Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln
 130 135 140
 Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg
 145 150 155 160
 Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln
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 Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser
 180 185 190
 Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp
 195 200 205
 Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys
 210 215 220
 Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln
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 Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser
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 260 265 270
 Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr

275 280 285
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys
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325 330 335
Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu
340 345 350
Arg Phe Asn Leu Phe Pro Cys Val Leu Gly Ser Pro Cys Phe Ile Ala
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370 375 380
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420 425 430
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435 440 445
Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe Ser His Ala
450 455 460
Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser Tyr Ser Gly
465 470 475 480
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500

505

510

Pro

<210> 281

<211> 2687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (359).. (1432)

<400> 281

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gctcagtgcg gagctcggcg ccggggccca tgcccgtgcg ccccgccagg ccggcgcc      358
atg gcc tcc ggg agt gtg gcc gag tgc ctg cag cag gag acc acc tgc      406
Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys
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ccc gtg tgc ctg cag tac ttc gca gag ccc atg atg ctc gac tgc ggc      454
Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly
20          25          30
cat aac atc tgt tgc gcg tgc ctc gcc cgc tgc tgg ggc acg gca gag      502
His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu
35          40          45

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Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln	
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Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys	
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Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln	
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Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp	
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 aatgtgccat agttttatta actccattaa agaagcctgt atgtgttttg gttagttaca 2182
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 aaaataaact gaatatggat gtta 2687

<210> 282

<211> 358

<212> PRT

<213> Homo sapiens

<400> 282

Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys
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 Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly
 20 25 30
 His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu
 35 40 45
 Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His
 50 55 60
 Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln
 65 70 75 80
 Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys
 85 90 95
 Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met
 100 105 110
 Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser
 115 120 125
 Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln
 130 135 140
 Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg
 145 150 155 160
 Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln

	165	170	175
Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser			
	180	185	190
Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp			
	195	200	205
Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys			
	210	215	220
Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln			
225	230	235	240
Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser			
	245	250	255
Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp			
	260	265	270
Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr			
	275	280	285
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys			
	290	295	300
Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu			
305	310	315	320
Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg			
	325	330	335
Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu			
	340	345	350
Arg Ser Pro Ser Thr Thr			
	355		

<210> 283

<211> 4777

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (548).. (2704)

<400> 283

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ctctcatccc ctcccgctgg ccccgcccc ccttgcccct accagccag tagtagttcc 180

ccagcgtgcg cccggggaga ccgggaacat ggcgctggga gcgctgtagc agctgagaag 240

gggctgaggc accgccgctt cgctgacagc cggccaccag atgttcatgc attctagaga 300

aagtggaaaa cttagaagcc taattaatga ctgtcttctg gacctctgag accatgtttc 360

tagtggttttc cgtggaatat tatcagaaat aactgttgtt gaaatgcttc cacctcttgc 420

taaaatgaac actgaggaaa aatgaagaag actgacaagc accagcgaaa agttgcagaa 480

tagaaatagc cacactcctc tggagtcttt aattcatcca cagccatcat ataaaggttt 540

tggcatc atg ttt ggg aag aaa aag aaa aag att gaa ata tct ggc ccg 589

Met Phe Gly Lys Lys Lys Lys Lys Ile Glu Ile Ser Gly Pro

1

5

10

tcc aac ttt gaa cac agg gtt cat act ggg ttt gat cca caa gag cag 637

Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Pro Gln Glu Gln

15

20

25

30

aag ttt acc ggc ctt ccc cag cag tgg cac agc ctg tta gca gat acg 685

Lys Phe Thr Gly Leu Pro Gln Gln Trp His Ser Leu Leu Ala Asp Thr

35

40

45

gcc aac agg cca aag cct atg gtg gac cct tca tgc atc aca ccc atc 733

Ala Asn Arg Pro Lys Pro Met Val Asp Pro Ser Cys Ile Thr Pro Ile

50	55	60	
cag ctg gct cct atg aag aca atc gtt aga gga aac aaa ccc tgc aag			781
Gln Leu Ala Pro Met Lys Thr Ile Val Arg Gly Asn Lys Pro Cys Lys			
65	70	75	
gaa acc tcc atc aac ggc ctg cta gag gat ttt gac aac atc tcg gtg			829
Glu Thr Ser Ile Asn Gly Leu Leu Glu Asp Phe Asp Asn Ile Ser Val			
80	85	90	
act cgc tcc aac tcc cta agg aaa gaa agc cca ccc acc cca gat cag			877
Thr Arg Ser Asn Ser Leu Arg Lys Glu Ser Pro Pro Thr Pro Asp Gln			
95	100	105	110
gga gcc tcc agc cac ggt cca ggc cac gcg gaa gaa aat ggc ttc atc			925
Gly Ala Ser Ser His Gly Pro Gly His Ala Glu Glu Asn Gly Phe Ile			
115	120	125	
acc ttc tcc cag tat tcc agc gaa tcc gat act act gct gac tac acg			973
Thr Phe Ser Gln Tyr Ser Ser Glu Ser Asp Thr Thr Ala Asp Tyr Thr			
130	135	140	
acc gaa aag tac agg gag aag agt ctc tat gga gat gat ctg gat ccg			1021
Thr Glu Lys Tyr Arg Glu Lys Ser Leu Tyr Gly Asp Asp Leu Asp Pro			
145	150	155	
tat tat aga ggc agc cac gca gcc aag caa aat ggg cac gta atg aaa			1069
Tyr Tyr Arg Gly Ser His Ala Ala Lys Gln Asn Gly His Val Met Lys			
160	165	170	
atg aag cac ggg gag gcc tac tat tct gag gtg aag cct ttg aaa tcc			1117
Met Lys His Gly Glu Ala Tyr Tyr Ser Glu Val Lys Pro Leu Lys Ser			
175	180	185	190
gat ttt gcc aga ttt tct gcc gat tat cac tca cat ttg gac tca ctg			1165
Asp Phe Ala Arg Phe Ser Ala Asp Tyr His Ser His Leu Asp Ser Leu			

195	200	205	
agc aaa cca agt gaa tac agt gac ctc aag tgg gag tat cag aga gcc			1213
Ser Lys Pro Ser Glu Tyr Ser Asp Leu Lys Trp Glu Tyr Gln Arg Ala			
210	215	220	
tcg agt agc tcc cct ctg gat tat tca ttc caa ttc aca cct tct aga			1261
Ser Ser Ser Ser Pro Leu Asp Tyr Ser Phe Gln Phe Thr Pro Ser Arg			
225	230	235	
act gca ggg acc agc ggg tgc tcc aag gag agc ctg gcg tac agt gaa			1309
Thr Ala Gly Thr Ser Gly Cys Ser Lys Glu Ser Leu Ala Tyr Ser Glu			
240	245	250	
agt gaa tgg gga ccc agc ctg gat gac tat gac agg agg cca aag tct			1357
Ser Glu Trp Gly Pro Ser Leu Asp Asp Tyr Asp Arg Arg Pro Lys Ser			
255	260	265	270
tcg tac ctg aat cag aca agc cct cag ccc acc atg cgg cag agg tcc			1405
Ser Tyr Leu Asn Gln Thr Ser Pro Gln Pro Thr Met Arg Gln Arg Ser			
275	280	285	
agg tca ggc tcg gga ctc cag gaa ccg atg atg cca ttt gga gca agt			1453
Arg Ser Gly Ser Gly Leu Gln Glu Pro Met Met Pro Phe Gly Ala Ser			
290	295	300	
gca ttt aaa acc cat ccc caa gga cac tcc tac aac tcc tac acc tac			1501
Ala Phe Lys Thr His Pro Gln Gly His Ser Tyr Asn Ser Tyr Thr Tyr			
305	310	315	
cct cgc ttg tcc gag ccc aca atg tgc att cca aag gtg gat tac gat			1549
Pro Arg Leu Ser Glu Pro Thr Met Cys Ile Pro Lys Val Asp Tyr Asp			
320	325	330	
cga gca cag atg gtc ctc agc cct cca ctg tca ggg tct gac acc tac			1597
Arg Ala Gln Met Val Leu Ser Pro Pro Leu Ser Gly Ser Asp Thr Tyr			

335	340	345	350	
ccc agg ggc cct gcc aaa cta cct caa agt caa agc aaa tcg ggc tat				1645
Pro Arg Gly Pro Ala Lys Leu Pro Gln Ser Gln Ser Lys Ser Gly Tyr				
	355	360	365	
tcc tca agc agt cac cag tac ccg tct ggg tac cac aaa gcc acc ttg				1693
Ser Ser Ser Ser His Gln Tyr Pro Ser Gly Tyr His Lys Ala Thr Leu				
	370	375	380	
tac cat cac ccc tcc ctg cag agc agt tcg cag tac atc tcc acg gct				1741
Tyr His His Pro Ser Leu Gln Ser Ser Ser Gln Tyr Ile Ser Thr Ala				
	385	390	395	
tcc tac ctg agc tcc ctc agc ctc tca tcc agc acc tac ccg ccg ccc				1789
Ser Tyr Leu Ser Ser Leu Ser Leu Ser Ser Ser Thr Tyr Pro Pro Pro				
	400	405	410	
agc tgg ggc tcc tcc tcc gac cag cag ccc tcc agg gtg tcc cat gaa				1837
Ser Trp Gly Ser Ser Ser Asp Gln Gln Pro Ser Arg Val Ser His Glu				
415	420	425	430	
cag ttt cgg gcg gcc ctg cag ctg gtg gtc agc cca gga gac ccc agg				1885
Gln Phe Arg Ala Ala Leu Gln Leu Val Val Ser Pro Gly Asp Pro Arg				
	435	440	445	
gaa tac ttg gcc aac ttt atc aaa atc ggg gaa ggc tca acc ggc atc				1933
Glu Tyr Leu Ala Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile				
	450	455	460	
gta tgc atc gcc acc gag aaa cac aca ggg aaa caa gtt gca gtg aag				1981
Val Cys Ile Ala Thr Glu Lys His Thr Gly Lys Gln Val Ala Val Lys				
	465	470	475	
aaa atg gac ctc cgg aag caa cag aga cga gaa ctg ctt ttc aat gag				2029
Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu				

480	485	490	
gtc gtg atc atg cgg gat tac cac cat gac aat gtg gtt gac atg tac			2077
Val Val Ile Met Arg Asp Tyr His His Asp Asn Val Val Asp Met Tyr			
495	500	505	510
agc agc tac ctt gtc ggc gat gag ctc tgg gtg gtc atg gag ttt cta			2125
Ser Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu			
	515	520	525
gaa ggt ggt gcc ttg aca gac att gtg act cac acc aga atg aat gaa			2173
Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu			
	530	535	540
gaa cag ata gct act gtc tgc ctg tca gtt ctg aga gct ctc tcc tac			2221
Glu Gln Ile Ala Thr Val Cys Leu Ser Val Leu Arg Ala Leu Ser Tyr			
	545	550	555
ctt cat aac caa gga gtg att cac agg gac ata aaa agt gac tcc atc			2269
Leu His Asn Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile			
	560	565	570
ctc ctg aca agc gat ggc cgg ata aag ttg tct gat ttt ggt ttc tgt			2317
Leu Leu Thr Ser Asp Gly Arg Ile Lys Leu Ser Asp Phe Gly Phe Cys			
575	580	585	590
gct caa gtt tcc aaa gag gtg ccg aag agg aaa tca ttg gtt ggc act			2365
Ala Gln Val Ser Lys Glu Val Pro Lys Arg Lys Ser Leu Val Gly Thr			
	595	600	605
ccc tac tgg atg gcc cct gag gtg att tct agg cta cct tat ggg aca			2413
Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Leu Pro Tyr Gly Thr			
	610	615	620
gag gtg gac atc tgg tcc ctc ggg atc atg gtg ata gaa atg att gat			2461
Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Ile Asp			

625	630	635	
ggc gag ccc ccc tac ttc aat gag cct ccc ctc cag gcg atg cgg agg			2509
Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Gln Ala Met Arg Arg			
640	645	650	
atc cgg gac agt tta cct cca aga gtg aag gac cta cac aag gtt tct			2557
Ile Arg Asp Ser Leu Pro Pro Arg Val Lys Asp Leu His Lys Val Ser			
655	660	665	670
tca gtg ctc cgg gga ttc cta gac ttg atg ttg gtg agg gag ccc tct			2605
Ser Val Leu Arg Gly Phe Leu Asp Leu Met Leu Val Arg Glu Pro Ser			
675	680	685	
cag aga gca aca gcc cag gaa ctc ctc gga cat cca ttc tta aaa cta			2653
Gln Arg Ala Thr Ala Gln Glu Leu Leu Gly His Pro Phe Leu Lys Leu			
690	695	700	
gca ggt cca ccg tct tgc atc gtc ccc ctc atg aga caa tac agg cat			2701
Ala Gly Pro Pro Ser Cys Ile Val Pro Leu Met Arg Gln Tyr Arg His			
705	710	715	
cac tgagcagagg attcgtgtag gtggcaaagc tagatgagga catgagaata			2754
His			
attcaggaga acaaaaggaa acacagaaca tgcaaaaggc ctgtgcattc tagaccagcc			2814
aattggtggg acagcgtgat gaccggcagg gttcaacaga ccagggcata ttcttgtgtc			2874
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 tttaaaccag aataaacatt aaaaactatt gcagaaaata gtggattttg gattccaaac 4614
 attttcgaca gtgtaatgga aatttttctg taattttctt accatcggtt atttttttaa 4674
 gtattcattg agttttacca aagttactgt agcttaaaag gttttgtgag cactaactat 4734
 tggcagaaac tgcatattgca aataaaaata aatgtttgcc ttt 4777

<211> 719

<212> PRT

<213> Homo sapiens

<400> 284

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20 25 30
Thr Gly Leu Pro Gln Gln Trp His Ser Leu Leu Ala Asp Thr Ala Asn
35 40 45
Arg Pro Lys Pro Met Val Asp Pro Ser Cys Ile Thr Pro Ile Gln Leu
50 55 60
Ala Pro Met Lys Thr Ile Val Arg Gly Asn Lys Pro Cys Lys Glu Thr
65 70 75 80
Ser Ile Asn Gly Leu Leu Glu Asp Phe Asp Asn Ile Ser Val Thr Arg
85 90 95
Ser Asn Ser Leu Arg Lys Glu Ser Pro Pro Thr Pro Asp Gln Gly Ala
100 105 110
Ser Ser His Gly Pro Gly His Ala Glu Glu Asn Gly Phe Ile Thr Phe
115 120 125
Ser Gln Tyr Ser Ser Glu Ser Asp Thr Thr Ala Asp Tyr Thr Thr Glu
130 135 140
Lys Tyr Arg Glu Lys Ser Leu Tyr Gly Asp Asp Leu Asp Pro Tyr Tyr
145 150 155 160
Arg Gly Ser His Ala Ala Lys Gln Asn Gly His Val Met Lys Met Lys
165 170 175
His Gly Glu Ala Tyr Tyr Ser Glu Val Lys Pro Leu Lys Ser Asp Phe

180	185	190
Ala Arg Phe Ser Ala Asp Tyr His Ser His Leu Asp Ser Leu Ser Lys		
195	200	205
Pro Ser Glu Tyr Ser Asp Leu Lys Trp Glu Tyr Gln Arg Ala Ser Ser		
210	215	220
Ser Ser Pro Leu Asp Tyr Ser Phe Gln Phe Thr Pro Ser Arg Thr Ala		
225	230	235
Gly Thr Ser Gly Cys Ser Lys Glu Ser Leu Ala Tyr Ser Glu Ser Glu		
245	250	255
Trp Gly Pro Ser Leu Asp Asp Tyr Asp Arg Arg Pro Lys Ser Ser Tyr		
260	265	270
Leu Asn Gln Thr Ser Pro Gln Pro Thr Met Arg Gln Arg Ser Arg Ser		
275	280	285
Gly Ser Gly Leu Gln Glu Pro Met Met Pro Phe Gly Ala Ser Ala Phe		
290	295	300
Lys Thr His Pro Gln Gly His Ser Tyr Asn Ser Tyr Thr Tyr Pro Arg		
305	310	315
Leu Ser Glu Pro Thr Met Cys Ile Pro Lys Val Asp Tyr Asp Arg Ala		
325	330	335
Gln Met Val Leu Ser Pro Pro Leu Ser Gly Ser Asp Thr Tyr Pro Arg		
340	345	350
Gly Pro Ala Lys Leu Pro Gln Ser Gln Ser Lys Ser Gly Tyr Ser Ser		
355	360	365
Ser Ser His Gln Tyr Pro Ser Gly Tyr His Lys Ala Thr Leu Tyr His		
370	375	380
His Pro Ser Leu Gln Ser Ser Ser Gln Tyr Ile Ser Thr Ala Ser Tyr		
385	390	395
		400

Leu Ser Ser Leu Ser Leu Ser Ser Ser Thr Tyr Pro Pro Pro Ser Trp
 405 . 410 415
 Gly Ser Ser Ser Asp Gln Gln Pro Ser Arg Val Ser His Glu Gln Phe
 420 425 430
 Arg Ala Ala Leu Gln Leu Val Val Ser Pro Gly Asp Pro Arg Glu Tyr
 435 440 445
 Leu Ala Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys
 450 455 460
 Ile Ala Thr Glu Lys His Thr Gly Lys Gln Val Ala Val Lys Lys Met
 465 470 475 480
 Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val
 485 490 495
 Ile Met Arg Asp Tyr His His Asp Asn Val Val Asp Met Tyr Ser Ser
 500 505 510
 Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly
 515 520 525
 Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu Gln
 530 535 540
 Ile Ala Thr Val Cys Leu Ser Val Leu Arg Ala Leu Ser Tyr Leu His
 545 550 555 560
 Asn Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu
 565 570 575
 Thr Ser Asp Gly Arg Ile Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln
 580 585 590
 Val Ser Lys Glu Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr
 595 600 605
 Trp Met Ala Pro Glu Val Ile Ser Arg Leu Pro Tyr Gly Thr Glu Val

610	615	620	
Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Ile Asp Gly Glu			
625	630	635	640
Pro Pro Tyr Phe Asn Glu Pro Pro Leu Gln Ala Met Arg Arg Ile Arg			
	645	650	655
Asp Ser Leu Pro Pro Arg Val Lys Asp Leu His Lys Val Ser Ser Val			
	660	665	670
Leu Arg Gly Phe Leu Asp Leu Met Leu Val Arg Glu Pro Ser Gln Arg			
	675	680	685
Ala Thr Ala Gln Glu Leu Leu Gly His Pro Phe Leu Lys Leu Ala Gly			
	690	695	700
Pro Pro Ser Cys Ile Val Pro Leu Met Arg Gln Tyr Arg His His			
705	710	715	

<210> 285

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108).. (971)

<400> 285

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gac ggg acg	cg caa ggt	gg agc acg	ctt gtc cgg	gag cag	atg ccg	gaa	116
					Met	Pro Glu	
					1		
gct ggt	ttt cag	gcc aca	aat gct	ttc aca	gag tgc	aaa ttc	acc tgc 164

Ala Gly Phe Gln Ala Thr Asn Ala Phe Thr Glu Cys Lys Phe Thr Cys
 5 10 15
 acc agt ggt aaa tgc ttg tat ctt ggt tgc ctg gtc tgt aac caa cag 212
 Thr Ser Gly Lys Cys Leu Tyr Leu Gly Ser Leu Val Cys Asn Gln Gln
 20 25 30 35
 aac gac tgt ggg gac aac agt gac gaa gag aac tgt ctc ctg gtg acc 260
 Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Asn Cys Leu Leu Val Thr
 40 45 50
 gag cac ccg cct ccg ggc atc ttc aac tgc gag ctg gag ttc gcc caa 308
 Glu His Pro Pro Pro Gly Ile Phe Asn Ser Glu Leu Glu Phe Ala Gln
 55 60 65
 atc atc atc atc gtc gtg gtg gtc acg gtg atg gtg gtg gtc atc gtc 356
 Ile Ile Ile Ile Val Val Val Val Thr Val Met Val Val Val Ile Val
 70 75 80
 tgc ctg ctg aac cac tac aaa gtc tcc acg cgg tcc ttc atc aac cgc 404
 Cys Leu Leu Asn His Tyr Lys Val Ser Thr Arg Ser Phe Ile Asn Arg
 85 90 95
 ccg aac cag agc cgg agg cgg gag gac ggg ctg ccg cag atc atg cat 452
 Pro Asn Gln Ser Arg Arg Arg Glu Asp Gly Leu Pro Gln Ile Met His
 100 105 110 115
 gcc ccg cgg tcc agg gac agg ttc aca gcg ccg tcc ttc atc cag agg 500
 Ala Pro Arg Ser Arg Asp Arg Phe Thr Ala Pro Ser Phe Ile Gln Arg
 120 125 130
 gat cgc ttc agc cgc ttc cag ccc acc tac ccc tat gtg cag cac gag 548
 Asp Arg Phe Ser Arg Phe Gln Pro Thr Tyr Pro Tyr Val Gln His Glu
 135 140 145
 att gat ctt cct ccc acc atc tcc ctg tcc gac ggt gaa gag cca cct 596

Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro
 150 155 160
 cct tac cag ggg ccc tgc acc ctg cag ctc cgg gac cct gaa cag cag 644
 Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln
 165 170 175
 atg gaa ctc aac cga gag tcc gtg agg gcc cca ccc aac cga acc ata 692
 Met Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile
 180 185 190 195
 ttt gac agt gat tta ata gac att gct atg tat agc ggg ggt cca tgc 740
 Phe Asp Ser Asp Leu Ile Asp Ile Ala Met Tyr Ser Gly Gly Pro Cys
 200 205 210
 cca ccc agc agc aac tcg ggc atc agt gca agc acc tgc agc agt aac 788
 Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Ser Thr Cys Ser Ser Asn
 215 220 225
 ggg agg atg gag ggg cca ccc ccc aca tac agc gag gtg atg ggc cac 836
 Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Met Gly His
 230 235 240
 cac cca ggc gcc tct ttc ctc cat cac cag cgc agc aac gca cac agg 884
 His Pro Gly Ala Ser Phe Leu His His Gln Arg Ser Asn Ala His Arg
 245 250 255
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 Pro Ile Lys Gly Lys Asp Arg Lys Pro Gly Asn Leu Val
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Phe Thr Cys Thr Ser Gly Lys Cys Leu Tyr Leu Gly Ser Leu Val Cys

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Asn Gln Gln Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Asn Cys Leu

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40

45

Leu Val Thr Glu His Pro Pro Pro Gly Ile Phe Asn Ser Glu Leu Glu

50

55

60

Phe Ala Gln Ile Ile Ile Ile Val Val Val Val Thr Val Met Val Val

65

70

75

80

Val Ile Val Cys Leu Leu Asn His Tyr Lys Val Ser Thr Arg Ser Phe

85

90

95

Ile Asn Arg Pro Asn Gln Ser Arg Arg Arg Glu Asp Gly Leu Pro Gln

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Ile Gln Arg Asp Arg Phe Ser Arg Phe Gln Pro Thr Tyr Pro Tyr Val		
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Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu		
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Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro		
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Glu Gln Gln Met Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn		
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Arg Thr Ile Phe Asp Ser Asp Leu Ile Asp Ile Ala Met Tyr Ser Gly		
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 Glu Arg Tyr Ser Ser Phe Pro Leu Asp Ala Ile Leu Asn Ala Arg Arg
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 Ala Ala Arg Pro Cys Gln Ala His Asp Lys Val Lys Leu Phe Cys Leu
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Thr Ile Trp Lys Ser Leu Phe Gln Asp Ile His Pro Val Pro Ala Ala	
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<400> 288

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 Ser Leu Lys Leu Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu
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 Asp Ala Ile Leu Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His
 85 90 95
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 Phe Cys Asp Glu Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile
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 Lys Arg Gln Leu Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr
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 180 185 190
 Gln Lys Ala Met Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu
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 Thr Asp Ile Glu Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys
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 225 230 235 240
 Arg His Thr Phe Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys

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	275		280		285										
Asp	Ile	His	Pro	Val	Pro	Ala	Ala	Leu	Thr	Leu	Asp	Pro	Gly	Thr	Ala
	290		295		300										
His	Gln	Arg	Leu	Ile	Leu	Ser	Asp	Asp	Cys	Thr	Ile	Val	Ala	Tyr	Gly
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Trp	Glu	Val	Val	Val	Ala	Glu	Lys	Thr	Gln	Trp	Val	Ile	Gly	Leu	Ala
	355		360		365										
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Organization
International Bureau



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(51) International Patent Classification⁷: **C07K 14/47**,
C12N 15/12, 15/63, 15/11, 5/10, C12Q 1/68, A61K 38/17,
G01N 33/50, A61K 48/00

(74) Agent: SIKS & CO.; 8th Floor, Kyobashi-Nisshoku Bldg.,
8-7, Kyobashi 1-chome, Chuo-ku, Tokyo 104-0031 (JP).

(21) International Application Number:
PCT/JP2002/012644

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2002-291302 3 October 2002 (03.10.2002) JP
60/415,769 4 October 2002 (04.10.2002) US

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AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,
MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK,
SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN,
YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK,
TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): ASAHI
KASEI PHARMA CORPORATION [JP/JP]; 9-1, Kanda
Mitoshiro, Chiyoda-ku, Tokyo, 101-8481 (JP).

Published:
— with international search report

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): MATSUDA, Akio
[JP/JP]; 1-37-404, Minami-machi, Fuji-shi, Shizuoka 417-
0026 (JP). MURAMATSU, Shuji [JP/JP]; 17-13, Tade-
wara, Fuji-shi, Shizuoka 416-0931 (JP).

(88) Date of publication of the international search report:
1 July 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NF-KAPPAB ACTIVATING GENES

(57) Abstract: Provided are proteins capable of activating NF- κ B, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of NF- κ B. Using plasmid pNF κ B-Luc, cDNA encoding a protein capable of activating NF- κ B has been cloned from a cDNA library constructed from human lung fibroblasts and the like, and the DNA sequence and the deduced amino acid sequence determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting NF- κ B activation.

WO 2003/048202 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/47 C12N15/12 C12N15/63 C12N15/11 C12N5/10
C12Q1/68 A61K38/17 G01N33/50 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, SEQUENCE SEARCH, PAJ, WPI Data, MEDLINE, BIOSIS, EMBASE, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! Homo sapiens, TTK protein kinase, retrieved from EBI Database accession no. BC000633 XP002233369 abstract</p> <p>---</p> <p>-/--</p>	1-13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

5 March 2003

Date of mailing of the international search report

09.07.03

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3018

Authorized officer

Mossier, B

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/JP 02/12644

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>MILLS G B ET AL: "EXPRESSION OF TTK A NOVEL HUMAN PROTEIN KINASE IS ASSOCIATED WITH CELL PROLIFERATION" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 22, 1992, pages 16000-16006, XP002233366 ISSN: 0021-9258 page 16001, column 1, paragraph 5 -column 2, paragraph 2; figure 1 & DATABASE EMBL 'Online! 27 February 1992 (1992-02-27) retrieved from EBI Database accession no. M86699 abstract</p>	1-13
X	<p>DOUVILLE E M J ET AL: "MULTIPLE CDNAS ENCODING THE ESK KINASE PREDICT TRANSMEMBRANE AND INTRACELLULAR ENZYME ISOFORMS" MOLECULAR AND CELLULAR BIOLOGY, vol. 12, no. 6, 1992, pages 2681-2689, XP009006945 ISSN: 0270-7306 figure 3 & DATABASE EMBL 'Online! 1 April 1992 (1992-04-01) retrieved from EBI Database accession no. M86377 abstract</p>	1-13
Y	<p>US 5 932 425 A (CIECHANOVER AARON ET AL) 3 August 1999 (1999-08-03)</p> <p>abstract column 1, line 16 - line 42 column 2, line 47 -column 3, line 15; examples 1-3</p>	1-16, 18-26, 30-33, 36,37
Y	<p>EP 0 955 372 A (SUNTORY LTD) 10 November 1999 (1999-11-10)</p> <p>page 2, line 5 - line 10 page 3, line 2 - line 17; claims 1-13; examples 1-10; table 1</p>	1-16, 18-26, 30-33, 36,37
Y	<p>WO 96 17927 A (KAROBIO AB ;NILSSON STEFAN (SE)) 13 June 1996 (1996-06-13)</p> <p>abstract page 10, line 21 -page 11, line 11 page 13, line 14 - line 16; claims 1-3,15; figures 2B,3B</p>	1-16, 18-26, 30-33, 36,37
	-/--	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>KWON BYUNGSUK ET AL: "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand"</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY, THE AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, INC.,, US, vol. 274, no. 10, 5 March 1999 (1999-03-05), pages 6056-6061, XP002147323 ISSN: 0021-9258 abstract page 6056, column 2, paragraph 2 page 6057, column 1, paragraph 1 -column 2, paragraph 2 page 6060, column 1, paragraph 2; figure 2 page 6060, column 2, paragraph 4</p>	1-16, 18-26, 30-33, 36,37
Y	<p>WANG CUN-YU ET AL: "NK-kappaB antiapoptosis: Induction of TRAF1 and TRAF2 and c-IAP1 and c-IAP2 to suppress caspase-8 activation."</p> <p>SCIENCE (WASHINGTON D C), vol. 281, no. 5383, pages 1680-1683, XP002233368 ISSN: 0036-8075 abstract</p>	1-16, 18-26, 30-33, 36,37
A	<p>WO 94 23045 A (BAEUEERLE PATRICK ;BOEHRINGER INGELHEIM INT (DE); HENKEL THOMAS (US) 13 October 1994 (1994-10-13)</p> <p>abstract column 2, line 4 - line 37 column 6, line 49 -column 9, line 36</p>	1-16, 18-26, 30-33, 36,37
A	<p>WO 01 72296 A (ANDERSSON TOVE ;ASTACAROTENE AB (SE); PETTERSSON SVEN (SE)) 4 October 2001 (2001-10-04)</p> <p>the whole document</p>	1-16, 18-26, 30-33, 36,37

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP 02/12644

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 34 and 35
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.: 17, 27-29
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-16, 18-26, 30-33, 36, 37 (all partial)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-16, 18-26, 30-33, 36,
37 (all partially)

A purified protein comprising the amino acid sequence as depicted in SEQ ID NO:2 and the subject matter relating to said protein, respectively an isolated polynucleotide comprising the polynucleotide sequence as depicted in SEQ ID NO:1 and the subject matter relating to said sequence.

Invention 2-144: Claims 1-16, 18-26, 30-33, 36,
37 (all partially)

As for subject 1, but respectively relating to SEQ ID NOs: 3 - 288 (i.e. subject 2, corresponding to amino acid sequence SEQ ID NO:4 and polynucleotide sequence SEQ ID NO:3; subject 3, corresponding to SEQ IDs NO:6 and 5;.....; subject 144, corresponding to SEQ IDs NO:288 and 287).

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claim 14 is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Although claims 14, 23, 26, 29 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Claims Nos.: 34 and 35

With regard to claim 34:

Claim 34 relates to subject matter for which no search is required according to Rule 39.1(v)PCT.

Given that the claim is formulated in terms of such subject matter or merely specifies features relating to presentation of information.

With regard to claim 35:

Claim 35 relates to subject matter for which no search is required according to Rule 39.1(vi) PCT.

Continuation of Box I.2

Claims Nos.: 17, 27-29

Present claims 17, 27-29 relate to an extremely large number of possible compounds. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is not to be found. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search is impossible. Consequently, no search has been carried out for those claims.

Present claim 26 relates to an extremely large number of possible compounds. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the compounds claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely those parts relating to monoclonal or polyclonal antibodies according to claim 21 or 22, antisense oligonucleotides according to claim 24 and/or ribozymes or desoxyribozymes according to claim 25.

The applicant's attention is drawn to the fact that claims, or parts of

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

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